Movement and Structure of Atmospheric Population of *Fusarium*

Binbin Lin

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David G. Schmale III, Chair
Shane D. Ross, Co-Chair
Antonius B. Baudoin
Boris A.Vinatzer

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ABSTRACT

Fusarium is one of the most important genera of fungi on earth. Many species of *Fusarium* are well-suited for atmospheric dispersal, yet little is known about their aerobiology. Previous research has shown that large-scale features known as atmospheric transport barriers (Lagrangian coherent structures) guide the transport and mixing of atmospheric populations of *Fusarium*. The overall goal of this work is to expand our knowledge on the movement and structure of atmospheric populations of *Fusarium*. The first objective was to monitor changes in colony forming units (CFUs) in atmospheric populations of *Fusarium* over small time intervals (10 min to several hours). We hypothesized that consecutive collections of *Fusarium* with unmanned aerial vehicles (UAVs) demonstrate small variations in colony counts. To test this hypothesis, sampling devices on UAVs were separated into two groups, four inner sampling devices opened during the first 10 minutes and four outer sampling devices opened during the second 10 minutes. Results indicated that (1) consecutive collections of *Fusarium* at 100 m demonstrated small variations in counts and (2) the similarity between collections decreased as the time between sampling intervals increased. The second objective was to determine the structure of atmospheric populations of *Fusarium* species and relate this to potential source regions. We hypothesized that diverse atmospheric populations of *Fusarium* are associated with multiple source regions. To test this hypothesis, *Fusarium* samples were collected with UAVs and identified to the level of species by sequencing a portion of the translation elongation factor 1-alpha gene (TEF-1α). Potential source regions were identified using the atmospheric transport model HYSPLIT. Results indicated that (1) diverse atmospheric populations of *Fusarium* appeared to be associated with multiple source regions, and (2) the number of *Fusarium* species collected with UAVs increased with back-trajectory distance of the sampled air. The third objective was to examine the associations between concentrations of populations of *Fusarium* at ground level (1 m) and in the lower atmosphere (100 m). We hypothesized that concentrations of *Fusarium* in the atmosphere vary between 1m and 100m. To test this hypothesis, *Fusarium* was collected with a Burkard volumetric sampler (BVS) and UAVs. Colony counts were converted to spore concentrations (spores per cubic meter of air). Sampling efficiency was used to correct spore concentrations. Results indicated that (1) the distribution of spore concentrations was similar for both samplers over different times of the day, (2) spore concentrations were generally higher in the fall, spring, and summer, and lower in the winter, and (3) spore concentrations were generally higher with BVS samplers than those with UAVs for both hourly and seasonal data. The fourth objective was to assess the ability of strains of *Fusarium* collected in the lower atmosphere to cause plant disease. We hypothesized that certain isolates of *Fusarium* collected with UAVs cause plant diseases. To test this hypothesis, we randomly selected isolates of three different species (*F. circinatum, F. avenaceum, and F. sporotrichioides*) of *Fusarium* collected with UAVs to inoculate three different hosts (wheat, corn, and pine). Known *Fusarium* strains were obtained from J. Leslie at Kansas State University as controls. Results indicated showed that the three different isolates tested were able to cause plant diseases in three different hosts (wheat, corn, and pine), confirming that these were potential agents of disease. This work sets the stage for future work examining potential source regions, transport distances, and seasonal patterns of *Fusarium*. An increased understanding of the dynamics and population structure of plant pathogenic *Fusarium* in the lower atmosphere is essential for predicting the spread of plant disease and optimizing disease management strategies in the future.

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Attributions

Several colleagues have assisted with the completion of the research in chapters of this dissertation. The following is a brief description of their contributions.

David Schmale, Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA

Dr. Schmale served as the major adviser and provided funding and guidance during the implementation and completion of the research project and dissertation. He is listed as co-author of publications represented in Chapters 2, 3, and 4.

Shane Ross, Department of Engineering Science and Mechanics, Virginia Tech, Blacksburg, VA

Dr. Ross served as the co-adviser and provided funding and guidance during the implementation and completion of the research project and dissertation. He is listed as co-author of publications represented in Chapters 2, 3, and 4.

