Genetic diversity and population structure analysis of *Colletotrichum capsici* isolates using SRAP and URP markers

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Abstract

Colletotrichum capsici *causing anthracnose is a major quality and yield-limiting factor of chilli in India and elsewhere. The present study was undertaken to determine genetic variability and population structure among 12 indigenous and one exotic isolate of* C. capsici *using SRAP and URP markers. Out of 15, each of SRAP and URP markers screened, 13 SRAP and 10 URP markers gave reproducible banding pattern. At a similarity coefficient of 0.77, thirteen isolates of* C. capsici *were classified into three major clusters based on unweighted paired-grouping method with arithmetic averages of NTSYSpc and the Bayesian analysis of population structure. The exotic isolates from USA grouped in cluster III along with two indigenous isolates from Bagalkot and Parbhani. The various genetic diversity parameters like percent polymorphism, number of different alleles, number of effective alleles, expected heterozygosity, polymorphism information content, Shannon's information index, resolution power, effective multiplex ratio and marker index were studied, which revealed that there is genetic variability with three different populations among isolates in Karnataka region only. Therefore, the information generated in the present study could be used for devising breeding strategy for developing disease resistant varieties at regional level.*

Keywords: Chilli, *Colletotrichum capsici*, genetic variability, population structure, SRAP, URP.

Introduction

Chilli (*Capsicum annum* L.) is an economically important spice cum vegetable crop not only for India but also for the world (Saxena *et al.,* 2014). It is a rich source of phytochemical compounds, like ascorbic acid, capsaicinoids, carotenoids, flavonoids, and tocopherols, which helps in preventing many chronic diseases (Wahyuni *et al.,* 2013). Several fungal, bacterial and viral diseases worldwide affect the quality and yield of chilli crop and among these, anthracnose is one of the most destructive disease, which results up to 50% yield losses (Pakdeevaraporn *et al.,* 2005). In India, anthracnose of chilli is mainly caused by C. *capsici* and transmitted through seeds carrying up to 5.0% infection index (Akhtar *et al.,* 2017). However, this disease is reported to be caused by a number of *Colletotrichum* species, *C. acutatum, C. brevisporum,* C. *capsici, C. fructicola, C. gloeosporioides, C. nigrum, C. siamense, C. sichuanensis, C. scovillei* and *C. truncatum* in different geographical regions (Don *et al.,* 2007; Liu *et al.,* 2016). *C. capsici* is a seed and soil-borne pathogen and has wide putative host range including cotton, peppers, tomatoes, legume species (Shenoy *et al.,* 2007) and also reported from weeds and flowering plants (Pring *et al.,* 1995).

In India, there is little information available regarding the population structure and genetic variability of *C. capsici* causing anthracnose disease of chilli. Traditionally, characterization methods of *C. capsici* are based on cultural and morphological characteristics. Due to vide range of variations in morphological characters under different environmental conditions, these may not be adequate for characterization of *C. capsici*. Molecular approaches provide alternative ways for the isolate level differentiation of pathogens. Molecular markers such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), inter simple sequence repeats (ISSR) have been applied to assess genetic diversity among populations of *Colletotrichum* sp. (Saxena *et al.,* 2014; Silva *et al.,* 2018). Sequence-related amplified polymorphism (SRAP) markers have also been extensively used in the genetic diversity analysis of other fungal species (Tripathi and Dubey, 2015). Universal rice primers (URPs) have not only extensively used for the genetic diversity of different plant pathogenic fungi but also for diverse plants, animals and other microbes (Dubey *et al.,* 2012; Kandan *et al.,* 2014; Kumar *et al.,*