Phylogenetic tree of Costa Rican TYLCV sequences (black boxes) and representative TYLCV sequences (n = 40) reported throughout the world. Sequences were aligned (Muscle), manually edited, and the phylogenetic tree constructed (neighbor joining method with 5,000 bootstrap replications, evolutionary distances computed using the Kimura 2-parameter method (K2P) and expressed as the number of base substitutions per site) using MEGA 5.2 (2). Only bootstrap values higher than 50% are shown. Bar indicates substitutions per site.