

PROJECT SUMMARY



RURAL
INDUSTRIES

Research & Development
Corporation

Australian honeybee pathogen survey

The issue

Australia has one of the healthiest honeybee (*Apis mellifera*) populations in the world, but beekeepers still need to manage a range of established pests and diseases. While we have good understanding for some of these pathogens, there are significant gaps in our knowledge of honeybee viruses. The last survey for honeybee viruses was conducted in eastern Australia in 1987.

Since then there has been little published research on viruses in Australia and several new pests and diseases have arrived, including the Asian honeybee (*Apis cerana*) in 2007. Molecular tools have also become standard practice overseas to detect honeybee pathogens but are not widely adopted in Australia. This puts Australia's biosecurity at risk and has raised concerns overseas that importing Australian honeybees could spread unwanted viruses. As a consequence, the US has prohibited imports of Australian queens and packaged bees and other export markets may be at risk.

The research project summarised here, *Upgrading knowledge on pathogens (particularly viruses) of Australian honeybees*, (completed in August 2015), was Australia's first national survey for honeybee viruses and provided valuable monitoring of endemic pathogens.



Outcomes

Using molecular tools we screened 1,240 hives representing 155 apiaries across Australia for 10 honeybee viruses, including Slow paralysis virus (SPV) which is a biosecurity concern for overseas export markets, and Deformed wing virus (DWV) which is a major factor in global colony losses and a local biosecurity threat. We also used hive inspections at each apiary and molecular testing to monitor the spread of non-viral pests and diseases, in particular *Nosema ceranae* and European foulbrood, which have not yet spread to all regions of Australia.

Five honeybee viruses were detected in Australia, but SPV and DWV were not found during the survey. There was good statistical support for this result, with > 0.99 probability 'freedom from disease' for many of the scenarios tested. Black queen cell virus (BQCV) was the most common virus followed by Lake Sinai virus 1 (LSV1), Sacbrood virus (SBV), Israeli acute paralysis virus (IAPV) and Lake Sinai virus 2 (LSV2). BQCV and SBV are long established honeybee viruses and were common in most regions. IAPV, LSV1 and LSV2 are more recently identified from overseas studies and are new records for most regions in Australia. Only 17% of samples were virus-free and 56% of samples were infected by more than one virus.





Nosema spore levels were generally high across Australia with 92% of samples having medium to high estimates, 6% of samples having low spore levels and only 2% had no detectable *Nosema* infection. *Nosema apis* was recorded in all regions except for NT and was not found north of Bundaberg, QLD. *Nosema ceranae* was common throughout its known distribution but was more common as a single infection in QLD. There was no evidence for *N. ceranae* displacing *N. apis*, with 49% of samples infected by both species where their distributions overlap.

Importantly, *N. ceranae* was detected for the first time in one Kununurra (north WA) sample from locally based hives. The confirmed absence of *N. ceranae* in south WA and its dominance in NT suggests a natural spread from

NT to Kununurra via the feral bee population. *Nosema ceranae* was also only found in two TAS samples, despite being found in one beekeeper's hives in 2010. The limited spread of *N. ceranae* in TAS is surprising and may be influenced by climate.

Lastly, no exotic pathogens or pests (e.g. *Varroa* and *Tropilaelaps* mites) were found and no endemic brood diseases or hive pests had increased their distribution. Chalkbrood was the most common brood disease present and 26% of detections were considered to be high infections. European foulbrood was confirmed in only seven samples from NSW, QLD and TAS, although diseased brood showing possible EFB-like symptoms were collected and tested from all regions except NT and Kununurra.

Implications

The findings of this project will benefit the Australian honeybee industry by improving current biosecurity knowledge for honeybee pathogens and assist with accessing and maintaining overseas export markets for live honeybees. The absence of both SPV and DWV also has implications for importing new honeybee stock into Australia. Introduction of these viruses with imported stock needs to be managed to protect industry's current honeybee health status and valuable export markets.

This project also highlighted potential issues with the management of some pest and disease, as shown by the high levels of *Nosema* infections, multiple viruses and chalkbrood outbreaks. Improving the management of these cryptic pathogens needs higher priority as a valuable strategy for increasing industry productivity.

