

Insights gained from metagenomic sequencing of apple fruit surface

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Introduction

Plant microbiota at fruit surface have been the source of the majority of biocontrol agents (BCAs)

Their role and evolution as a community has been poorly addressed because their holistic study was an unattainable objective due to the absence of survey techniques.



Recent developments in high-throughput sequencing (HTS) have now enabled the holistic analysis of the microbiota genomes.

A pioneering assay has been carried out to get insight into the microbiota of apple (Pinova) surface through metagenome sequencing.

Methods

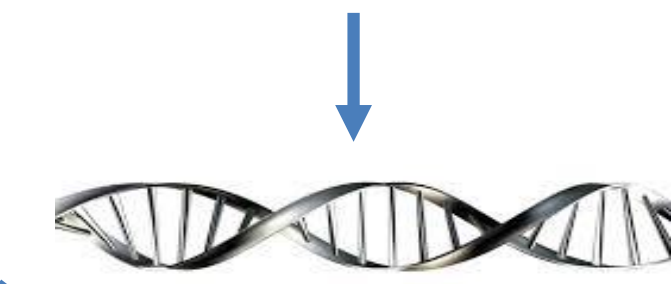


Survey in 2 apple Pinova orchards

2 samples/orchard
1sample = 4 apples



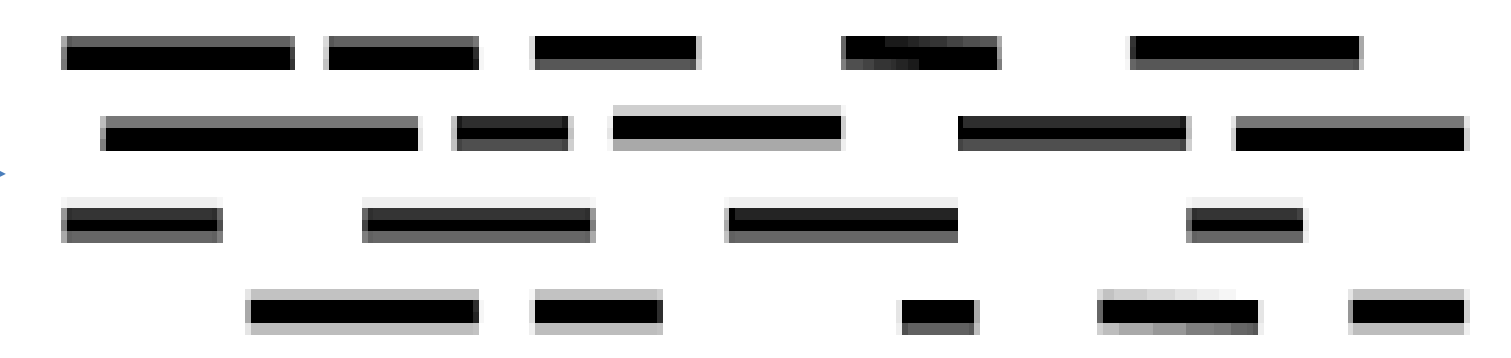
Microbiota extraction by phosphate washing buffer



