

Special Research Report # 128: Disease Management

Integrated Management of *Fusarium* in Florists' Crops

Molecular Identification of Fusarial Floricultural Pathogens

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BACKGROUND

A broad spectrum of *Fusarium* species is responsible for floricultural diseases, including familiar names such as *F. oxysporum*, *F. solani*, and *F. avenaceum*. Unfortunately, *Fusarium* species are notoriously difficult to identify, hindered by a lack of clear morphological traits, and conflicting and problematic taxonomic systems. But fortunately, in recent years extensive DNA sequence based phylogenetic studies have generated a wealth of data that allow us connect floricultural pathogens with clearly defined species based on their evolutionary histories. These studies have revealed that “species” such as *F. oxysporum* and *F. solani* comprise dozens of independent lineages, many

of which are themselves best considered species, and also to the discovery of new species associated with floricultural diseases (e.g., *F. hostae*, *F. begoniae*, *F. foetens*).

Our objectives were to use DNA sequence characters to identify important fusarial pathogens of lisianthus (Fig. 1) and connect the pathogens to the already known spectrum of species and isolates from other hosts and the environment.

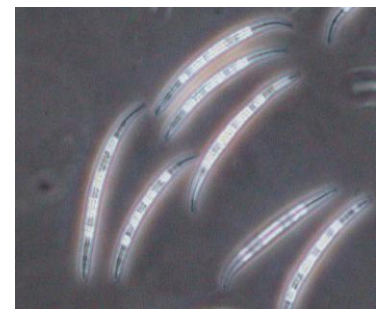


**Fig. 1 –
Fusarium stem rot of
lisianthus**

MATERIALS AND METHODS

A total of 34 *F. avenaceum* isolates were analyzed in this study (Fig. 2). Fifteen *F. avenaceum* from diseased lisianthus plants collected in Florida, California, and Connecticut, and 19 *F.*

avenaceum chosen from the Fusarium Research Center (FRC) culture collection to represent a wide host and geographic diversity. 33 *F. oxysporum* isolates (11 from Ecuador, and 22 from Florida) were analyzed.



**Fig. 2 - Spores of *Fusarium
avenaceum***

DNA was extracted and sequence data from multiple loci (including translation elongation factor 1-alpha (TEF), the nuclear ribosomal internal transcribed spacers (ITS), intergeneric spacer (IGS) and large subunit (LSU) genes, and beta-tubulin (BT)) were generated and added to alignments of sequences from other hosts and sources. These alignments inform us as to whether or not isolates from lisianthus are closely related to each other and, thus, indicate a specific pathogenic group (Fig. 3).

Lisianthus pathogens:

All isolates were also tested for pathogenicity in the greenhouse (Fig. 4). Spore inoculum was produced by growing the cultures on carnation leaf agar plates for 10 days under cool white light at 20 C night/ 25 C day temperature. Spores were washed from the plates with distilled water and spore concentration adjusted to 10^6 spores/ml. Twenty ml of inoculum were poured around the base of the seedlings. Four seedlings per isolate were inoculated and border cells on both sides of inoculated plants were left untreated. Control plants were treated with distilled water.



Fig. 4 Pathogenicity test showing healthy lisianthus plants on either side of plant inoculated with a virulent isolate of *F. avenaceum*.

RESULTS AND CONCLUSIONS

Lisianthus is susceptible both to wilt disease caused by *F. oxysporum* and crown and stem rot caused by *F. avenaceum*. *F. oxysporum* isolates from lisianthus were found to represent at least five different groups within the diversity of this complex, and showed similarity to isolates from a wide variety of hosts and from the environment. It is a common phenomenon in *F. oxysporum* that isolates pathogenic on a particular host have multiple evolutionary origins. *F. avenaceum* isolates from lisianthus were found to represent multiple genotypes scattered among isolates of *F. avenaceum* from other hosts and soil. This strongly suggested that the lisianthus pathogens did not represent unique types, but instead that lisianthus crown and stem rot could be caused by any *F. avenaceum* isolate.

Similarly, a wide spectrum of *F. oxysporum* isolates can be expected to be capable of causing disease on lisianthus. Pathogenicity tests confirmed that *F. avenaceum* isolates from other hosts could cause the disease.

IMPACT TO THE INDUSTRY

Given that any isolate of *F. avenaceum* may have the ability to infect and cause disease on lisianthus, growers must guard against sporadic outbreaks in their operation. Our findings suggest that if conditions are suitable, opportunistic isolates of *F. avenaceum* from alternate hosts may also lead to epidemics. An integrated approach to disease management including frequent scouting, weed management, sanitation of containers and production surfaces, fungus gnat control, and preventive use of fungicides will minimize the number of outbreaks. Similarly, the broad genetic spectrum of *F. oxysporum* isolates associated with disease on lisianthus suggests taking steps to avoid the establishment of *F. oxysporum* in the soil, potting materials, and irrigation systems.

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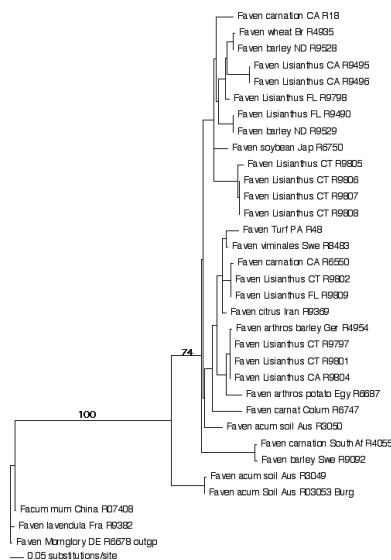


Fig. 3 Phylogenetic tree based on the IGS region showing relationships among *F. avenaceum* isolates from Lisianthus and other hosts/substrates. Note that isolates from Lisianthus do not form a single cohesive group.