



## First report of lethal yellowing disease associated with subgroup 16SrIV, a phytoplasma on St. Kitts in the Lesser Antilles

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Received: 18 Jun 2012. Published: 01 Dec 2012.

Coconuts (*Cocos nucifera*) are grown as a crop and as amenity trees in many tropical countries. Caribbean countries use coconuts to enhance the aesthetics of sandy coastal beaches. Lethal yellowing (LY) as a phytoplasma disease, is the single most important plant disease affecting coconut production in some countries. This disease also affects 35 other palm species in Florida, and in various countries. LY was first observed in the Cayman Islands and Jamaica 100 years ago and became a devastating malady in the 1970s in Jamaica. Widespread mortality of coconut palm on St. Kitts, in the Leeward Islands (Lesser Antilles), became a cause for alarm during 2011. This disease had already been observed in nearby Nevis island, the other part of St. Kitts and Nevis, in 2006 (Myrie *et al.*, 2006). Tall-type coconuts (Atlantic tall ecotype), in areas of high planting density near Conarre Bay and Dieppe Bay, have been most severely affected, although Christmas palm (*Adonidia merrillii*) and date palm (*Phoenix dactylifera*) have also died. Yellow to brown discoloration of leaves leading to defoliation and death are the most prominent symptoms observed on coconut palms. Bud rot caused by *Phytophthora palmivora* or LY were suspected as the most likely cause.

To determine the possible involvement of LY disease, DNA samples extracted from 50 g interior stem tissue and trunk tissue (Harrison *et al.*, 2008) of 10 palms in late stages of decline were each evaluated for phytoplasma infection by a nested PCR assay employing rRNA operon primer pair P1 (Deng & Hiruki, 1991) /P7 (Smart *et al.*, 1996) followed by LY group (16SrIV)-specific primer pair LY16Sf2/LY16-23Sr2 (Harrison *et al.*, 2008). An rDNA product (1.64 kb) was readily amplified from five out of 10 affected palms but not from DNA of a symptomless coconut used as a negative control. *AluI* or *HinfI* endonuclease digests of nested PCR products revealed no differences in fragment profiles (Wei *et al.*, 2007) amongst the five diseased palms, and profiles matched those generated from a known LY phytoplasma DNA included as a positive control. A phylogenetic distance tree was constructed by the neighbour-joining method and visualised by MEGA 5.0 software (Fig. 1). The branching pattern in the tree verified that the samples analysed were part of the existing lineage subgroup 16SrIV-A. Comparison of rDNA sequences (1.64 kb) derived from nested PCR products of LYWM1 (Lethal Yellowing Wayne Myrie 1) and LYWM2 (Lethal Yellowing Wayne Myrie 2), GenBank Accession Nos. JX070936 and JX070937 respectively, revealed that they were 100% identical to sequences of

phytoplasma strains LYFL (Lethal Yellowing Florida, HQ613874) associated with coconut LY in Florida. In addition, the phytoplasmas infecting coconut on St. Kitts were identified and classified as members of subgroup 16SrIV-A upon analysis of 16S rDNA sequences using the *i*PhyClassifier program (Zhao *et al.*, 2009). LY continues to be a major threat to coconut and other palms. The disease is spreading and is of quarantine importance for many countries. This report will help in informing the stakeholders that are implementing phytosanitary measures in their respective countries.

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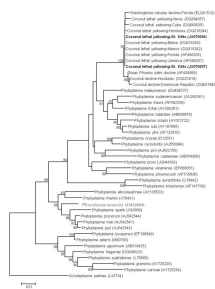


Figure 1

**To cite this report:** Myrie WA, Douglas L, Harrison NA, McLaughlin W, James M, 2012. First report of lethal yellowing disease associated with subgroup 16SrIV, a phytoplasma on St. Kitts in the Lesser Antilles. *New Disease Reports* **26**, 25. [http://dx.doi.org/10.5197/j.2044-0588.2012.026.025]

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