

METAGENOMIC ANALYSIS OF RHIZOSPHERE MICROBES FROM BANANA PLANTATION SUKABUMI-WEST JAVA

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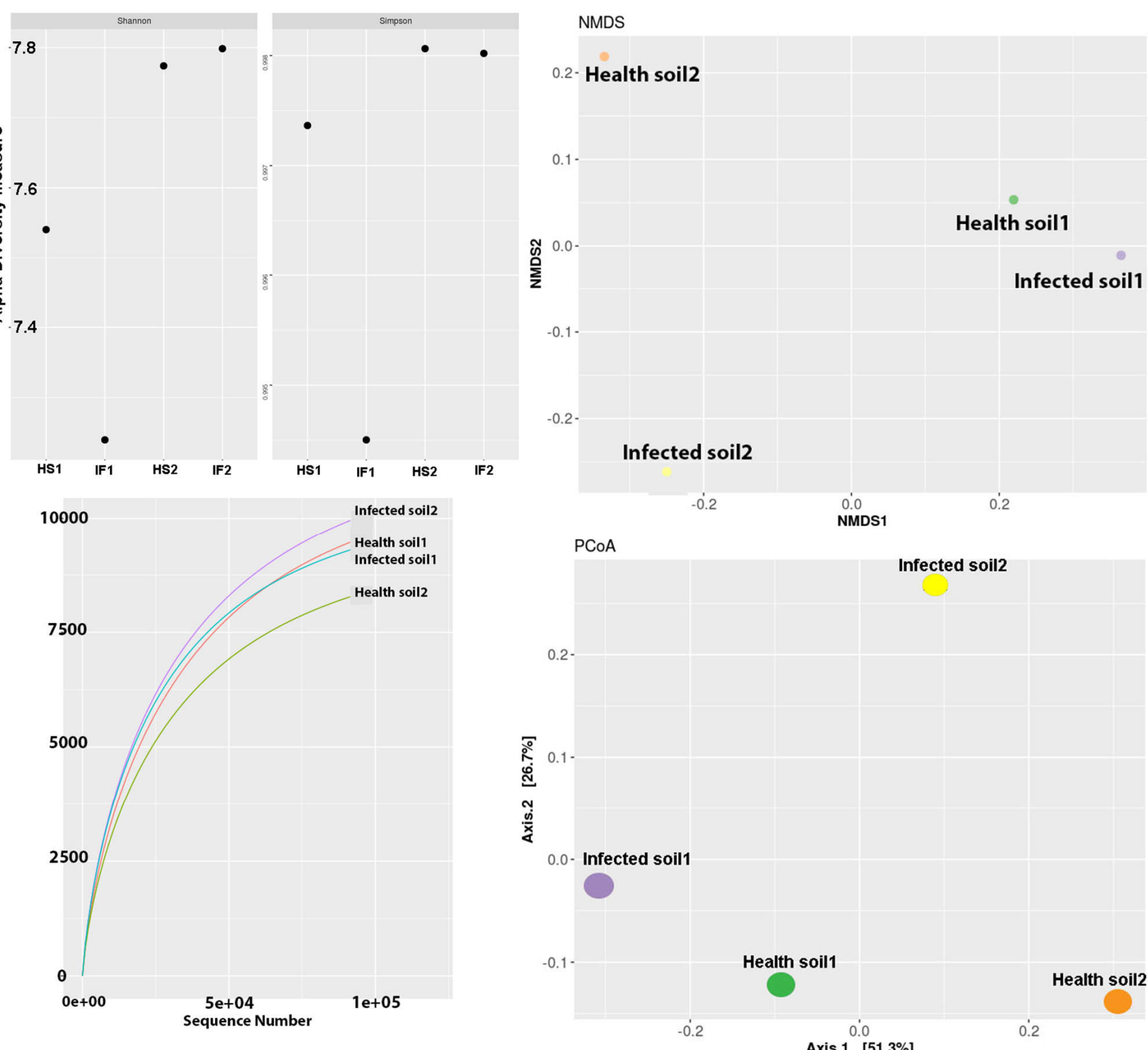
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Abstract

