Genetic Characterization and Utilization of Muskmelon (*Cucumis melo* L.) Germplasm

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Abstract—Muskmelon is a highly relished cucurbit because of its attractive fruit with unique aromatic musky flavour, sweet taste and being rich in vitamins and minerals which is extensively being grown worldwide during frost free period. Cucumis melo L. is a highly polymorphic taxon encompassing a large number of botanical and horticultural varieties or groups exhibiting wide range of variability in morphological, physiological and biochemical traits that govern their preferences. Phenotypic variations have been used to characterize the relationships among intra-specific and landraces of melon genotypes across the horticultural groups. Muskmelon germplasm exhibited tremendous variation in fruit traits such as size, shape, colour, taste, texture, and phytonutrients composition. Wide range of variation for average fruit weight, number of primary branches per plant, vine length, days from pollination to fruit harvest, node number of first pistillate flower, yield per plant and TSS were found in the germplasm which indicated that sufficient variability existed for yield and quality contributing characters and considerable improvement could be achieved in most of these characters by selection. Sixty seven muskmelon genotypes were classified into 22 distinct clusters and largest cluster II comprised of 22 exotic genotypes mostly from inodorous group followed by cluster III possessing 7 genotypes and two clusters had single genotypes. Based on quality traits, these genotypes were categorized into 13 groups and broadly these groups were in line with clustering based on yield traits. However, genotypes from momordica group were grouped separately in a distinct cluster from other groups. Promising genotypes of muskmelon with high fruit yield and better fruit quality; DMM-148, DMM151, DMM-159, DMM -56, DMM -145 and DMM -163 could be developed by selection for their unique traits. Novel source of Fusarim wilt resistance have been identified from Indian snapmelon genotype DSM-11 which is being utilized for introgression of resistance to cultivated muskmelon varieties.