Marker Assisted Breeding for Resistance against *Fusarium* wilt in Muskmelon

Harshawardhan Choudhary¹, Sri Dhar², T.K. Behera³ and V Shanmugam⁴

^{1,2,3,4}Division of Vegetable Science, Indian Agricultural Research Institute, Pusa, New Delhi-12 E-mail: harshahit2001@yahoo.co.in

Abstract—Muskmelon wilt caused by Fusarium oxysporum Schlecht f. sp. melonis is the most devastating disease which sometime result in complete crop loss and it continues to be a limiting factor for muskmelon cultivation in northern Indian plain as most of the varieties/hybrids under commercial cultivation lacks resistance for this disease. Farmers are prone to severe economic loss after investing about 60-70 days time and all other agricultural inputs including labour as they could not get any return due to total and sudden loss of crop. Host plant resistance has been considered as the most dependable approach for sustainable disease management in many crops. Novel source of resistance in Indian snapmelon line has been identified after continuous field screening against Fusarium wilt for 5 continuous years at IARI, New Delhi. One genotype DSM-11-6 of snapmelon (Cucumis melo var. momordica) has been made homozygous by selfing for 6 generations from a population collected from Ganganagar area of Punjab. The fungus (Fusarium oxysporum f.sp. melonis) was isolated from the diseased plant from IARI field and DSM-11-6 has showed resistance under artificial inoculation test. Highly susceptible lines Hara Madhu and Kashi Madhu were crossed with resistant line DSM-11-6 as pollen parent and inheritance of the resistance gene was found to be governed by single dominant gene in both the crosses. Sixty seven lines of melon germplasm were screened for resistance to Fusarium wilt and the same set of lines were used for genotyping with 12 SSR/STS markers from Fom-2 region of genetic map and 2 functional SCAR markers Fom2- R_{408} and Fom2- S_{342} developed from LRR domain of Fom-2 gene for resistant and susceptible alleles respectively. Two lines MR-1 and DSM-11-6 were identified with resistant allele in homozygous condition and no recombinants were observed. DSM-11-6 was distinct from MR-based on morphological as well as on the basis of SSR138. The identification of new source of resistance in Indian snapmelon line and development of gene based marker for Fom-2 gene will be useful in introgression of this gene to Indian muskmelon cultivars by marker assisted breeding.