Fusarium oxysporum is a soil borne pathogen fungus that has been known as caused Panama Disease in many horticulture plants, especially banana for *Fusarium oxysporum* cv Cubense TR4 (*Foc*). Currently, there is no effective method for controlling Panama Disease in banana has been applied. Utilization of novel Rhizosphere microbes as bio-agent for preventing the dispersal of microbial pathogens is a method that recently has been developing in agriculture system of many countries. In this study, metagenomic analysis of 16srRNA gene was utilized for analysing composition, richness, and abundance of soil microbes which is living in the rhizospheral area of banana plants. Comparison soil bacterial structure of healthy soils and *Foc*-infected soils was also performed for identifying key bacteria OTU which different in both soil conditions. Data showed more than 9000 OTU of bacteria was identified in both soil conditions. Of it, the *Foc*-infected soils showed a higher species abundance than healthy soil (ACE index 73,6 and 68,8 respectively). However, healthy soil has more taxa richness than infected-soil (Fisher index 447,7 and 343,4 respectively). Beta diversity analysis indicated infected-soils have lower bacterial diversity in comparison with health soils. No statistically difference between both soil conditions in phylum taxa. About 43 phyla have been identified and no significantly difference between both soil conditions. However, *Acidobacteria* (22%) and *Verrucomicrobia* (13%) were more abundance in the health soils in comparison in the infected soils 19% and 10% respectively, whereas *Proteobacteria* was found more abundance in the infected soil (11%) in comparison with the health soil (7%). High abundance of *Xantomonadaceae*, member of *Proteobacteria* in the infected soils might contribute on Fusarium development in soils .

