Plant Pathology Seminar Series

“Population Dynamics and Activities of Native Yeasts in Washington State Vineyards and during Alcoholic Fermentation”

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Native yeasts are an important part of the microbiota in vineyards and some are recognized for their biocontrol activity and their contributions to the wine fermentation process. To assess biocontrol activity, 11 yeast and yeast-like strains isolated from Washington vineyards were tested for their ability to colonize grape berries, inhibit the growth of *Botrytis cinerea in vitro*, and suppress disease symptoms on berries. Strains of *Aureobasidium pullulans*, *Candida saitoana*, *Curvibasidium pallidicorallinum*, *Metschnikowia chrysoperlae*, *Metschnikowia pulcherrima*, *Meyerozyma guilliermondii*, *Saccharomyces cerevisiae*, and *Wickerhamomyces anomalus* multiplied rapidly on grapes berries by 2 days after inoculation, and the population sizes reached log 7 CFU mL^{-1} of tissue by 10 days. *B. cinerea* isolates from Washington State varied in virulence on berries, and *B. prunorum*, which is significantly less virulent, was identified for the first time from Washington grapes. Consistent disease suppression occurred on berries inoculated with *B. cinerea* and treated with *A. pullulans*, *Mt. chrysoperlae*, *Mt. pulcherrima*, *Me. guilliermondii*, and *S. cerevisiae*. Specific real-time PCR primers were designed to the internal transcribed spacer (ITS) and large ribosome subunit region of the 26S ribosomal RNA subunit. Real-time PCR assays were developed to target strains of *Brettanomyces bruxellensis*, *C. californica*, *Cur. pallidicorallinum*, *H. uvarum*, *H. opuntiae*, *Mt. pulcherrima*, *Mt. chrysoperlae*, *Me. caribbica*, *Me. guilliermondii*, *S. cerevisiae*, and *A. pullulans*. A strong correlation existed between cell populations and amounts of purified DNA (pg) for six of the yeasts; exceptions were *A. pullulans* and *Cur. pallidicorallinum*. The utility of the real-time assays for detecting *Mt. pulcherrima/chrysoperlae*, *Me. caribbica/guilliermondii*, and *S. cerevisiae* was further validated using fermentation samples. Next-generation sequencing was used to characterize native yeast communities on Cabernet Sauvignon from two Washington vineyards, and in natural fermentations in 2015 and 2016. Yeast diversity was assessed using the ITS1 region of the 26S rRNA gene. Yeast community richness (number of taxa), structure, population sizes and dynamics were correlated with geographic location, vintage year, grape growth stages, sampling points during fermentations and sulfite addition. Vineyard location and year were the primary factors that accounted for the variation among yeast communities in vineyards and during alcoholic fermentation.

1:10 pm | Friday, April 20 | Johnson Hall 343

PhD Exit Seminar

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