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SCREENING FOR RESISTANCE TO FUSARIUM WILT IN TUNISIAN MELON CULTIVARS USING MOLECULAR MARKERS

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Fusarium wilt of melon caused by *Fusarium oxysporum* f.sp. *melonis* (FOM) is one of the most threatening fungal diseases of melon crops. Four races (0, 1, 2, and 1-2) of the pathogen are defined. Resistance to race 1 and race 2 is conferred by a single dominant gene Fom-2 and Fom-1, respectively. Both genes also confer resistance to race 0. Host-plant resistance is one of the management strategies that can be used to control this pathogen. In this study, we screened 15 Tunisian melon cultivars to identify new sources of resistance to Fusarium wilt using phenotypic data from melon plants inoculation by FOM (races 0 and 1) and further molecular markers validation. Melon plants (at the 1st true leaf stage) were inoculated by FOM conidial suspension (10^6 conidia/ml) and symptoms were evaluated. Following inoculation phenotyping, DNA analysis was carried out to amplify resistant and susceptible alleles. For PCR assays, two markers previously reported to be linked to Fom-2 gene were used. The Spanish accession Tortuga and the Korean accession PI161375 were used as negative and positive controls, respectively, for the Fom-2 gene. Results revealed that among the Tunisian melon cultivars evaluated, four genotypes showed resistance to races 0 and 1 by inoculation method. All genotypes were further screened for presence of alleles conferring resistance to FOM. Molecular and phenotypic screening revealed that two genotypes (TUN-5 and TUN-12) have a strong resistance to FOM races 0 and 1. These genotypes should be explored as potential source of resistance genes that can be used in breeding programs to develop new resistant melon cultivars.

Key words: Melon, Disease resistance, Fusarium wilt, Molecular marker