

Genomics-assisted mapping in *Cicer-Ascochyta* pathosystem to unravel the quantitative resistance genes

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Abstract: In many plant-pathogen interactions the host resistance is governed by a combinatorial action of multiple genes termed as quantitative disease resistance (QDR). Three decades of genetic research on economically important interaction of chickpea (*Cicer arietinum* L.) and *Ascochyta rabiei* has revealed quantitative nature of host resistance. Despite various genomic studies in chickpea-*Ascochyta* system, identification of narrowed QTL/gene remain elusive. We utilized next-generation genomic tool namely multiple quantitative trait loci sequencing (mQTL-seq), to trounce the hurdles in revealing QDR genes against *Ascochyta* blight (AB). The mQTL-seq analysis revealed two major QTLs (*qABR4.1* and *qABR4.2*) and a novel minor QTL (*qABR4.3*) on assembled Ca4 chickpea chromosome that provides resistance against AB. Under the major *qABR4.1*, a transcriptional regulator *CaAHL18* was identified as a candidate gene and CaNIP8 marker was developed from its polymorphic cis-regulatory region for molecular breeding. We are further fine-mapping the major *qABR4.2* (27.55-33.49 Mb) and novel minor *qABR4.3* (38.78-39.48 Mb) to elucidate the candidate genes and their molecular mechanism of resistance. Up till now, the second major QTL, *qABR4.2* is narrowed to ~1.41 Mb from 5.41 Mb region via utilizing bi-parental CRIL-7 population genotyping and association analysis in various chickpea accessions. Further, to translate the obtained genetic information from our AB resistance study, we intend to introgress multiple fungal resistance loci (for AB and FW resistant desi accessions) in few selected higher yielding cultivated chickpea varieties. Our combinatorial approaches have helped in overcoming the chickpea-AB genetic mapping associated problems of AB resistance loci fine-mapping and their utilization in molecular breeding. Consequently, our work will provide landmark information on chickpea AB resistance for the convenience of biotechnologists and breeders.

Keywords: *Ascochyta rabiei*; CaAHL18; QTL