

Plant Pathology Seminar Series

“Studies on viruses associated with redleaf symptoms in Washington Vineyards”

Jati Adiputra

Viral diseases are one of the significant constraints to sustainability of the grape and wine industry that contributes nearly \$5 billion annually to Washington State’s economy. This study was undertaken to gain a better understanding of grapevine leafroll (GLD) and red blotch (GRBD) diseases causing red leaf symptoms for managing these two virus diseases in vineyards. In the first objective, a state-wide survey was conducted for three growing seasons to assess the prevalence of GRBD and GLD in vineyards. Overall results indicated that *Grapevine leafroll-associated virus 3* (GLRaV-3) was more predominant and wide spread than *Grapevine red blotch virus* (GRBV). The data underscored the critical need for reliable identification of GLRaV-3 and GRBV in vines showing red leaf symptoms and to differentiate virus symptoms from those induced by other biotic factors and abiotic stresses. A multiplex PCR was developed for the simultaneous detection of GLRaV-3 and GRBV. Phylogenetic analysis indicated the presence of GRBV variants in Washington vineyards that segregated into two well-separated clades. In the second objective, impacts of GRBD were studied in a vineyard field-grafted with cv. Sangiovese showing atypical symptoms of the disease. A comparative analysis between symptomatic vines tested positive for GRBV and non-symptomatic vines negative for GRBV indicated that virus infection can cause significant impacts on shoot biomass, fruit yield and grape quality in field-grafted Sangiovese vines. Since field-grafting results in grafted vines with a blend of characteristics inherited from two distinct types of grapevines, the data provided a foundation for further studies on elucidating the influence of grafting vinifera to vinifera on host-virus interactions. Among the GLRaVs reported earlier from Washington vineyards, very little information is available on the genome characteristics of GLRaV-4 and its strains. In this third objective, the complete genome sequence of GLRaV-4 strains -4, -5, and -9 was determined. The genome sequences of these strains were compared with corresponding sequences of GLRaV-4 and its strains reported from other grapevine-growing regions. Together with sequence information available for GLRaV-1, 2, and -3, the data generated in this objective will provide new avenues for investigating the comparative molecular biology of GLRaVs infecting grapevines.

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PhD Exit Seminar



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