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# Plant Pathology Seminar Series

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

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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.

10:10 am | Friday, September 15, 2017 | Johnson Hall 343

*PhD Exit Seminar*



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