BS25625 – Psa genomic surveillance

Project summary

Background:

Since *Pseudomonas syringae* pv. *actinidiae* (Psa) was first detected in New Zealand in late 2010, the kiwifruit industry has worked tirelessly to limit the spread of the disease and minimise its impact on production. In general, the industry is in a good position; Psa can be managed through good on-orchard practices using a combination of tools available including copper-based products, the elicitor Actigard®, bio-bactericide Aureo®Gold and various other biologicals, with the option of antibiotics-based bactericides, such as streptomycin and kasugamycin, when necessary. However, as with any other bacteria, Psa can rapidly evolve and adapt to new conditions. For example, we have seen the development of copper tolerance within the Psa populations in kiwifruit orchards over the last decade through acquisition of new genetic elements. While these Psa can still be controlled by currently available tools in the Psa toolbox, it remains possible that Psa could evolve further to be highly copper-tolerant, more pathogenic and virulent on the existing cultivars including Gold3.

Aim:

The aim of this Zespri Innovation project was to determine whether there is any genetic evidence for adaption in Psa population to Gold3 cultivar and current Psa control products. This was carried out through:

- the identification and characterisation of copper resistance elements in Psa genome,
- identification of mobile genetic elements (e.g. Plasmids, ICEs – integrated conjugative elements), and
- analysis of single nucleotide polymorphisms (SNPs) distribution across Psa genomes.

Methodology:

The project analysed 146 Psa isolates that were collected during orchard surveys in the 2022, 2023 and 2024 growing seasons. This included 101 isolates collected through Psa resistance monitoring programmes in 2022 and 2023 run by Zespri/KVH, and 45 isolates submitted by growers in 2024 who were concerned that control of Psa was not as effective as expected. The isolates were sequenced on Illumina high-throughput sequencing platform by Novogene. The sequenced Psa genomes were analysed with a set of bioinformatic tools with an aim to identify the acquisition of new genes, and genetic mutation of existing genes that might increase the pathogenicity or environmental fitness of Psa.

Key Findings:

- There was a clear trend of the dominance of a copper resistance elements harboured by known ICE element called PacICE-10 among the Psa isolates. This resistance conferred by PacICE-10 genetic element can be controlled by currently available copper formulations at label rate.
- Two new mobile genetic elements were identified but both conferred less copper resistance than PacICE-10.
- Four isolates were found that had both PacICE-10 and another element known as pMG2_SR198 but these isolates did not exhibit greater resistance than the isolates that harboured only PacICE-10 genetic element.
- A number of different plasmids were found in the Psa genomes (p47-like and p64-like) but only one - p64-like plasmid appears to be accumulating in the population. There was no correlation between the presence of p64-like plasmids and copper resistance elements.
- Other plasmids were detected but were present at low frequency. Most of the genes in these new plasmids are of uncharacterised function making it difficult to determine their selective advantage to Psa (if any).
- Genome comparison across all Psa isolates showed the SNPs (genetic mutations) to be accumulating evenly across the genome. There was no evidence for the accumulation of SNPs in specific genes within the wider Psa orchard population, nor is there evidence for the domination of a particular genotype.
- No significant changes were found in the complement of genes known to be involved in pathogenicity.
- Although all the isolates submitted by growers in 2024 were copper-resistant and in the majority of cases this was due to the presence of the genetic element PacICE-10, there were no obvious genetic differences observed between these isolates and those collected from the previous years' Psa resistance monitoring programmes in 2022 and 2023.

Overall conclusion

This Psa genomic surveillance work ensures the continued vigilance of Psa populations in kiwifruit orchards for early detection of any new forms of Psa or any exotic Psa biovars that are absent in New Zealand by monitoring genetic changes in Psa populations that could impact this crop in the future. The survey did not find any concerning genetic trends at this stage or found any evidence that warrants any changes to current copper use on orchard.