



Unveiling The Grapevine Red Blotch Virus (GRBV) Host-Pathogen Arms-Race Via Multi-Omics For Enhanced Viral Defense

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Abstract (250 words)

The Grapevine Red Blotch Virus (GRBV) poses a critical challenge to the wine sector, lacking a uniquely identified vector. Current control methods involve costly and labor-intensive vine removal, emphasizing the urgency for targeted alternatives. The limited understanding of intricate host-virus interactions underscores the need for foundational knowledge to develop innovative disease control strategies. These include efforts to boost the plant's RNA interference (RNAi) response, including RNA-based topical applications. Our research investigates the early GRBV infection stages, aiming to unravel the "arms race" between the plant's RNAi machinery and the viral counter-defense strategies. Following an *Agrobacterium tumefaciens*-mediated infiltration with an infectious clone containing the GRBV genome, we detected a peak of viral activity in infected microvine plants one-week post-infection. Small RNA sequencing from infected tissues identified 21, 22, and 24 nucleotides virus-derived small-interfering RNAs (vsiRNAs), suggesting post-transcriptional and transcriptional gene silencing activity. We utilized a custom bioinformatics pipeline to identify GRBV "hotspots," that were further validated as RNAi precursors through secondary structure predictions. GRBV-targeted bisulfite sequencing revealed hypermethylation within GRBV hotspots, establishing a crucial link between small RNA production and effective methylation of the virus, culminating at 24 days post-infection (dpi).

Examining the plant transcriptome and methylome during early infection dates (3, 6, 12 and 24 dpi) unveiled molecular strategies employed by both organisms to counteract each other. The multilayered OMICs data we generated constitute the foundation for innovative viral defense strategies. This strategy could enhance GRBV management, ensuring sustainable vineyard practices by integrating molecular biology insights into agriculture.

Keywords: Grapevine Red Blotch Virus (GRBV), Host-virus interactions, small RNA-seq, genome-wide OMICs