Supplemental Tables and Figures

Table S1. The list of genera that comprised the core microbiomes associated with citrus leaves and roots. Core taxa identified down to genus-level are listed in alphabetical order by taxonomic group (a blank cell or a cell that contains "Other" means that it is an unclassified taxon within an assigned higher group). The relative abundance of the microbiota in all trees, in only aymptomatic trees, or in only HLB-symptomatic trees sampled in Fall 2015 are listed. Results from a Student's t-test and Power calculation to evaluate differences in asymptomatic and HLB-symptomatic trees are listed. Significant differences ($p<0.05$) with a Power > 0.9 are indicated in bold font; green bold font indicates higher abundance in asymptomatic trees and red indicates higher abundance in diseased trees.

(See Dataset_Table S1 excel file for table)

Table S2. Pairwise comparisons of leaf microbiota from Valencia trees sampled in Immokalee (n=5), Vero Beach (n=4), Ft. Pierce (n=14), and Gainesville (n=8) in Fall 2015. The R statistic for each ANOSIM test is shown above the x-line and the statistical significance based on 999 permutations is shown below the x-line. An R statistic of 0 means the communities are identical; whereas, R of 1 means the communities have no overlap.

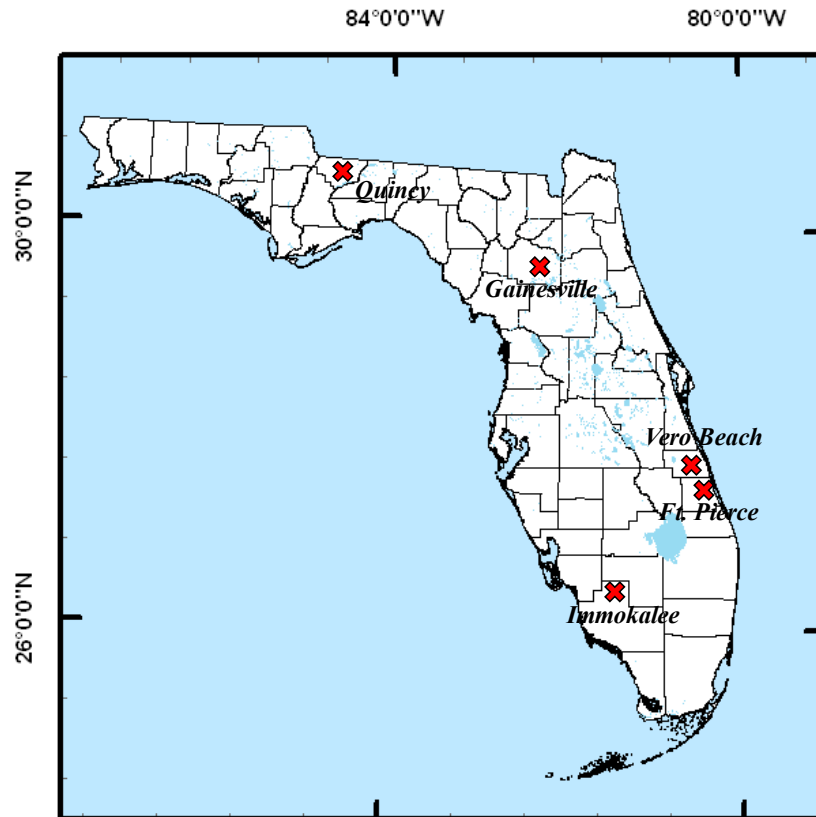| Location	Immokalee	Vero Beach	Fort Pierce	Gainesville
Immokalee	x	0.513	0.749	0.387
Vero Beach	0.034	x	0.871	0.555
Fort Pierce	0.002	0.001	x	0.732
Gainesville	0.011	0.003	0.001	x

Fig. S1. Locations where the citrus trees were sampled. The image template was obtained from the Hydrographic Internet Map Service Data Library (USGS. 2009. Florida Counties. <http://www.envirobase.usgs.gov/FlGisData/FLWSC/descriptions/counties_state_polygon.htm>. accessed on 12/8/17). The city labels were overlaid in Microsoft® PowerPoint (version 15.11.2) based on their approximate locations identified using Map data ©2016 Google.

