

Identification of Genomic Regions Associated with Fusarium Wilt Resistance in Cowpea

Abstract

Fusarium wilt (FW), caused by the soil-borne fungal pathogen *Fusarium oxysporum* f. sp. *Tracheiphilum*, is a serious threat to cowpea production worldwide. Understanding the genetic architecture of FW resistance is a prerequisite to combatting this disease and developing FW resistance varieties. In the current study, a genetic diversity panel of 99 cowpea accessions was collected, and they were infected by a single strain, FW-HZ. The disease index (DI) based on the two indicators of leaf damage (LFD) and vascular discoloration (VD) varied highly across the population: most accessions were susceptible, and only seven accessions showed resistant phenotypes by both indicators. Through a genome-wide association study (GWAS), 3 and 7 single nucleotide polymorphisms (SNPs) significantly associated with LFD and VD were detected, respectively, which were distributed on chromosomes 3, 4, 5, 6 and 9, accounting for 0.68–13.92% of phenotypic variation. Based on the cowpea reference genome, 30 putative genes were identified and proposed as the likely candidates, including leucine-rich repeat protein kinase family protein, protein kinase superfamily protein and zinc finger family protein. These results provide novel insights into the genetic architecture of FW resistance and a basis for molecular breeding of FW resistant cultivars in cowpea.

Keywords: cowpea • fusarium wilt • GWAS • candidate genes

Introduction

Cowpea (*Vigna placentalis* Walp.) is one in all the foremost vital legume crops worldwide. As a multiple-purpose crop, most the surface elements of the cowpea plant area unit edible and often consumed. The dry grains area unit used as a staple food in sub-Saharan continent, and therefore the dry haulms area unit harvested and oversubscribed as fodder for placental mammal [1]. In addition, the immature pods area unit typically used as a vegetable, particularly in East Asia and Southeast Asia. Being made in nutrients like super molecule, carotene, vitamins and mineral parts in tender pods, vegetable cowpea is wide cultivated in China, and the pods are often poached in stew, stir-fried, served cold in an exceedingly dish or processed into pickled vegetables. China has been the world's largest producer and client of vegetable cowpea, with AN annual planting space of over 533,333 hectares and total yield of additional than twenty million tons. GWAS could be a powerful technology for exploiting genes/quantitative attribute loci (QTLs) controlling complicated traits. This methodology doesn't have to be compelled to construct quarantined populations [2].

Thereby mostly reducing analysis time and price. Additionally, additional natural alleles for one trait may well be detected at the same time. GWAS has been wide employed in crops like rice, corn, soybean and watermelon. In cowpea, mistreatment the GWAS supported the Cowpea I Select syndicate Array (Illumina, Inc., San Diego, CA, USA) containing fifty one, 128 SNP markers, Xu et al. known seventy two SNPs related to pod length, Lo et al. known seventeen SNPs for grain size and Wu et al. known thirty SNPs loci for cowpea

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drought tolerance. the target of this study was to screen the FW resistant accessions in Chinese cowpea germplasms and known the genes/QTLs conferring FW resistance. The experiment was dispensed within the greenhouse of the Haining Experimental Base of Zhejiang Academy of Agricultural Sciences within the autumns of 2020 and 2021. All the accessions were seeded in plastic pots (20 cm in diameter) containing sterile vermiculite and matrix, and four-five uniform seedlings for every accession were unbroken once one week. When the third trifoliolate leaves began to emerge, a changed root-dip methodology was wont to inoculate. The check seedlings were gently uprooted and lord tic for one min in suspended inoculum, and so transferred back to the pots [3]. Then, the plants were coated with a plastic sheet for two days to retain wetness. From the third day, the plastic shed was removed and traditional management was applied with the greenhouse day temperature set to twenty-eight laptop and the night temperature to sixteen laptop. Cowpea is a vital legume crop in China. It absolutely was among the highest six of edible [4].

Description

Legumes and prime 10 of vegetables in terms of consumption. FW is one in all the 3 devastating diseases in cowpea production, and therefore the destruction and yield loss caused by FW exaggerated quickly in recent years. Screening the resistant germ plasms is that the beginning for FW resistance breeding. In China, nearly 5000 cowpea

accessions had been collected until now; but, solely a little variety had been exactly known for FW resistance. In a previous study, resistance of ninety nine cowpea accessions and obtained ten resistant accessions. Within the current study, another ninety nine cowpea accessions were evaluated for FW resistance, and seven resistant accessions were obtained. Taken along, these seventeen accessions give a helpful resistant resource for cowpea malady resistance breeding [5].

Conflict of Interests

None

Acknowledgments

None

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