WASHINGTON STATE UNIVERSITY

WSU PLANT PATHOLOGY SEMINAR
October 20, 2025, 4:10 PM

Beyond the grove: Unveiling the ecology and diversity of X-disease, '*Candidatus* Phytoplasma pruni', strains in extra-orchard environments

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Attend in Person
10/20/25 @ 4:10 pm (Pacific)
Clark 149, Pullman, WA

Attend on Zoom

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> **Meeting ID:** 953 7682 7690
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ABOUT THE PRESENTER

Mason C. Hoskins is an M.S. student in the Department of Plant Pathology at Washington State University's Irrigated Agriculture Research and Extension Center in Prosser, WA. Under the advisement of Dr. Scott Harper, his research focuses on '*Candidatus* Phytoplasma pruni', the causal agent of X-disease, the focus of his presentation. Outside of the lab, Mason serves as Treasurer of the Prosser Graduate Student Association and as the Prosser Steward for WSU's ASE Union Local 4591. He is also an active member of the department's Community Resource Committee and the FUN Committee.

ABSTRACT

Commercial cherry growers throughout North America have experienced significant crop losses over the last decade due to an outbreak of X-disease, caused by '*Candidatus* Phytoplasma pruni' [1]. The X-disease phytoplasma is part of '*Ca.* Phytoplasma' 16SrIII group. This group comprises 21 subgroups determined on the basis of 16S rRNA sequence, with true '*Ca*. P. pruni' strains belonging to subgroup "A" and '*Ca*. P. pruni'-related strains classified into the remaining 20 subgroups [2]. In previous epidemics, this phytoplasma was thought to have originated in uncultivated *Prunus* spp. adjacent to orchards [3]. Building on recent research into the diversity of '*Ca*. P. pruni'—which identified seven distinct genotypes, five associated with commercial *Prunus* spp. and two specific to uncultivated *Prunus* spp. [4]—we aimed to test that hypothesis by determining which genotypes were present in cultivated vs. uncultivated *Prunus* spp. across the western and mountain states of the United States during the 2023 and 2024 growing seasons. Additionally, we aimed to understand the placement of these '*Ca*. P. pruni' strains within the broader context of the '*Ca.* Phytoplasma' 16SrIII group.

Chokecherry (*Prunus virginiana*) samples (n = 518) were collected across 13 states and tested for '*Ca*. P. pruni' presence using a species-specific quantitative real-time PCR assay [5], followed by rapid genotype identification using the *imp* gene [6]. Multi-locus sequence analysis (MLSA) was performed using the 16S, *secY*, *secA*, *imp*, and *Ef-Tu* genes to increase the resolution of strain relationships and genetic diversity [7]. Metagenomic analysis was also conducted to better understand strain relationships at the highest resolution.

'*Ca*. P. pruni' presence was almost universal in chokecherry across the western and midwestern states. MLSA revealed clear geographic segregation among strains found in uncultivated *Prunus* spp., but not among strains in commercial orchards in most states. This pattern suggests that strain introductions into orchards may occur independently of native uncultivated *Prunus* spp. populations. Several novel strain populations were also identified, indicating that this phytoplasma is more genetically diverse than previously recognized. Notably, the Rocky Mountains emerged as a potential barrier to strain movement, with increased strain diversification observed on the western side of the mountains compared to the eastern side. We present an additional 29 genomes representing the 16SrIII group, expanding coverage of the '*Ca*. P. pruni' subgroup A. Metagenomic analyses indicated distinct grouping among the strains in the 16SrIII group, and revealed that some '*Ca*. P. pruni'-related strains (as classified by 16S rRNA analysis) fall below the established average nucleotide identity (ANI) threshold of 95% for species delineation [7]. In addition to these genetic differences, these strains possess distinct biological characteristics, including differences in primary host range, putative insect vectors, and geographic origins—that are not shared with classical X-disease inducing strains. This highlights the need to reconsider their taxonomic classification and to incorporate biological criteria into taxonomic frameworks [8].

LITERATURE CITED

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