

## **Molecular characterization of '*Candidatus Liberibacter*' species/strains causing huanglongbing disease of citrus in Kenya**

This study was undertaken to characterize the alpha subgroup of the proteobacteria causing the huanglongbing (HLB) disease of citrus from three different ecological zones of Kenya namely the Lower highlands (LH2, LH3, 1800-1900 m above sea level); Upper midlands (UM3, UM4, 1390-1475m), Lower midlands (LM5, LM4, LM3 of 1290-1340-1390m), by isolation and sequencing DNA encoding the L10 and L12 ribosomal proteins and the intergenic region. A 716-basepair DNA fragment was amplified and sequenced and consisted of 536 basepairs of DNA encoding the L10 protein, 44 basepairs of DNA intergenic region and 136 basepairs of DNA that partially encodes the L12 protein. Sequences of rpL10/L12 protein genes from Kenyan strains were 98% and 81% similar to the South African '*Candidatus Liberibacter africanus* strain Nelspruit' and the Asian '*Candidatus Liberibacter asiaticus*' strains, respectively. The intergenic rDNA sequence of Kenyan strain from UM and LM showed 84% similarity with '*Candidatus L. africanus* strain Nelspruit' and 50% similarity with '*Candidatus L. asiaticus*' strain. However, the LH strain had an 11-basepairs deletion, while the LM4 had a 5-basepair deletion in the intergenic region compared to '*Candidatus L. africanus* strain Nelspruit'. The L10 amino acid sequence was 100% homologous among HLB bacteria obtained from the agro-ecological zones in Kenya and the L10 protein sequence was also homologous to '*Candidatus L. africanus* strain Nelspruit'. Nevertheless, the L10 amino acid sequence of '*Candidatus L. asiaticus*' and the '*Candidatus L. africanus* subsp. *capensis*' differed from the Kenyan strains by 18.36% and 11.82%, respectively. Phylogenetic analysis of both the L10/L12 rDNA sequences and the L10 amino acid sequences clustered the Kenyan strains of the '*Candidatus Liberibacter*' species with members of alpha subdivision of proteobacteria.