Fusarioid community structure among conifer nurseries of the contiguous USA and virulence of conifer-associated *Fusarium commune*

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Fusaria can be introduced into novel landscapes through latent-infected nursery stock and cause seedling mortality. Molecular tools can rapidly identify and track Fusarioid pathogens to mitigate novel pathogen introductions by informing both pathogen composition and pathogenicity of different *Fusarium* spp. Understanding the community structure and population genetics of *Fusarium* spp. is a prerequisite for developing robust primers to detect pathogenic species. Accessory chromosomes have been identified in fungi that house virulence genes that can be horizontally transferred among species and populations. These accessory chromosomes and/or associated virulence genes are prime targets for developing diagnostic probes to identify conifer pathogens. *Fusarium commune* is an understudied species that can be pathogenic to both herbaceous crops and timber trees; however, its virulence mechanisms for conifers have not been elucidated. *Fusarium annulatum* has recently been described as a distinct species from *F. proliferatum*, a species that is a known pathogen of conifers. Subsequently, *F. annulatum* virulence to conifers is not well studied. Our work has three objectives: 1) evaluate Fusarioid fungal community structure in conifer nurseries across the U.S.A. by identifying host associations and geographic distributions, 2) evaluate virulence of conifer-associated Fusarioid isolates on ponderosa pine (*Pinus ponderosa*), loblolly pine (*P. taeda*), and Douglas-fir (*Pseudotsuga menziesii*) seedlings, and 3) use genomic tools to identify candidate virulence genes in host-pathogen interactions that allow design of diagnostic primers for rapid identification and tracking of Fusarioid pathogens. In this study, ca. 26 *Fusarium* spp., including *F. commune* and *F. annulatum*, were collected from conifer nurseries. Unique genomic regions and virulence genes of 15 Fusarioid fungal genomes were compared to identify diagnostic primer targets. Further, three conifer-derived *F. commune* isolates (two from Douglas-fir and one from ponderosa pine) were compared with two non-conifer *F. commune* isolates [from rice (*Oryza sativa*) and tomato (*Solanum lycopersicum*)] to identify genes involved in pathogenicity to conifer hosts (Figure 1). This work will identify virulence factors of *Fusarium* that determine host specificity and genomic regions for developing tools that quantify the inoculum density of *Fusarium* pathogen in conifer nurseries and/or track Fusarioid pathogens from nurseries to prevent/monitor their spread into the forest landscape.

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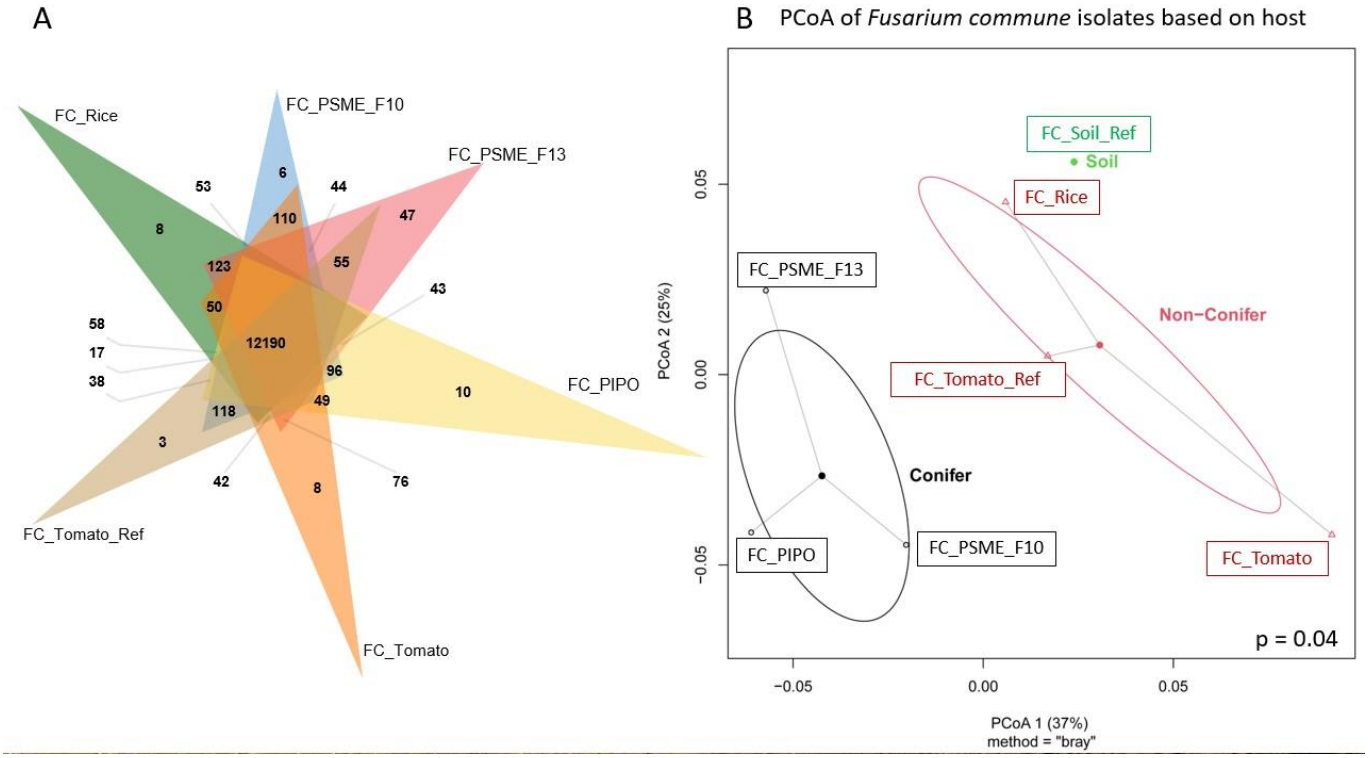

Figure 1: (A) Comparisons of orthologous proteins based on shared orthogroups among *Fusarium commune* (FC) isolates collected from conifer [Douglas-fir (*Pseudotsuga menziesii*; PSME) and ponderosa pine (*Pinus ponderosa*; PIPO)] and non-conifer hosts [rice (*Oryza sativa*) and tomato (*Solanum lycopersicum*)]. These isolates were also compared with two *F. commune* reference genomes collected from tomato (Accession #: JABFES000000000) and soil (Accession #: BCHB00000000) retrieved from GenBank. (B) A principal coordinate analysis was used to assess the similarity of isolates based on hosts from which they were collected and showed significant groupings of isolates based on their host origins.

Proceedings of the 68th Western International Forest Disease Work Conference

DoubleTree Hotel

Rohnert Park, California

June 5-9, 2023

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Citation:

Brooks, R.K. (comps.) 2024. Proceedings of the 68th Western International Forest Disease Work Conference, Rohnert Park, California, 5-9 June 2023. https://www.wifdwc.org/

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