John G. Jelesko, Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA

Dr. Jelesko was co-author of the publication represented by Chapters 3. He provide phylogenetic methods to analyze the population structure of *Fusarium.*

Amir Bozorgmagham, Department of Engineering Science and Mechanics, Virginia Tech, Blacksburg, VA

Amir Bozorgmagham is a graduate student in Dr. Ross lab. He was listed as co-author of publications represented in Chapters 2 and 3. He provided HYSPLIT models and turbulence information for calculating potential source regions.

Aaron J. Prussin II, Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA

Aaron J. Prussin is a graduate student in Dr. Schmale lab. He was listed as co-author of the publication represented in Chapter 4. He provided sampling efficiency calculations to correct spore concentrations.

CHAPTER 1

Introduction

Members of the genus *Fusarium* are some of the most important fungi on earth that not only cause plant diseases, but may also produce toxins that can threaten the health of both humans and domestic animals (Berek et al., 2001; Leslie, 2006; McMullen et al., 1997). The genus *Fusarium* is cosmopolitan and contains at least 80 biological species, with at least 100 or more proposed phylogenetic species (Leslie and Summerell, 2006; O'Donnell, 1996). These species may cause very different symptoms on different plants and under various environmental conditions, such as rot (Wang and Jeffers, 2000), cankers (Schmale and Gordon, 2003), blights (Schmale and Bergstrom, 2003), and wilts (Chaimovitsh et al., 2006). Certain species are capable of producing dangerous mycotoxins (Bush et al., 2004; Ichinoe et al., 1983; McMullen et al., 1997). Others may be saprophytes that live on dead plant tissues (Dill-Macky and Jones, 2000).

Aerobiology is the study of factors and processes that influence the movement of biota in the atmosphere and involves liberation from inoculum sources, horizontal transport, and deposition (Isard and Gage, 2001). Biotas have adapted to move long distances in the atmosphere by taking advantage of aerial transport. Atmospheric movement may result in invasion of new sites, utilization of new resources, and gene transfer among populations (Rabb, 1985). It can also result in the introduction of a disease to a region or continent or the frequent re-introduction of a pathogen to a region (Aylor, 1986).

The aerobiology of the genus *Fusarium* is poorly understood. First, identification of *Fusarium* based on *Fusarium* selective medium (FSM) and microscopic examination from airborne samples is difficult due to the presence of other fungi with similar conidial morphologies. Second, knowledge of the microclimate factors influencing spore release and dispersal is limited. Third, knowledge of the long distance transport of *Fusarium* is limited. Fourth, little is known about how *Fusarium* populations are structured in the atmosphere and variations due to weather patterns. Fifth, technologies for tracking the movement of *Fusarium* in the atmosphere are limited. Finally, knowledge of potential inoculum sources and/or potential source regions of *Fusarium* are also limited.

There are a number of different ways to identify unknown isolates of *Fusarium* to the level of species. First, isolates of *Fusarium* may be identified using morphological species concepts, in which species delimitation is based in part on the morphology of asexual and sexual spores produced on standard culture medium (Leslie et al., 2001). Second, unknown isolates of *Fusarium* may be identified by biological species concepts, in which species delimitation is based on reproductive assays that can define mating populations, such as within the *F. fujikuroi* population (Kerényi et al., 1999). Third, unknown isolates of *Fusarium* may be identified to species using phylogenetic species concepts, based largely on DNA sequence identity and similarity (Geiser et al., 2004; Nirenberg and O'Donnell, 1998). This last approach has gained considerable traction in recent years, as most modern labs generate and analyze DNA sequence data on a regular basis. These techniques leverage DNA sequence analyses of a portion of the translation elongation factor 1-alpha gene (TEF-1α), which has high phylogenetic utility because sequence variation at this locus can distinguish between in *Fusarium* species and universal primers that work across the *Fusarium* genus (Geiser et al., 2004).

