



VI21072: Wild and cultivated kiwifruit microbiomes

PROJECT SUMMARY

Background

People, animals and plants live with and alongside a large number of microorganisms (bacteria, viruses, fungi etc.) that affect many aspects of their life. The collection of microorganisms living in a given environment is called the 'microbiome'. There is growing evidence that the plant microbiome increases resistance to biotic (e.g., insects, plants) and abiotic factors (e.g., drought, floods, chemical treatments); and some specific microorganism(s) from a microbiome can directly affect the ability of *Pseudomonas syringae* pv. *actinidiae* (Psa) to cause infection. However, little is known about the plant microbiome of perennial plants such as kiwifruit.

Aim

The aim of this project was to determine whether kiwifruit vines affected by Psa were associated with a different microbiome than vines not affected by Psa, and to determine the differences in microbiome diversity between 'commercial' and 'wild' kiwifruit vines living in similar environments and/or within close proximity. This information could lead to the development of novel ways of reducing the incidence of Psa, including through the identification of new biological control agents.

Methods

Microbiomes from the leaf surfaces were characterised from four asymptomatic vines (i.e., no clear sign of Psa infection) and four symptomatic (i.e., clear sign of infection) vines from both the gully and the orchard at Tauriko (n=16 vines) and Rangioru (n=16 vines). Fine feeder roots (i.e., non-woody) from the same 32 vines were also sampled and microbiome from inside root tissues, and the root-surface microbiome were explored.

Key findings

- No consistent differences were found in microbiomes from samples from vines showing and those not showing Psa symptoms. This could indicate that the asymptomatic vines were already infected but not showing symptoms (latency stage) or that a few symptoms were present but not detected at the time of the sampling.
- There were major differences in the microbiomes between wild and commercial kiwifruit in the two different locations examined. The differences between the orchard and the gully samples in Rangioru or in Tauriko might simply reflect the impact of orchard management practices on the microbiome. The differences between the orchard samples from Rangioru



and those from Tauriko could be due to the local climatic differences or due to different management practices.

- This study also identified a core group of bacteria and fungi that were present in all the samples examined, regardless of whether they were from commercial or wild vines, their growing location, or vine health status. These microorganisms may play a key role in the establishment and growth of kiwifruit vines.

Conclusion

In conclusion, this project highlighted the strong influence of the environment on the composition of the kiwifruit microbiome. We found major differences between wild and commercial kiwifruit in the two different locations of the Bay of Plenty we examined. Further analysis of the results obtained in this project along with other ongoing projects will help define the core microbiome of kiwifruit and the impact of different management strategies on the microbiome.