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Title

Development of genome-wide KASPar markers from a comparative transcriptomic analysis for mapping QTLs associated with the pungent trait of pepper (Capsicum annuum L.)

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Abstract

BACKGROUND Pepper (Capsicum spp.), belonging to the Solanaceae family, is an important vegetable crop worldwide owing to its nutritional value and flavor. There are five domesticated pepper species (C. annuum L., C. frutescens L., C. chinense Jacq., C. baccatum L., and C. pubescens Ruiz et Pav.) and more than 20 wild relative species. Global pepper production is approximately 34.5 million tons annually. Under the threat of a changing environment, new varieties with enhanced resistance to biotic and abiotic stresses are demanded by farmers. Marker-assisted selection (MAS) has been used to introduce new and desirable characters into plants, such as disease resistance. The lack of sufficient molecular markers for pepper has been a bottleneck for genetic and linkage studies [1]. MATERIALS & METHODS Transcriptomes from five C. annuum L. accessions (Yolo Wonder, CM334, Perennial, PM687 and PM217) were sequenced. Unigenes of CM334, Perennial, PM687, and PM217 were mapped to the reference transcriptome of Yolo wonder [1]. Positions of SNPs and their flanking sequences were extracted to design KASPar markers. A genetic map based on KASPars was constructed by using Joinmap 4 thanks to 113 F9-recombinant-inbred-lines (RIL) issued from the intraspecific cross 'Perennial x 83-58'. Capsaicin and dihydrocapsaicin were quantified in the RIL progeny by ultra-high performance liquid chromatography (UPLC, Waters, USA) and a QTL analysis was performed by using the software MapQTL3.0. RESULTS Comparison of the Perennial transcriptome with the Yolo Wonder transcriptome revealed 9,037 SNPs corresponding to 4,333 unigenes. Comparison of the transcriptomes of CM334, PM687, and PM217 with the Perennial transcriptome revealed 2,077 SNPs corresponding to 1,674 unigenes. We developed KBioscience Competitive Allele-Specific PCR (KASPar) markers for a set of SNPs. Out of the 975 KASPars developed, 303 (31%) were polymorphic between Perennial and 83-58. We constructed a genetic linkage map with 372 markers (including 278 KASPars) and detected quantitative

trait loci (QTL) for the pungent trait (capsaicin and dihydrocapsaicin content) using the F9 RIL progeny. Four QTLs determining the capsaicin and dihydrocapsaicin content were identified. For traits related to the capsaicin content, one major QTL was located between marker BD76366 and Pun1 on chromosome P2; it explained 29% to 41.5% of the phenotyptic variation. Two minor QTLs located on chromosome P2 and P12 explained 8.0% and 11.0%. For the dihydrocapsaicin content, one major and two minor QTLs were located at the same positions as the QTLs of capsaicin content on chromosomes P2 and P12; an additional minor QTL located on chromosome P12 explained 9.9% of the phenotypic variation. DISCUSSION & CONCLUSION This research identified thousands of polymorphic positions among the genomes of pepper accessions. We developed KASPar markers covering the whole-genome and that can be used to locate QTLs or genes at any position. 31% of 975 KASPar markers were polymorphic; they were used to construct a molecular linkage map and identified QTLs associated with the pungent trait. The KASPar markers we have developed have potential value for pepper crop improvement and breeding for altered capsaicin content.

REFERENCES [1] Nicolaï et al., 2012, Genetics and Molecular Research, 11 (3): 2295-2300. DOI: 10.4238/2012.August.13.3 215 BG-P/21 | Capsicum and Eggplant EUCARPIA Meeting 2019

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