Many species of *Fusarium* are well-suited for atmospheric dispersal (Fernando et al., 2000; Katan et al., 1997; Maldonado-Ramirez et al., 2005; Schmale et al., 2005). The dispersal of *Fusarium* in the atmosphere is complex and the transport processes (release, horizontal transport, and deposition) take place in different boundary layers (Isard and Gage, 2001; Isard et al., 2005). The boundary layers associated with the atmospheric transport processes are the surface boundary layer (SBL) (1-50 m) and the planetary boundary layer (PBL) (~50-1,000 m) (Isard and Gage, 2001).

Liberation occurs primarily in the SBL and is critical for *Fusarium* to colonize new habitats. Once spores have escaped into the turbulent layers of the atmosphere (Isard and Gage, 2001), spores can move throughout the crop canopy or escape into the lower atmosphere for long distance transport. Drift includes long range transport of *Fusarium* spores in the PBL in which the turbulence tends to be homogeneous over horizontal distances (Maldonado-Ramirez et al., 2005; Zdunkowski and Bott, 2003). Vertical mixing occurs in the PBL when the sun heats the surface of the earth, warming the air in contact with the surface. Warm air then rises carrying spores from near the surface upward. Cooler air replaces the rising warm air to be subsequently warmed in contact with the earth's surface. Solar radiation and moderate wind speeds increase daytime convection while night-time cooling of surface air inhibits convection in the atmosphere (Sparks et al., 1985). Because of turbulence, the SBL contains very strong vertical gradients in wind speed, temperature and humidity (Isard and Gage, 2001). Deposition occurs in the SBL when turbulence in the atmosphere slows down. At night, an inversion layer, with little to no wind, allows spores to remain above a crop canopy preventing escape and allowing spores to settle (Oke, 1992).

Other factors to consider regarding the variations observed among samples are that samples at different times correspond to air coming from different locations across different seasons (Doohan et al., 2003). There are different environmental factors during different seasons of the year. Seasonal changes, such as temperature, rainfall, humidity, ultraviolet (UV) light, and wind speed and direction, are thought to play an important role in spore release, survival, and dispersal (Jones and Harrison, 2004; Lyon et al., 1984). When conditions are warm and humid with strong turbulence and complete cloud cover (no sunlight), which are favorable for spore release, survival, and dispersal, the diseases caused by *Fusarium* can develop rapidly on either local (within the same field) or susceptible crops at some distance (Dill-Macky and Jones, 2000; Schmale et al., 2005). Therefore, the whole aerobiological process of the movement and structure of *Fusarium* may be influenced by various ecological and environmental factors.

Population genetic analyses may be used to develop predictions about potential sources of fungal populations (Bennett et al., 2005), and may contribute to developing strategies for disease management and control (Bissegger et al., 1997). To date, population genetic analyses have been applied to only a few species of *Fusarium*. High levels of genetic diversity have been reported for *F. graminearum* (*G. zeae*) (Astolfi et al., 2012; Gale et al., 2007; Lee et al., 2010; Schmale et al., 2006; Talas et al., 2011; Zeller et al., 2004), *F. pseudograminearum* (Bentley et al., 2008), *F. verticillioides* (Reynoso et al., 2009), *F. solani* (Mohammadi and Mofrad, 2009), *F. circinatum* (Wikler and Gordon, 2000) and *F. oxysporum* (Bayraktar, 2010), but little is known about the population structure of other species of *Fusarium*, particularly for species that may be transported over long distances through the atmosphere.

It is very important to have appropriate methods for studying the aerobiology of these fungi. Members of the Schmale Lab have developed technologies with autonomous unmanned aerial vehicles (UAVs) to track the movement and structure of populations of *Fusarium* in the lower atmosphere (Schmale et al., 2008; Tallapragada et al., 2011). The UAVs were equipped with microbe-sampling devices that contained Petri plates with *Fusarium* selective medium on the wings. The UAVs flew defined sampling altitudes (100 m above ground level), sampling speeds (90km/h) and sampling patterns (circle). The sampling devices were opened and closed by remote control from the ground once the UAV reached the target altitude of 100 m and then exposed to the atmosphere for durations of 10-20 min.

