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Disease Notes



First Report of a 16SrV-C Phytoplasma Causing Little Leaf and Bunchy Top of *Tossa* Jute (*Corchorus olitorius*) in India

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Abstract

Jute is the most important phloem fiber crop of the world, and is mainly grown in the South East Asian countries of India, Bangladesh, Nepal, China, Indonesia, Thailand, and Myanmar, and few South American countries. The fiber is used in making sacks, ropes, bags, carpets, shoes, geo-textiles, and home decorations. There are two kinds of jute: *tossa* jute (*Corchorus olitorius* L.) and white jute (*C. capsularis*). In June 2012, symptoms suggestive of phytoplasma infection (little leaf and bunchy top) were noticed on *tossa* jute in different experimental fields of the CRIJAF research farm, Barrackpore, India, and the incidence of the disease varied from 5 to 20%. The infected plants showed profuse lateral branching with a bushy appearance. In many plants, branching at the apical portion developed a bunchy top symptom with tufts of smaller leaves. Leafy stem was also common in many plants with main stems covered with numerous little leaves. Total DNA was extracted from leaf midveins of 15 symptomatic and 5 asymptomatic plants by using an improved salt concentration and simple sodium acetate CTAB method (1). PCR

was carried out with universal P1/P7 primer set followed by nested primer pair R16F2n/R16R2 (3), resulting in DNA amplicons that were 1.8 kb and 1.2 kb, respectively, in all symptomatic samples tested. Phytoplasma was not detected in symptomless samples. The five purified nested products were cloned in a pGEM-T Easy vector (Promega) and sequenced. One of the sequences that proved to be identical was deposited in GenBank (Accession No. KF501045). The consensus sequence was analyzed by NCBI BLAST and found to share 99% similarity with the 16Sr DNA sequence of the alder yellows phytoplasma reference strain (GenBank Accession No. AY028789), which belongs to the 16SrV group. The phylogenetic tree based on the 16SrDNA sequence of phytoplasmas belonging to group 16SrV and other distinct phytoplasma groups also showed that the phytoplasma clustered with members of subgroup 16SrV (4). Subsequently, in silico RFLP analysis of the nested PCR product with the pDRAW32 program using *AluI* and *TruI* restriction site used for 16SrV subgroups A, B, C, D, and E indicated that the 16SrV *Corchorus* strain belonged to subgroup C. RFLP patterns from all symptomatic *C. olitorius* samples were identical to the 16SrV-C pattern (2). The vector species transmitting the concerned phytoplasma in *C. olitorius* still needs to be identified. The leaf hopper, *Amrasca biguttula biguttula*, may be a potential vector as it is often noticed in jute fields. To the best of our knowledge, this is the first report of 16SrV-C phytoplasma associated with *tossa* jute (*C. olitorius*) in India. Initiative has to be taken to manage this disease; otherwise, branching of the main stems would badly affect the fiber quality as well as yield.

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