

International Conference on

Agricultural & Horticultural Sciences

September 14-15, 2012 Hyderabad International Convention Centre, India

Mapping SSR markers linked to powdery mildew resistance gene in sesamum (Sesamum indicum L)

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 ${f P}$ owdery mildew (Oidium sesame) is a serious disease of sesamum (sesamum Indicum) and is one of the major constraints in sesamum production. F1 was developed by crossing the resistant parent (BB3-8 accession of Sesamum mulayanum) and the susceptible parent (Swetha til) during Late summer, 2009. F2 sesamum population(104 plants) produced from selfing of F1 in Kharif 2010 . On screening of 104 plants of ${\bf F_2}$ population, the plants segregated into 61 susceptible and 43 resistant plants. Chisquare analysis showed the observed ratio to confirm the expected ratio of 9:7 ratio (susceptible : resistant) and the resistance to disease was governed by two pairs of recessive genes contributed by S.mulayanum. The two parents were screened for parental polymorphism using 300 sesame microsatellite markers, of which 240 showed clear amplification pattern and 24 markers exhibited polymorphism (10%) and the same were used for genotyping. DNA from 104 ${\bf F_2}$ progenies were collected for genotyping with 24 Polymorphic SSR primers. Molecular linkage map was constructed with SSR markers SM10 178 and SM10 176 using the MAPMAKER/EXP version 3.0 Both the markers were mapped to one and the same linkage group at a distance of 14.2 cM. These two markers were found to be linked to the powdery mildew resistance gene.

Biography

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