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Study of Genetic Diversity in Phytopathogenic Fungal Populations Detected By RAPDS, AFLPS, SSR, SRAP, AND ISSR Markers

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Abstract

During the summer season are the ones that present the highest concentrations of Alternaria spores in the atmosphere. The months of July and June are the ones that have the most pleasant weather, which is the reason behind this. There is a possibility that symptoms of Alternaria black spot might be seen on any portion of the host plant at any moment in the life cycle of the organism. Both A. brassicicola and A. brassicae are responsible for the effect of damping on cruciferous plant seedlings. By puncturing the skin, taking advantage of stomata, and causing sores, insects or host plants that are produced in a farm environment may cause discomfort. The agroecological adaptations, geological concerns, and biological components were all taken into account when these discoveries were taken into consideration. A significant amount of genetic diversity was found in Chinese vegetable mustard accessions by using RAPDs, AFLPs, SSR, SRAP, and ISSR markers. This was accomplished by the use of these markers. The traditional categorization, which was based on the different edible organs of vegetable mustards and the geographical origin of the accessions that were investigated, the conclusions of the clusters that were based on the molecular marker data did not entirely correspond to the conventional classification.. Researchers are interested in this because it may be a sign of the spread of illness. The molecular connections seen in the wild A. species of brassicicola and A. This approach has been extensively used to study brassicae. The sources of these links include AFLPs inter-simple sequence repeat and random amplified polymorphic DNA reported these results. Using AFLPs, discovered polymorphic bands with percentages between 16.7 and 27.9 percent. Eighteen separate A. isolates exhibited these bands. species of brassicicola flower. The genetic diversity among 32 pathogenic A was determined in a 2013 study by Sharma et al. using five inter-simple sequence repeat primers. brassicae bacteria isolated from mustard and cauliflower plants.