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BSA-Seq Technologies Identify a Major QTL for Clubroot Resistance in Chinese Cabbage (*Brassica rapa* ssp. *pekinesis*)

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BSA-seq technologies, combined Bulked Segregant Analysis (BSA) and Next-Generation Sequencing (NGS), are making it faster and more efficient to establish the association of agronomic traits with molecular markers or candidate genes, which is the requirement for marker-assisted selection in molecular breeding. Clubroot disease, caused by *Plasmodiophora brassicae*, is a serious threat to Brassica crops. Even we have breed new clubroot resistant varieties of Chinese cabbage (*B. rapa* ssp. *pekinesis*), the underlying genetic mechanism is unclear. In this study, an F_2 population of 340 plants were inoculated with *P. brassicae* from Xinye (Pathotype 2 on the differentials of Williams). Resistance phenotype segregation ratio for the populations fit a 3:1 (R:S) segregation model, consistent with a single dominant gene model. Super-BSA ,using re-sequencing the parents, extremely R and S DNA pools with each 50 plants, revealed 3 potential candidate regions on the chromosome A03, with the most significant region falling between 24.30 Mb and 24.75 Mb. A linkage map with 31 markers in this region was constructed with several closely linked markers identified. A Major QTL for clubroot resistance, *CRq*, which was identified with the peak LOD score at 169.3, explaining 89.9% of the phenotypic variation. And we developed a new co-segregated InDel marker BrQ-2. Joint BSA-seq and traditional QTL analysis delimited *CRq* to an 250 kb genomic region, where four TIR-NBS-LRR genes (Bra019409, Bra019410, Bra019412 and Bra019413) clustered. The CR gene *CRq* and closely linked markers will be highly useful for breeding new resistant Chinese cabbage cultivars.