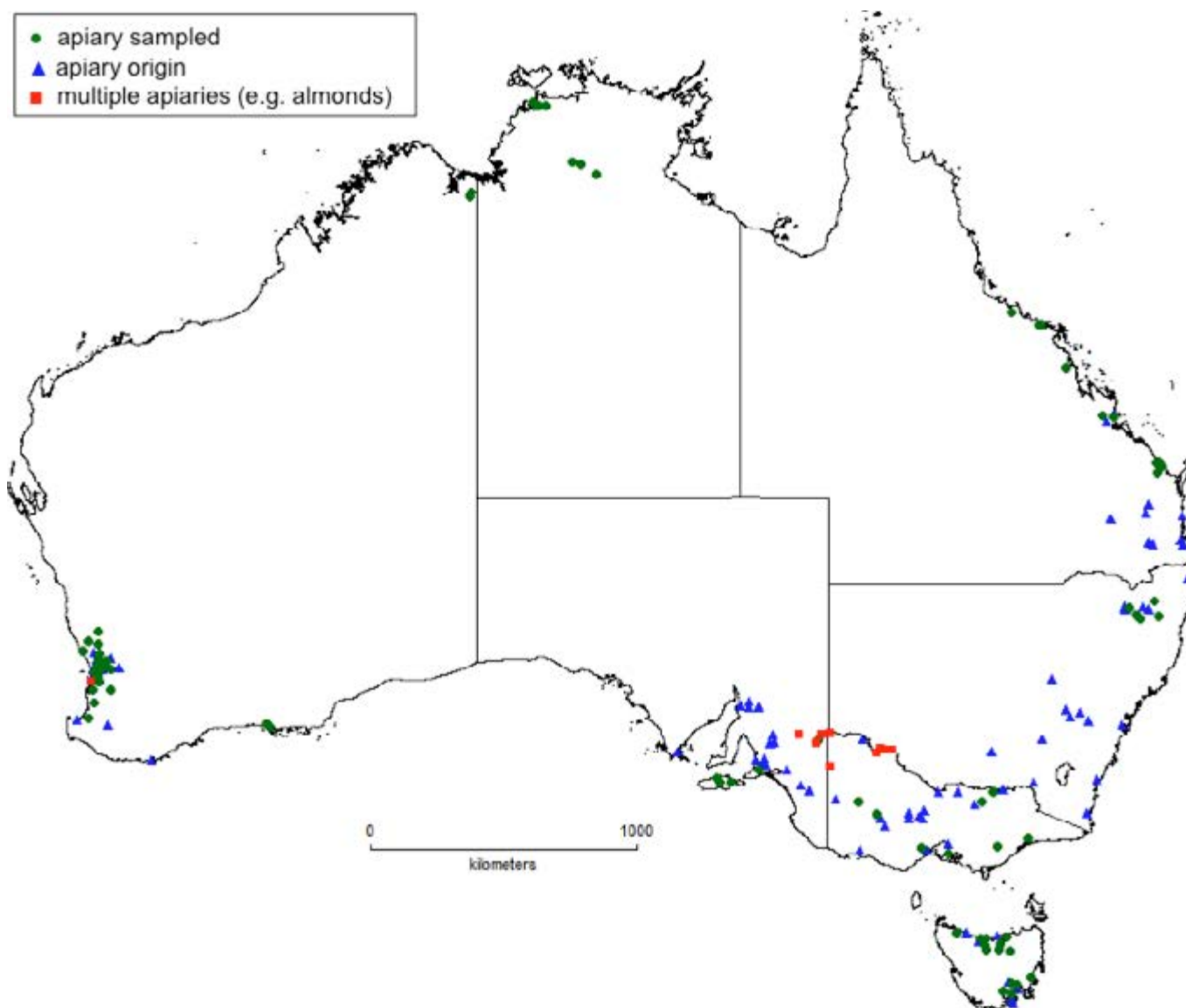


Figure 1. Locations of apiaries sampled and where they originate from (if different to sample location). Multiple apiaries were sampled during almond pollination in northwest VIC and east SA, and during the Rottne Island breeding program in WA.

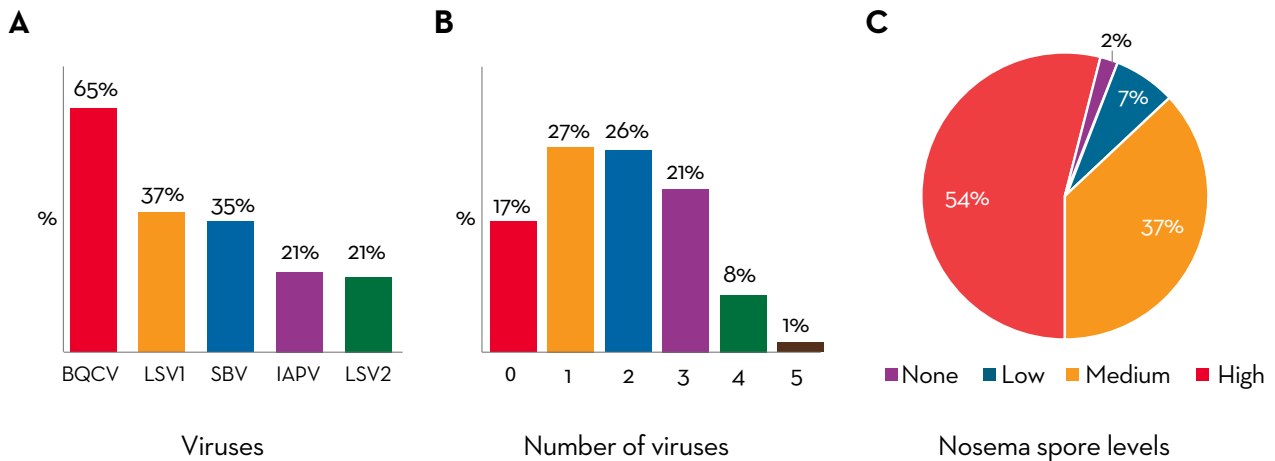


Figure 2.
A, Prevalence of five honeybee viruses found in Australia;
B, Frequency of multiple virus infections in apiaries;
C, Estimated *Nosema* spore levels in apiaries.

Future needs

Monitoring and surveillance of pests and diseases needs to be ongoing. It is essential for protecting honeybee biosecurity and would benefit from more targeted, risk-based approaches for specific pathogens.

More research is needed on viruses in Australia. We have little understanding of their impact on honeybee health or of virulence differences between strains, particularly for the newly identified Lake Sinai viruses.

Better management is needed to reduce *Nosema* and virus levels. We need more detailed knowledge and demonstration of how different management strategies affect pathogen levels.



For more information

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can be contacted for more information about the project.

A scientific journal article from the project is expected to be published in 2016.

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