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Molecular profiling of mapping population derived from Anthurium ornatum X Anthurium andreanum

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nthurium belongs to the family Araceae. In anthurium, flower colour and shape of the spathe are given more importance. The most devastating disease among the anthurium variety is the bacterial blight caused by Xanthomonas axonopodis. There has been no genetic resistance found against bacterial blight among anthurium. A programme on breeding novel characters in Anthurium omatum has lead to a natural mutant 'IIHRA1' at IIHR, Bangalore. A mapping population comprising of 43 progenies was developed from interspecific cross between Anthurium ornatum, var IIHR selection A1, and Anthurium andreanum var Eternity which is susceptible to bacterial blight. A total of 410 RAPD primers were screened among the parents of which 20 highly reproducible markers yielding 84 polymorphic bands were further used for screening the mapping population. The percent of polymorphism observed between the parent lines is less (5%) as both the parental lines belong to different species. The generated RAPD profiles play a key role in constructing a reference linkage map of anthurium and also help mapping the trait responsible for bacterial blight resistance. Thus identified marker improvises the breeding program of anthurium through Marker assisted selection (MAS).

Biography

Sudarshini. K is pursuing her doctoral degree from Jawaharlal Nehru technological university, Hyderabad. Currently working on various aspects of molecular markers, their applications and identification in Anthurium, muskmelon etc at Molecular Biology Lab in Division of Biotechnology, IIHR at Bangalore.

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