Fig. S2. Each set of replicate trees was categorized based on HLB symtom severity. Photographs illustrate the four categories: asymptomatic (i.e., no observable HLB symptoms), symptomatic-mild (i.e., some blotchy mottle and pointed leaves observed), symptomatic-moderate (i.e., blotchy mottle and some chlorosis/yellowing of leaves observed), and symptomatic-severe (i.e., thinning of canopy, severe chlorosis/yellowing of leaves, dead branches observed). I: Owari tree at the North Florida Research and Education Center in Quincy, FL (NF-REC) (10/20/15). II: Navel tree at the Southwest Florida Research Education Center in Immokalee, FL (SF-REC) (11/3/15). III: Valencia tree at the SF-REC (11/3/15). IV: Valencia tree at the University of Florida IFAS Research Center in Gainesville, FL (4/16/15).
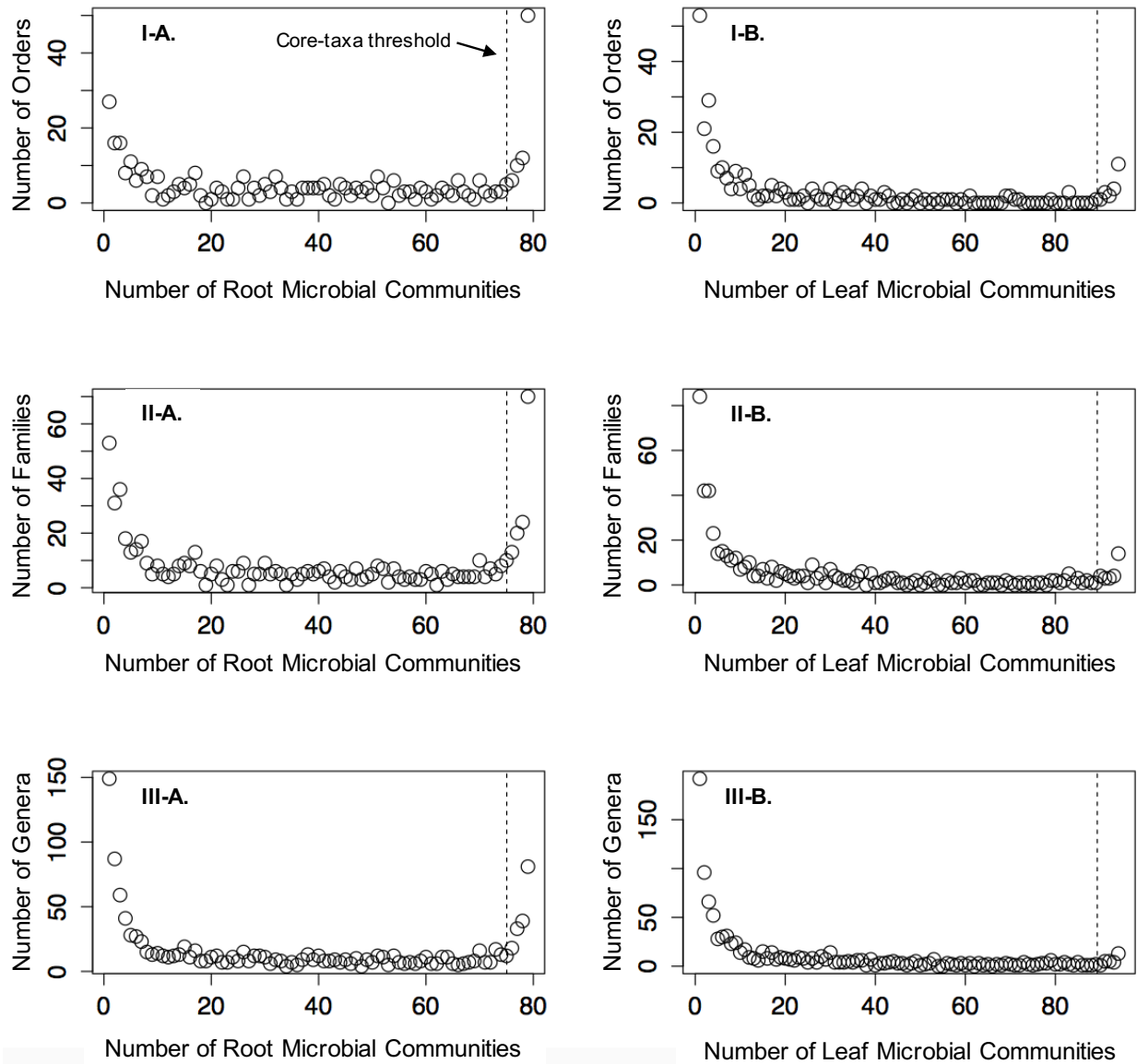
Fig. S3. Frequency of orders (I), families (II), and genera (III) assigned to 16S sequences detected in the leaf samples (A) (n=94) and root samples (B) (n=79). Points on the right of the dotted lines represent the core fraction of the microbiomes (i.e., present in >95% of respective samples [Huse et al., 2012]).

