



OCCURRENCE OF THE ROOT ROT PATHOGEN, *FUSARIUM COMMUNE*, IN MIDWESTERN AND WESTERN UNITED STATES

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ABSTRACT

Fusarium commune can cause damping-off and root rot of conifer seedlings in forest nurseries. The pathogen is only reported in Oregon, Idaho, and Washington within United States. *Fusarium* isolates were collected from midwestern and western United States to determine occurrence of this pathogen. DNA sequences of mitochondrial small subunit gene were used to identify *F. commune*. In addition to the aforementioned states, *F. commune* was found from nurseries in Nevada, Montana, Nebraska, and Michigan, USA.

BACKGROUND

The genus *Fusarium* is ubiquitous in most container and bareroot nurseries on healthy and diseased conifer seedlings, in nursery soils, and on conifer seeds of several species, especially Douglas-fir (*Pseudotsuga menziesii*), western white pine (*Pinus monticola*), and ponderosa pine (*Pinus ponderosa*) (James et al. 1990). Since the first report of this *Fusarium* root rot in forest nurseries, the major pathogen was previously identified as *Fusarium oxysporum* based on morphology (Bloomberg 1981). However, selected *Fusarium* spp. isolates that had previously been characterized as pathogenic on Douglas-fir seedlings displayed a range of high, moderate, and low virulence (Stewart et al. 2006). Stewart et al. (2006) showed that all the highly virulent isolates were identified as *F. commune*, a

recently named species (Skovgaard et al. 2003), based on DNA sequences. DNA sequences from the mitochondrial small subunit (mtSSU) and elongation factor-1 α (EF-1 α) regions are useful for distinguishing *F. commune* from *F. oxysporum*.

MATERIALS AND METHODS

A total of 260 isolates of *Fusarium* spp. were collected in forest nurseries throughout midwestern and western United States (Table 1). Isolates from each state were collected from one to five forest nurseries. *Fusarium* isolates were collected from diverse sources of host/substrate: diseased or healthy seedlings of Douglas-fir, western larch (*Larix occidentalis*), western redcedar (*Thuja plicata*), Pacific yew (*Taxus brevifolia*), lodgepole pine (*Pinus contorta*), western hemlock (*Tsuga heterophylla*), western white pine, ponderosa pine, grand fir (*Abies grandis*), rabbitbrush (*Chrysothamnus* sp.), sagebrush (*Artemisia* sp.), Austrian pine (*Pinus nigra*), blue spruce (*Picea pungens*), bitterbrush (*Purshia tridentata*), and eastern redcedar (*Juniperus virginiana*), containers of various conifer seedlings, and soil/growing medium.

Table 1: Number of *Fusarium* spp. isolates collected from midwestern and western United States.

State	Total # of isolates
Washington	31
Oregon	79
California	43
Idaho	56
Nevada	13
Montana	14
Utah	12
Nebraska	7
Michigan	5

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Molecular species identification. All 260 isolates were characterized using mtSSU sequences. Template DNA was derived from scrapings of actively growing mycelial cultures (3-5 days old), so

no DNA extractions were performed. The PCR products were sequenced with an ABI 3700 DNA Sequencer (Applied Biosystems, Inc.) at the University of Wisconsin – Biotechnology Center (Madison, WI, USA) and the sequences of mtSSU region were blasted to GenBank database.

Confirmation of species identification. Phylogenetic analyses were performed on the 29 *F. commune* isolates from this study, along with previously identified *F. oxysporum* and *F. commune* isolates (Figure 1; Stewart et al. 2006). Isolates of *F. subglutinans* (NRRL 22016: M1431/AF160289), *F. proliferatum* (NRRL22057: M1431/M1432) were included in the analyses as an outgroup. Sequences of *F. proliferatum* and *F. subglutinans* were retrieved from TreeBASE matrices (M1431, M1432) (www.treebase.org). Phylogenetic analyses were conducted using PAUP*4.0b10 (Swofford 2003) and MrBayes v.3.0b4 (Huelsenbeck and Ronquist 2001.)

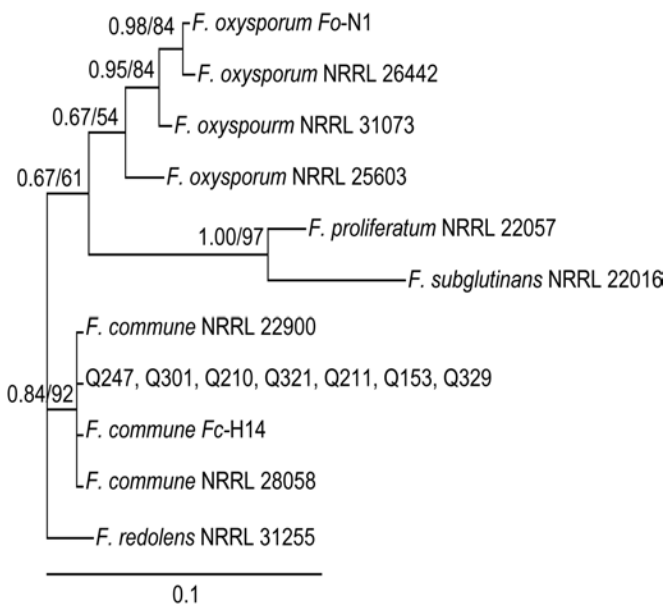


Figure 1: Phylogenetic analyses based on mtSSU region showed that the 29 *F. commune* from this study grouped with the previously identified *F. commune* (Stewart et al. 2006), which is genetically distinct from *F. oxysporum*. Isolates Q247 (WA), Q301 (OR), Q210 (ID), Q321 (NV), Q211 (MT), Q153 (NE), and Q329 (MI) represent strains from each state. Node confidence levels are shown by posterior probability (left) and bootstrap (right) support.