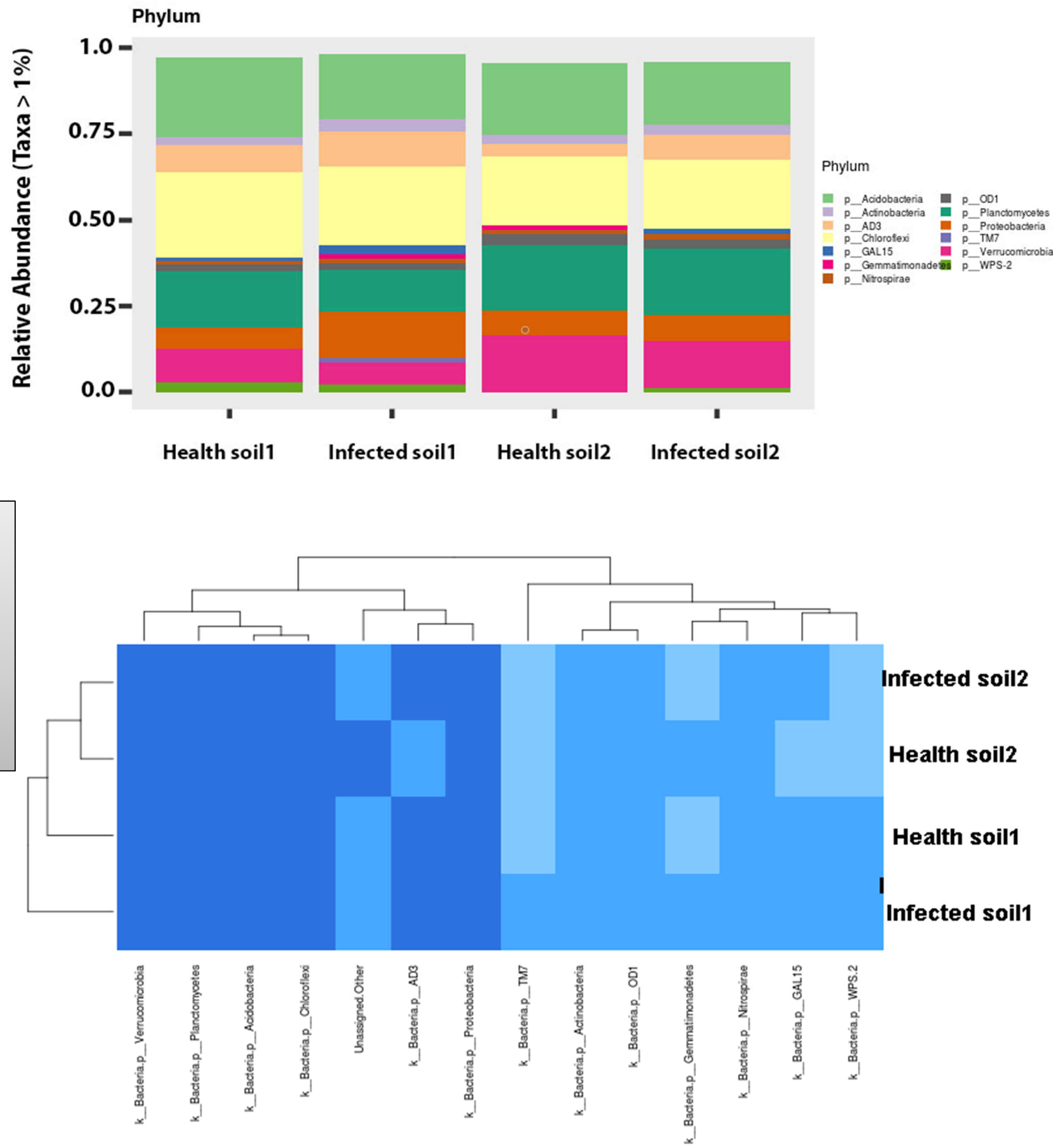
Alpha and Beta Diversity



Diversity index of bacterial community in health and infected soils. Within samples diversity all soil samples contain relative high richness in species except Infected soil1 (Shannon and Simpson index). Between both soil conditions, NMDS base on - Bray-curtis index indicates health soils contain higher diversity than *Foc*-infected soils. Number of OTU has been identified from read was between 7500-10000 OTU with no significant different between both soil conditions.

Relative abundance in phyla taxa. Various abundance of different taxa was identified between health and *Foc*-infected soils, but no significant different. *Verrucomicrobia*, *Planctomycetes*, *Acidobacteria*, *Chloroflexi* and *Protobacteria* were found the most abundance phyla in both soil conditions