Reference:

Huse SM, **Ye Y**, **Zhou Y**, **Fodor AA.** 2012. A core human microbiome as viewed through 16S rRNA sequence clusters. PLoS One **7**:1–12.

Fig. S4. Photographs that demonstrate progression of HLB symptoms over time (e.g., branch die-back in canopy). Two Valencia trees at the University of Florida IFAS Research Center in Gainesville, FL during Spring 2015 and Winter 2016; the same trees are pictured in each row.
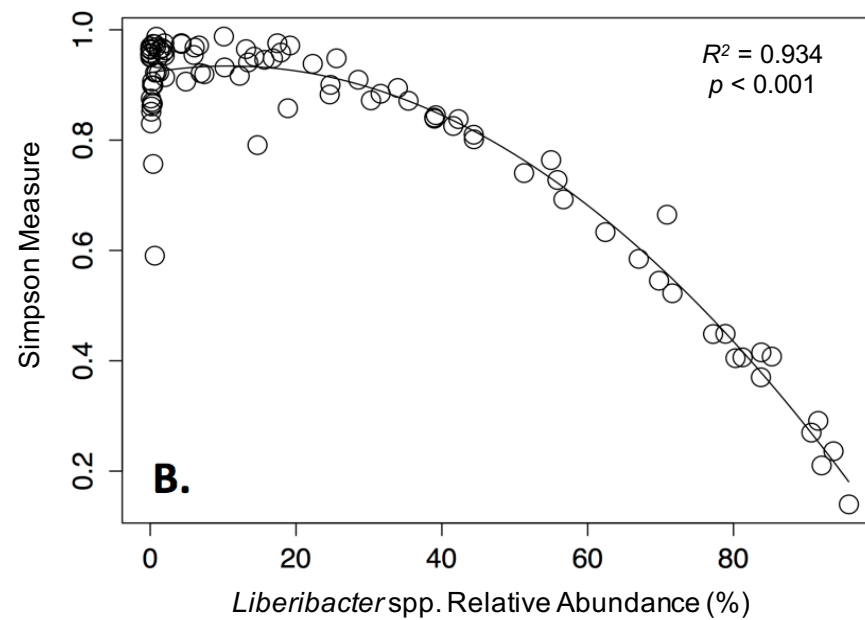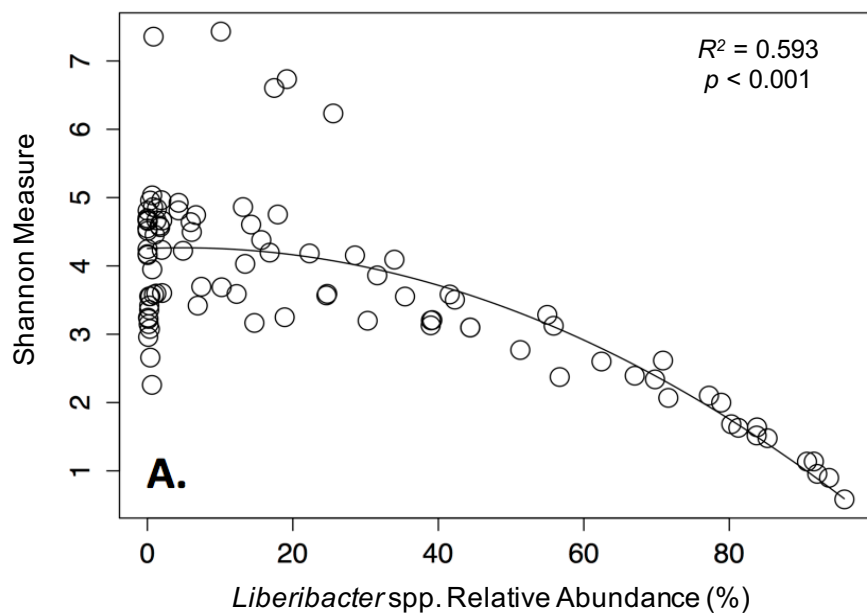
Fig. S5. Correlation between the relative abundance of *Liberibacter* spp. among all genera in leaf-associated