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Title:	Characterization and development of molecular marker for the detection of Fusarium oxysporum f. sp ciceries causing chickpea wilt
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Abstract: Fusarium wilt caused by Fusarium oxysporum f. sp. ciceris is a serious and wide spread disease of chickpea (Cicer arietinum) in all chickpea growing countries. Virulence analysis of 36 isolates of the pathogen collected from 12 states of india, on a new set of 10 differential cultivars of chickpea, namely, C104, JG 74, CPS 1, PUSA 212, WR 315, KWR 108, GPF 2, DCP 92-3, Chaffa and JG 62, grouped them into eight races. Except the isolates from Delhi, Haryana, Bihar, Uttar Pradesh and Madhya Pradesh, the races/virulence groups were corresponding to the area of the origin of the isolates. Genetic diversity of 14 representative isolates of pathogen determined through internal transcribed spacer (ITS) region of rDNA - Restriction Fragment Length Polymorphism(ITS-RFLP) and amplified products were digested with 7 restriction enzymes (Tru I, AluI, Rsa I, Kpn I, Eco RI, Sal I and Bam H I). Some of the isolates gave area specific ITS-RFLP patterns, whereas others from the same area showed distinct pattern and matched with the pattern of the isolates of the other areas. Clearly indicating the presence of highly variable population in chickpea growing areas of India. The ITS-RFLP pattern was partially related with the geographical origin of the isolates. The phylogenetic analysis based on ITS sequences of the isolates also grouped the grouped them into eight categories which were partially corresponding to the virulence groups or races of the pathogen. Genetic diversity of the population of F. oxysporum f.sp ciceris was also determined through random amplified polymorphic DNA (RAPD) markers. Unweighted paired group method with arithmetic average (UPGMA) cluster analysis of RAPD profiles grouped the isolates into eight categories showing high magnitude of genetic diversity. Each group had the isolates from different states of India. The molecular groups were not corresponding to the geographical origin of the isolates. The RAPD primer OPA 07 and OPA 11 produced specific fragments of 1.3 kb and 1.4 kb, repectively in all the isolates of the pathogen. Primers were designed with sequence information of these two fragments using primer 3 software. Two sets of Sequence characterized amplified region (SCAR) markers (CW-FOC 1 and CW-FOC 2) developed from the sequences of these fragments were found to be specific to F. oxysporum f. sp ciceris and produced an amplicon of 1.3 kb and 1.4 kb respectively. These set of markers were validated against the isolates of the pathogen collected from different locations of India, representing various races of the pathogen. First time SCAR markers have been developed to detect for Indian population of Fusarium oxysporum f. sp. ciceris through the present study.

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