RESULTS AND DISCUSSION

A total of 29 *F. commune* isolates was identified based on GenBank BLAST search using mtSSU sequences from Washington, Oregon, Nevada, Montana, Michigan, and Nebraska (Figure 2). Previous studies also identified *F. commune* in Idaho, Oregon, and Washington (Leon 2009; Skovgaard et al. 2003; Stewart et al. 2006). No *F. commune* was found in California or Utah. A total of 43 isolates was collected from California representing three nurseries, but all are *F. oxysporum*. *Fusarium* isolates representing one nursery in Utah also did not contain any *F. commune*. The majority of *Fusarium* isolates derived from midwestern and western United States were identified as *F. oxysporum* based on mtSSU sequences. Several isolates of *F. redolens* and a couple of *F. solani* were also identified (data not shown). Results from this study indicate that *F. commune* occurs widely throughout the midwestern and western United States. More intensive studies are needed to better characterize the distribution and host range of *F. commune* in tree nursery settings.

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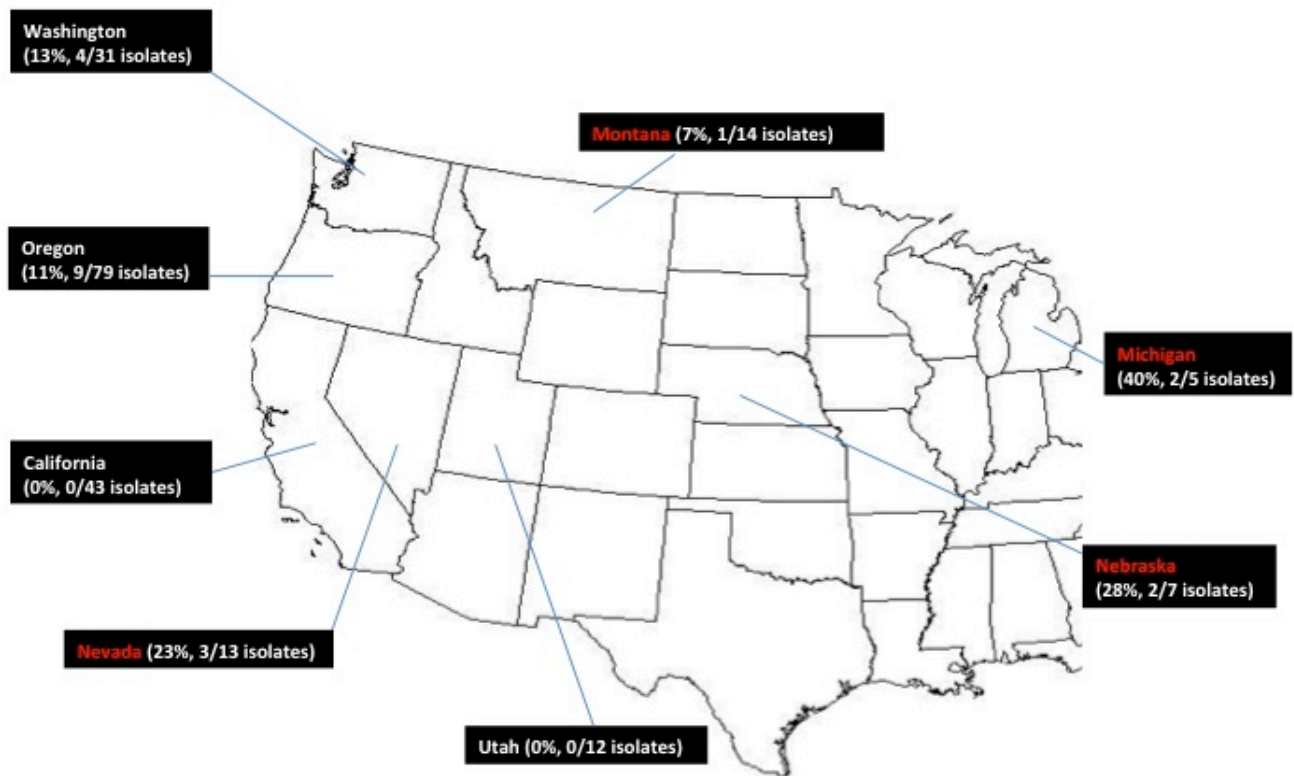


Figure 2: New reports of *F. commune* in four states: Nevada, Montana, Nebraska, and Michigan, USA.



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