microbial communities and community alpha diversity (A: Shannon measure; B: Simpson measure) (n=94). The R^2 and *p*-value from each regression are listed.
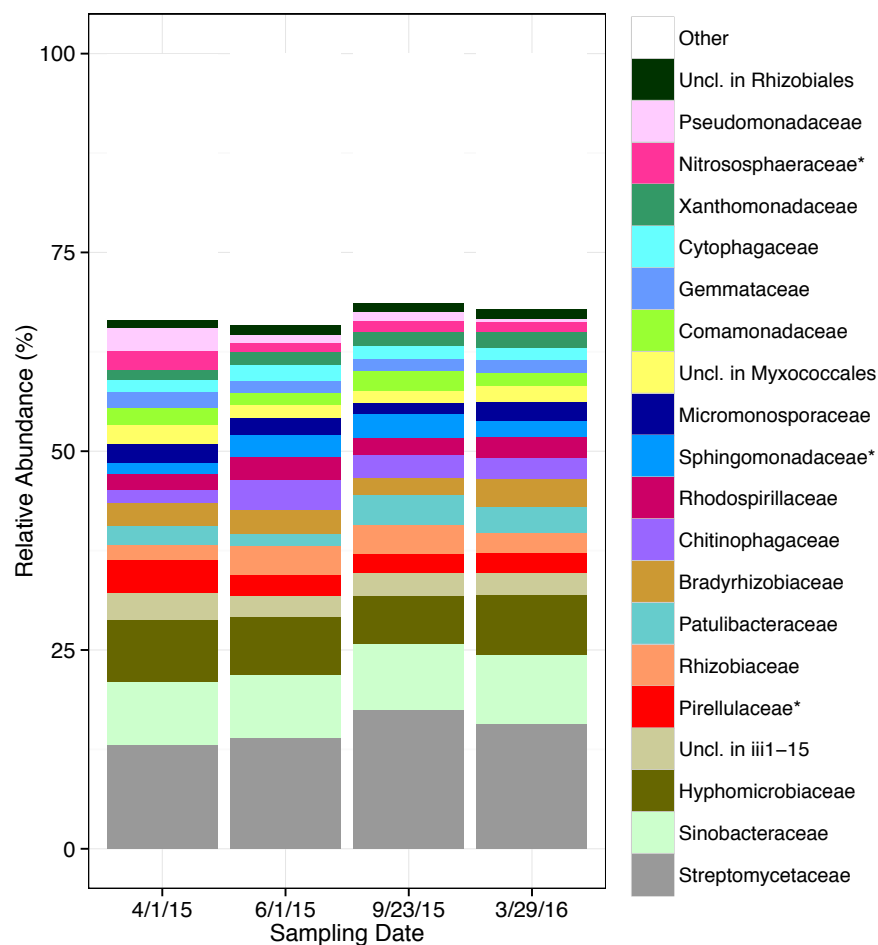
Fig. S6. Relative abundances of the 20 most abundant families assigned to 16S sequences detected in the root-associated microbial communities of Valencia trees sampled in Gainesville, FL on 4/1/15, 6/1/15, 9/23/15, and 3/29/16. All listed taxa were core root microbiota (i.e., detected in >95% of all root samples in the survey). The * indicates significant difference ($p < 0.05$) for different dates based on ANOVA.