Relative Abundance of Level Phylum Taxa

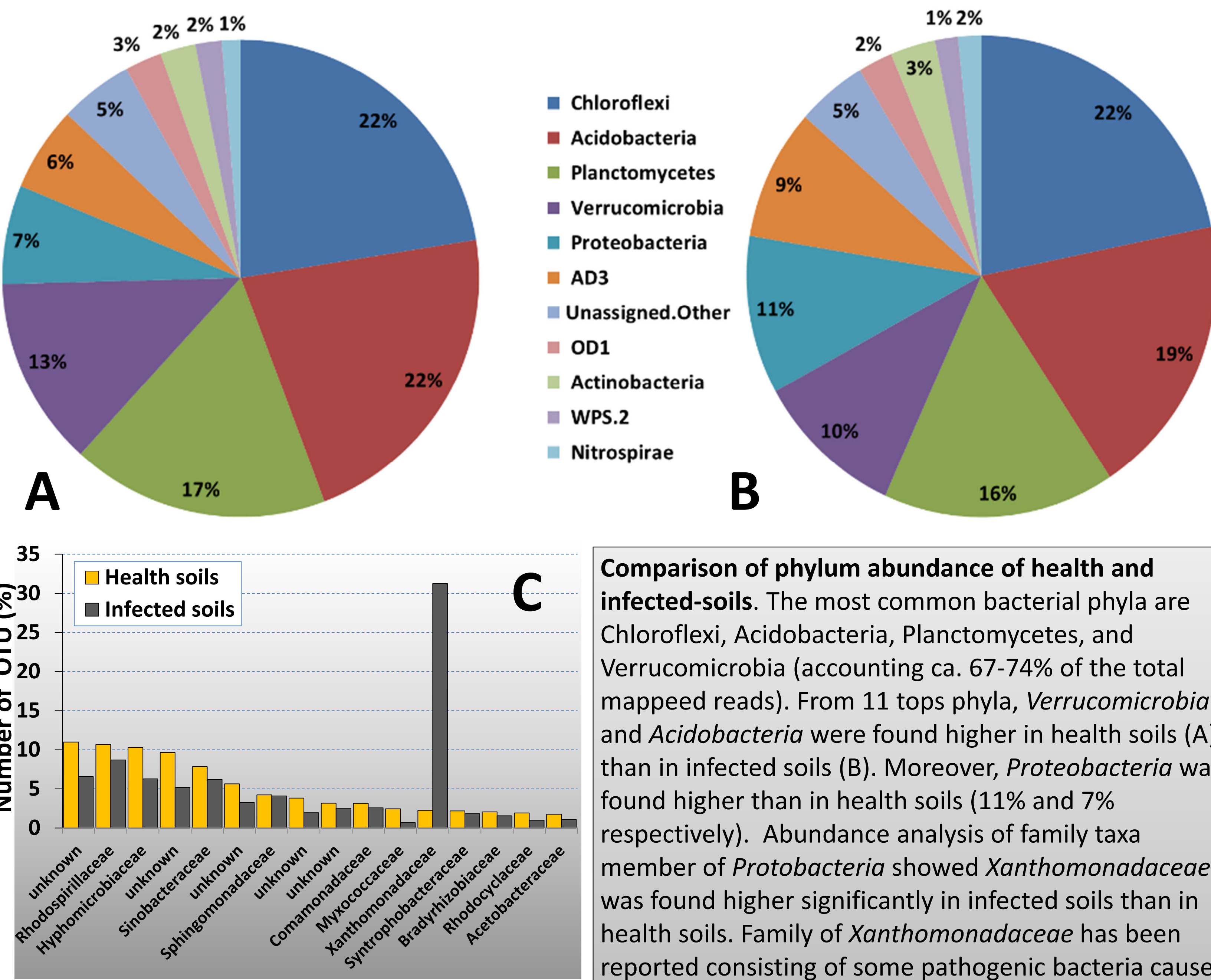


Pairwise comparison p-value of identified-phyla

Phylum	Health soil	Infected soil	<i>p-value</i>
Archaea			
Crenarchaeota	0.00033±0.00006	0.00017±0.00004	0.27
Euryarchaeota	0.00003±0.00002	0.00026±0.00020	0.07
Parvarchaeota.	0.00005±0.00005	0.00000±0.00000	0.26
Bacteria			
AD3	0.05517±0.02247	0.08320±0.01472	0.41
Acidobacteria	0.20938±0.01099	0.17915±0.00467	0.2
Actinobacteria	0.02296±0.00359	0.02922±0.00246	0.31
Armatimonadetes	0.00410±0.00054	0.00356±0.00041	0.42
BHI80.139	0.00010±0.00003	0.00009±0.00002	0.17
BRC1	0.00025±0.00025	0.00020±0.00020	0.56
Bacteroidetes	0.00289±0.00019	0.00732±0.00192	0.09
Chlamydiae	0.00094±0.00047	0.00102±0.00053	0.33
Chlorobi	0.00012±0.00001	0.00056±0.00044	0.11
Chloroflexi	0.21542±0.02283	0.20454±0.01260	0.46
Cyanobacteria	0.00129±0.00004	0.00194±0.00054	0.11
Elusimicrobia	0.00197±0.00028	0.00144±0.00011	0.25
FBP	0.00000±0.00000	0.00001±0.00001	0.21
FCPU426	0.00282±0.00067	0.00212±0.00015	0.51
Fibrobacteres	0.00014±0.00004	0.00042±0.00031	0.17
Firmicutes	0.00054±0.00032	0.00054±0.00012	0.55
GAL15	0.00716±0.00309	0.01918±0.00502	0.45
GN02	0.00001±0.00001	0.00001±0.00001	0.42
Gemmatimonadetes	0.00942±0.00192	0.00976±0.00069	0.51
Kazan.3B.28	0.00004±0.00004	0.00000±0.00000	0.34
NC10	0.00000±0.00000	0.00003±0.00003	0.44
NKB19	0.00124 ±0.00123	0.00058 ±0.00058	0.43
Nitrospirae	0.01218±0.00175	0.01494±0.00217	0.12
OD1	0.00004±0.00004	0.00000±0.00000	0.24
OP11	0.00000±0.00000	0.00003±0.00003	0.32
OP3	0.00124±0.00123	0.00058±0.00058	0.09
Planctomycetes	0.01218±0.00175	0.01494±0.00217	0.33
Proteobacteria	0.02411±0.00601	0.02245±0.00378	0.4
Synergistetes	0.00000±0.00000	0.00002±0.00002	0.23
TM6	0.00118±0.00092	0.00044±0.00025	0.15
TM7	0.16714±0.01058	0.00820±0.00639	0.37
Verrucomicrobia	0.06428±0.00510	0.10006±0.02639	0.56
WPS.2	0.00004±0.00004	0.00012±0.00009	0.55
WS3	0.00292±0.00269	0.00007±0.00002	0.44
Thermi	0.00294±0.00049	0.00820±0.00639	0.16

Pairwise comparison P value of phyla taxa indicates no significant different in abundance of 35 phyla of bacteria and 3 phyla of Archaea between health and infected-soils were found. However, some phyla were found more higher in health soils than in infected soils

Comparison of Relative abundance of 11 tops phyla



CONCLUSION

Metagenomic analysis of bacterial community in health and *Foc* infected-soils showed various abundance and richness of taxa in both soil conditions. The health soils have more richness of taxa in comparison to infected soils (Shannon, Simpson indexes and NMDS), however the OTU abundance between both soil conditions are statistically not difference. *Xanthomonas* member of *Protobacteria* was found relatively more abundance in *Foc*-infected soils which might has correlation with the present of *Fusarium oxysporum f.sp cubense* in banana planted-soils.