

ABSTRACT

In this study, PCR-based DNA fingerprinting techniques were used to study the molecular relatedness among accessions of dasheens (*Colocasia* sp.) and cocoyam (*Xanthosoma* sp.) collected randomly from 14 farms in 8 parishes of Jamaica. Analyses were carried out to assess the genetic diversity within species and to develop markers linked to important traits useful for the assessment and control of the Common Leaf Blight Disease, which affects the production of these important crops.

Random Amplified Polymorphic DNA (RAPD) analyses using UPGMA clustering, $-(CA)_8RY$ - microsatellite repeat unit, and chloroplast (*trnL* 03 - *trnL* 04) and mitochondrial (*rps14* - *COB*) specific primers revealed the 18 accessions as belonging to three species among the accessions of dasheen. Of the 18 accessions analyzed, 11 were identified as *C. esculenta*. Some of the *C. esculenta* accessions were identified as *C. esculenta* var. *esculenta* and *C. esculenta* var. *antiquorum*. This study also revealed four species among the accessions of cocoyam and cocoyam, two of which were identified to be *X. violaceum* and *X. caracu*. RAPD analyses using 10-mer primers and the $-(CA)_8RY$ - repeat microsatellite primer and chloroplast specific primers (*trnL* 03 - *trnL* 04 and *trnR* 01 - *trnQ* 01) revealed polymorphism within plastid and mitochondrial genomes of cocoyam and dasheen that can be used to differentiate between their genetic relatedness.

The *trnL* 03 – *trnL* 04 amplification profile of cocoyam accessions XSA1 & XSA2 and dasheen accession DM2 provided evidence that they possess 2 *trnL* sequences in comparison to most plants that possess only a single *trnL* sequence.

This study also revealed that *E. chrysanthemi* pv. *dieffenbachiae*, *X. campestris* pv. *dieffenbachiae*, *P. syringae* and a Non-fluorescent *Psuedomonas* are associated with the Common Leaf Blight Disease in dasheen and cocoyam. The *P. syringae* isolated in this study did not correspond to any known strain and was therefore named *P. syringae* pv. jamaica-DP. The causative agent of the Common Leaf Blight Disease in Jamaica was found to be *X. campestris* pv. *dieffenbachiae*, which was observed to be of three strains named in this study as strains DPJ1, DPJ2 and DPJ3.

These strains were found to be host specific producing symptoms of Common Leaf Blight Disease infection on dasheens and cocoyam and a hypersensitive response on the non-host pepper (*Capsicum chinense*). However, tobacco (*Nicotiana tabacum* L) and lettuce (*Lactuca sativa*) were tolerant to the phytopathogenic infections of *X. campestris* pv. *dieffenbachiae* strains DPJ1, DPJ2 and DPJ3. The insertion of the avirulence (*avrBs3*) gene into *X. campestris* pv. *dieffenbachiae* increased the hypersensitive response of pepper to the pathogen and increased the phytopathogenicity on dasheen and cocoyam.

DNA fingerprinting analyses of the bacterial DNA of *X. campestris* pv. *dieffenbachiae*, revealed that it contained sequences from the *hrpB6*, *hrpG* and ORF1 - ORF2 of a pathogenicity gene of *X. campestris* pv. *glycines*. The *hrp* cluster, conserved among the different pathovars of *X. campestris* is responsible for the phytopathogenic infection. The *hrp* cluster or pathogenicity gene of *X. campestris* pv. *dieffenbachiae* was identified, analyzed and sequenced. Any part of the sequence can be used as a probe or primer to provide a molecular diagnostic tool that can be used for assessing *X. campestris* pv. *dieffenbachiae* infections in plants.