Aster yellows group (16SrI), subgroups 16SrI-A and 16SrI-B, phytoplasmas associated with lettuce yellows in Texas

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Lettuce (Lactuca sativa) is an important vegetable crop grown in the United States. Lettuce yellows is a devastating disease commonly found in lettuce fields and causes significant economic loss to growers, damaging 40-100% of the crop in some seasons (Thompson, 1944). The causal pathogen was not verified until a phytoplasma aetiology was confirmed by molecular means (Lee et al., 1998). In 2013, an epidemic of lettuce yellows occurred in the Winter Garden region of Texas. The infected plants were stunted with blanching and chlorosis in young heart leaves (Fig. 1). A total of thirteen samples from two different farms, including three apparently lacking symptoms from Romaine and leaf lettuce cultivars, were collected and tested for phytoplasmas. DNA was extracted from leaf veinal tissue, and nested PCRs using universal primer pair P1/16S-SR, followed by R16F2n/R16R2n and P1A/16S-SR were performed as described previously (Lee et al., 2004) to detect the presence of phytoplasmas in the samples. The taxonomic affiliation of the putative phytoplasmas detected was determined by RFLP analysis using nested PCR products (Lee et al., 1998; Zhao et al., 2009). A nested PCR using primer pair rpF1/rpR1 followed by rpF1/rp(1)R1A as described previously (Lee et al., 2004) was used to amplify a phytoplasma DNA segment (about 1.2 kb) of the ribosomal protein (rp) operon that encompasses genes rpIV (rp422) and rpC (rp3); and a nested PCR using primer pair AYsecYF1/AYsecYR1(I) followed by AYsecYF1/AYsecYR1 (Lee et al., 2006) was used to amplify a phytoplasma DNA segment (about 1.3 kb) of the partial secY operon that includes the complete secY gene. Four PCR-amplified products from each of 16S rDNA, rp, and secY genes were cloned and sequenced as previously described (Lee et al., 2004, 2006), and deposited in GenBank (Accession Nos. KF573449-KF573456; rp, KF573441-KF573448; secY, KF573433-KF573440).

The results indicated all 13 lettuce samples were infected with phytoplasmas. Both lettuce cultivars were infected with 16SrI-A and 16SrI-B phytoplasmas (Fig. 2). Phylogenetic analysis with 16S rRNA (Fig. 3), rp (Fig. 4) and secY gene (Fig. 5) sequences confirmed the presence of two distinct lineages (Fig. 3). This is the first report confirming that lettuce yellows in Texas is associated with two distinct phytoplasma strains. The finding implicates that multiple vectors may be involved in the disease outbreak. The information on identities of associated phytoplasmas should facilitate formulating effective strategies to combat this newly emerging lettuce yellows in Texas.

References


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