MOLECULAR VARIATION OF VIRUSES INFECTING HOPS IN AUSTRALIA AND ASSOCIATED STUDIES

By

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Abstract

The objectives of this study were to investigate the virus incidence and molecular variation of *Apple mosaic virus* (ApMV), *Hop mosaic virus* (HpMV) and *Hop latent virus* (HpLV) and to examine the *Hop latent viroid* (HLVd) infection status of Australian hop varieties.

HLVd was found to be ubiquitous in all hop gardens surveyed. This was the first survey of HLVd in Australia. This confirms findings in the Czech Republic where infection was also found to be ubiquitous, while viroid status in other countries also indicates high levels of infection.

A virus survey, primarily to collect viruses for use in molecular analysis, was conducted. The percentage of infected plants detected in this study correlates with those previously undertaken by Pethybridge *et al.,* 2000b. Cultivar 'Victoria' had the greatest level of ilarvirus infections (61%) significantly more than 'Super Pride' (6%). Cultivar Opal had the greatest incidence of carlavirus infections (38%) but this was not significantly different to other cultivars sampled. Hops from the farm at Bushy Park recorded the highest incidences of Ilarvirus infection (44%) although this was not significantly different to the other sampled farms. However, hops sampled from the Gunns Plains farm showed significantly more carlavirus infections (40%) than the other three sampled farms.

Experiments testing transmission capacity of local aphid species (*Macrosiphum euphorbiae* and *Myzus persicae*) of the carlaviruses HpMV and HpLV was performed. It was found that both aphid species transmitted both carlaviruses, this being the first study to demonstrate transmission of HpLV by an aphid other than

the hop aphid, *Phorodon humuli*. This study also showed that prior infection by either virus did not significantly affect subsequent the efficiency of transmission of the other which may have explained observations of greater than expected co-infection of both carlaviruses within the field.

It was known that two serologically distinct ilarvirus strains infect hop. Prior literature indicated that these were strains of *Prunus necrotic ringspot virus* (PNRSV) designated –intermediate (PNRSV-I) type and PNRSV-A (apple serotype). This study undertook molecular analysis of hop-infecting ilarviruses to clarify strain diversity and taxonomic relationships. Analyses showed Australian hops are infected with two distinct strains of ApMV (and not PNRSV) these being distinct to ApMV strain commonly found in Apple. It was proposed that hop infecting strains of ilarvirus be termed ApMV-Hop (the former PNRSV-apple serotype) and ApMV-Intermediate (the former PNRSV intermediate serotype). PCR based assays were developed that could be used to distinguish the two strain types.

Suggestions of strains of HpMV had been described due to lethal and non-lethal response following infection in 'English Golding' hops. Molecular analysis of HpMV from Australian hop gardens indicated that there were at least two distinct clades of HpMV present with approximately 80% homology. Further work conducted at the conclusion of this study identified a possible third clade of HpMV. All HpLV isolates that were sequenced in this study had a high degree of identity. This was supported by recent publication of several further sequences on GenBank that also show this high degree of identity.

Statement of co-authorship and publications

Several of the chapters in this work have been published as scientific manuscripts. Unless stated as a percentage, experimental design, field and laboratory work, data analysis and interpretation, and manuscript preparation were the primary responsibility of the candidate. However, they were carried out with the supervision of the co-authors. These publications are presented in Chapter 8 – Appendix 4.

In Chapter 3, Shirofugen cherry virus indexing was conducted by Dr Michael Barkley, New South Wales Department of Agriculture, Camden, New South Wales, Australia.

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