DNA extraction



HTS



Sequenced DNA fragments

De novo assembly into 133,888 contigs and analysis by MG-RAST

Results

Taxonomic analysis

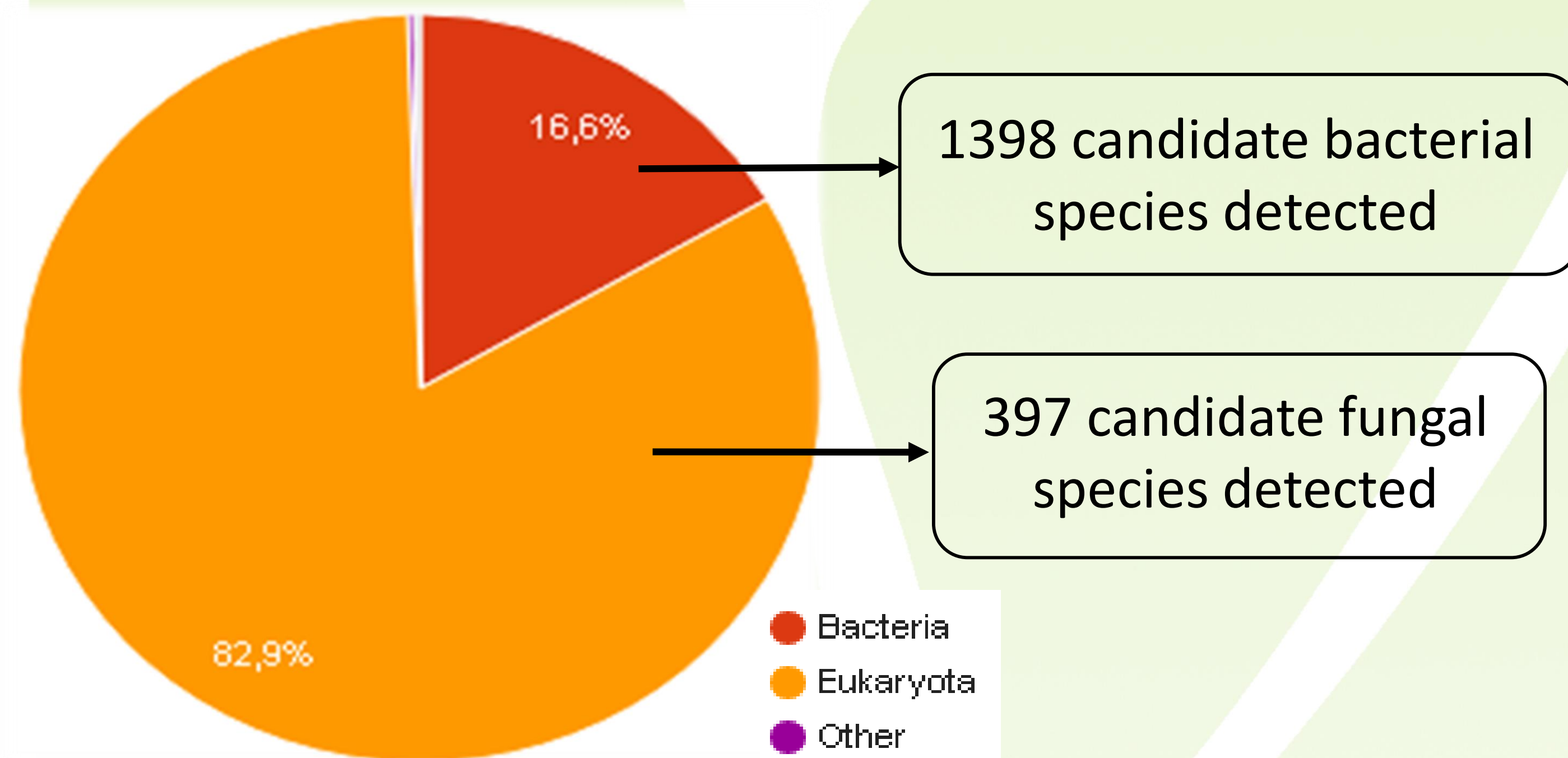
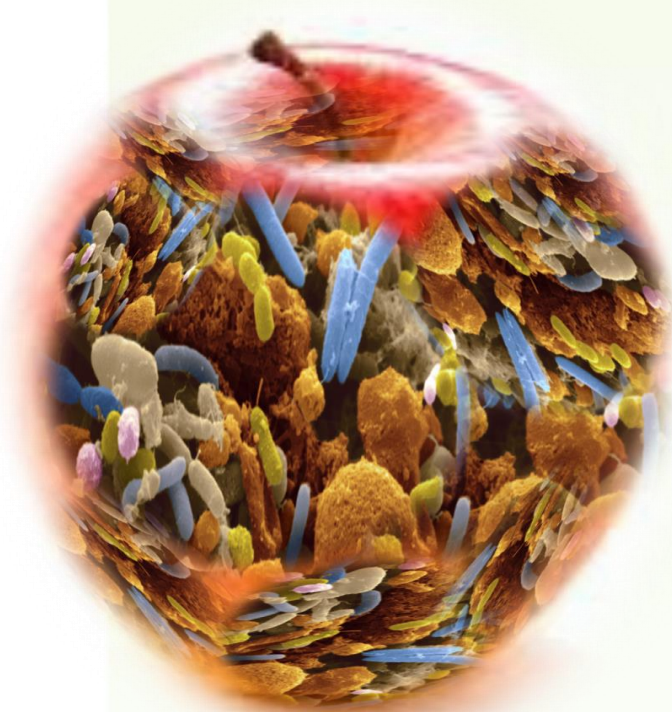


Fig. 1. Distribution of principal taxons

We have observed similar distribution for the 4 samples

What to keep in mind from Pinova's microbiota?



