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Abstract:	The study entitled "Molecular characterization of viruses in taro [Colocasia esculenta (L.) Schott]" was carried out at the Division of Crop Protection, Central Tuber Crops Research Institute , Sreekariyam, Thiruvananthapurarn during 2013- 2014. The objective of the study was to diagnose, clone and characterize viruses implicated in mixed infections of taro hence identifying an effective diagnostic strategy to detect virus infections in taro. Taro leaf samples with various virus infection symptoms were collected from Jharkhand, Bhuvaneshwar and the germplasm repository of CTCRI. The samples were mainly screened for Dasheen Mosaic Virus, Taro Bacilliform Virus, Taro vein chlorosis virus and Colocasia Bobone disease virus using both genus and species specific primers. This study found out Dasheen Mosaic and taro bacilliform virus to be the most common virus infecting taro in India, the former being ubiquitous in taro everywhere. Fortunately TaVCV and CBDV infection was not detected during virus screening and this should be because TaVCVand CBDV presence is mostly confined to PNG and other pacific islands. PCR based diagnostics carried out using MJl/MJ2, potyvirus group specific primers and DsMV 3F IDsMV 3R, DsMV specifc primers amplifying the partial CP region and 3'UTR giving an amplicon of 327 bp and 540 bp respectively was found to be an robust of detecting DsMV infecting taro in India. Whereas BadnaF/BadnaR badnavirus group specifc primer and TaBV l/TaBV4 TaBV specific primer amplifying the RT/RNaseH-coding region giving an amplicon of 530 bp and 320 bp respectively proved to be an efficient and consistent method in detecting TaBV infections. PNG BadnaF IPNG BadnaR for detecting TaBV like virus sequences also gave several positives. One sample each for DsMV and TaB V, were cloned and sequenced. The BLASI' results were analysed and sequence similiarity was studied. The obtained 334 nt DsMV sequence showed maximum similiarity of 93% to dasheen mosaic virus isolate DsMV-Amp3 polyprotein gene, DsMV isolate T10 (Accession KJ786965) and DsMV partial CP gene for coat protein of NiNG1 and NiNG4 isolate. Whereas the 410 nt TaBV sequence showed maximum sequence similiarity of 92% to TaBV isolates (NCl, SI2 and S17) polyprotein gene. The phylogenic tree was constructed with similar sequences. The trees constructed at 100 bootstrap replicates showed similiarity with the CP region of different DsMV isolates and the RT region of TaBV of different isolates respectively. Since the diagnosis of virus infections based on symptoms is unreliable due to complicated mixed infections in taro with multiple viruses and isolates, it is necessary sensitive diagnostic tests are developed region wise to confront this issue. As a prerequisite to this virus detection and identification has to be carried out in taro to determine the viruses of taro geographically.
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