

Analysis on virus-virus and virus-host interactions in Brassicaceae in natural environments

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Abstract

As research on plant viruses has focused mainly on crop diseases, little is known about plant viruses in natural environments. However, viruses are important factor in ecosystem, because they can alter host physiology and consequently become an important determinant of plant demography. Under natural environments, infection that produces severe symptoms is not considered to be adaptive for either plants or viruses. Indeed, increasing number of studies have reported asymptomatic infections in wild plants. Distributions and observed infection rate of viruses affected by surrounding natural environments, because they are an output of infection processes that involve viruses, vectors, hosts and their interactions. To understand the ecological interactions and behaviour of viruses in natural systems, comprehensive information on virus–virus and virus–host interactions is required. However, comprehensive detection of known and novel viruses is difficult, because viruses do not have conserved genome regions to be utilized for species identification. Therefore, in this study, I employed RNA-Seq with selective depression of rRNA which enables the detection of viral RNA comprehensively regardless of their genome molecule type (DNA/RNA) or presence/absence of polyA tail at their 3' ends. In addition, RNA-Seq enabled us to precise identifications of viruses and simultaneous analyses of host transcriptome. In this thesis, in chapter 1, I described several factors which must be considered in studying virus–virus and virus–host interactions in natural systems, by quoting the previous studies. In Chapter 2, to reveal these interaction at individual and population levels, I applied RNA-Seq to a natural population of *Arabidopsis halleri* subsp. *gemmifera* [Brassicaceae]. Four virus species, including a novel virus discovered by *de novo* assembly, were detected, and the asymptomatic infections were common. Analysis on host transcriptome revealed that *AhgAGO2*, a key gene in host defence systems, was upregulated in virus infected leaves. Among virus species, multiple infection was frequently observed in leaves infected by *Turnip mosaic virus* (TuMV), which has a suppressor gene for host RNA-silencing, a major plant defence-machinery for viruses. In Chapter 3, I conducted RNA-Seq on all Brassicaceae species inhabited in three natural plant-communities. Virus species composition was significantly different among the three locality and host plant species, and 5, 2 and 0 virus species were detected from the examined three communities. Virus infections were observed only in two perennial plants. Such viruses in perennial plants

with weak symptoms are expected to be hard to be eliminated from the natural plant communities. In Chapter 4, I discussed the following questions, i.e., the observed virus diversity in natural plants, characteristics of viruses and plants that enhance/reduce observed infection rate under natural conditions, and effects of virus-virus interactions on multiple infections. Revealing hidden plant–virus interactions in nature would enhance our understanding of biological interactions and may reveal natural sources of pathogenic viruses in agricultures.