25 apple pathogens species
37 BCA species of apple pathogens
Apple microbiota also harbored important genes for biological control such as Glycoside hydrolyse, Protease, Glucanase, Glucosaminidase, Chitinase and Antibiotic.

Fonctional analysis

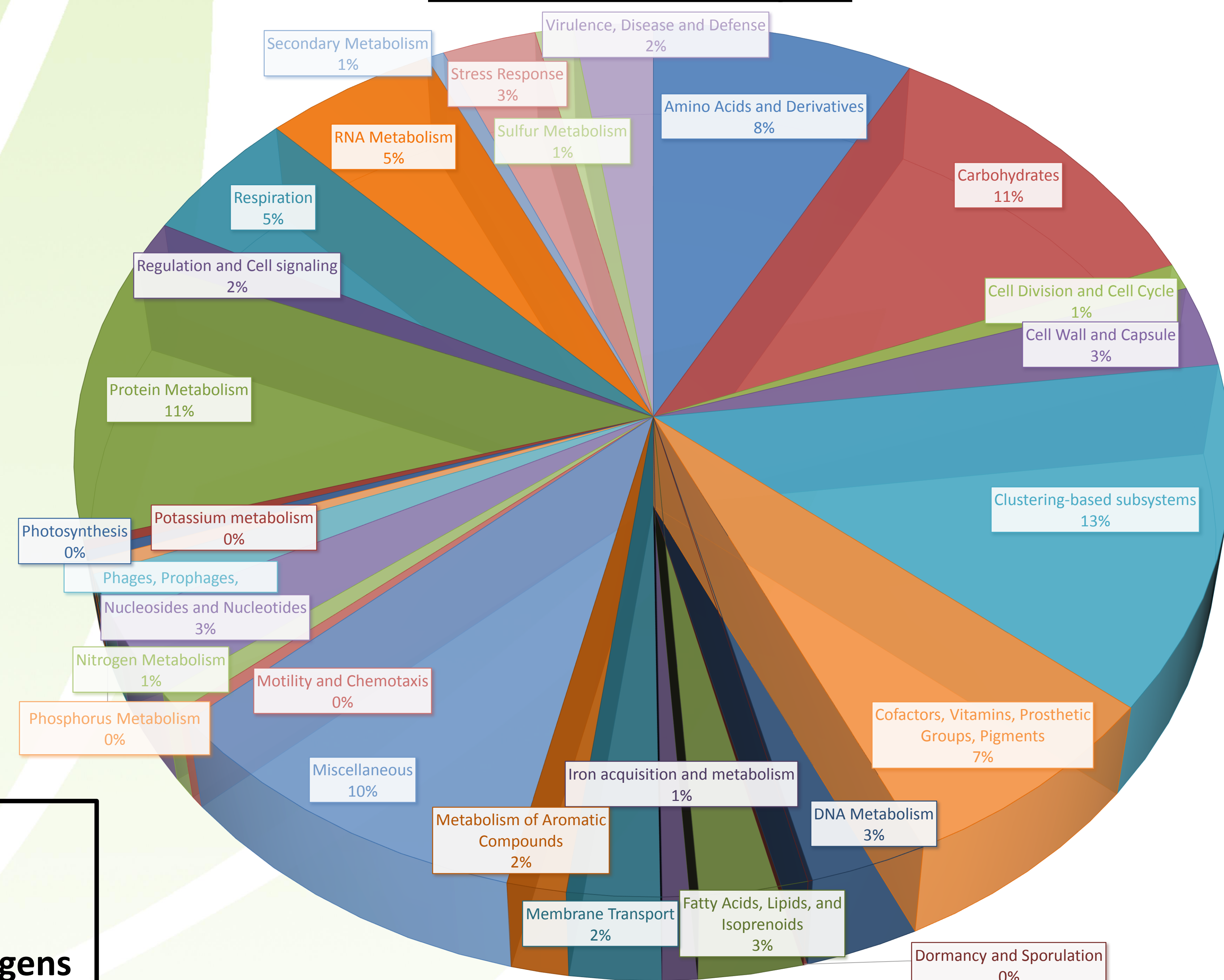


Fig. 2. Distribution of fonctional subsystem categories

We have observed similar distribution for the 4 samples

Conclusion

Apple microbiota presents 25 pathogens indicating high pressure on this fruit. Its also has diverse microbial community including 37 BCA species with high potential of biological control genes that need to be studied in detail to improve fruit biological control.