Previous work has shown that atmospheric populations of *Fusarium* in the lower atmosphere are influenced by large-scale atmospheric features known as Lagrangian coherent structures (LCSs) that may serve as atmospheric transport barriers (ATBs) (Schmale et al., 2012; Tallapragada et al., 2011). In these studies, LCSs/ATBs were associated with punctuated changes in colony forming units (CFUs) of *Fusarium* recovered from a series of collections with UAVs. Though these studies observed fluctuations in CFUs of *Fusarium* across varying temporal scales, they did not address the identity (i.e., species diversity), structure, composition and potential origin of atmospheric populations of *Fusarium*.

The overall goal of this work is to expand our knowledge on the movement and structure of atmospheric populations of *Fusarium,* leading to the hypotheses that: (i) consecutive collections of *Fusarium* with UAVs demonstrate small variations in colony counts, (ii) diverse atmospheric populations of *Fusarium* are associated with multiple source regions, (iii) spore concentrations of *Fusarium* in the atmosphere vary between 1m and 100m, and (iv) certain isolates of *Fusarium* collected with UAVs cause plant diseases.

Knowledge of a better understanding of the movement and structure of atmospheric populations of *Fusarium* in the lower atmosphere may help forecast plant disease epidemics and optimize disease measurement and control in the future (Aylor, 2003). Successful integrated pest management strategies depend upon an accurate evaluation of atmospheric sources of inoculum (Aylor, 1999). The aerobiology of *Fusarium* contributes to the overall knowledge of pathogen transport in the atmosphere.

Research Objectives

1. Monitor changes in colony forming units (CFUs) in atmospheric populations of *Fusarium* over small time intervals (10 minutes to several hours),

2. Determine the structure of atmospheric populations of *Fusarium* species and relate this to potential source regions,

3. Examine associations between the concentrations of population of *Fusarium* at ground level (1m) and in the lower atmosphere (100m),

4. Assess the ability of strains of *Fusarium* collected with UAVs to cause plant diseases.

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CHAPTER 2

Small fluctuations in the recovery of fusaria across consecutive sampling intervals with unmanned aircraft 100 m above ground level

Binbin Lin[1], Amir E. BozorgMagham[2], Shane Ross[2], David G. Schmale III[1*].

[1]Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA;

[2]Department of Engineering Science and Mechanics, Virginia Tech, Blacksburg, VA;

*Corresponding author: David G. Schmale III

Email: dschmale@vt.edu;

Phone: (540) 231-6943;

Fax: (540) 231-7477

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Abstract

The aerobiology of fungi in the genus *Fusarium* is poorly understood. Recent work has highlighted the role of Lagrangian coherent structures (LCSs) in the movement of fusaria in the lower atmosphere. Here, we extend this work by examining the relationship between the length of atmospheric sampling intervals with autonomous unmanned aerial vehicles (UAVs) and the recovery of fusaria. UAVs were equipped with an array of eight microbe-sampling devices with four ‘inner’ sampling arms and four ‘outer’ sampling arms. Each set of arms was used to collect consecutive aerobiological samples for periods of 10 minutes at 100 m above ground level at Kentland Farm in Blacksburg, Virginia. Fifty-one flights (102 consecutive sampling intervals) were conducted in 2010 and 2011. A correlation analysis showed that counts of fusaria did not vary between the inner and outer sampling arms from consecutive sampling periods of 10 min ($r = 0.93$, $P < 0.001$), and the frequency of colony counts had similar distributions for samples from the inner and outer sampling arms. An analysis of the temporal variation in collections of *Fusarium* showed that the similarity between collections decreased over time. This work supports the idea that atmospheric populations of fusaria are well-mixed, and large changes in the recovery of fusaria in the lower atmosphere may be attributed to large-scale phenomena (e.g., LCSs) operating across varying temporal and spatial scales. This work may contribute to effective control measures for diseases causes by fusaria in the future.

Keywords: Fungi; Aerobiological sampling; Pathogen; Unmanned aerial vehicles; UAV; Lagrangian coherent structure; Long-distance transport; Atmospheric transport barrier; Selective medium; UAV

1 Introduction

Fusarium is one of the most important genera of fungi on Earth (Leslie and Summerell 2006). Members of this genus cause a number of devastating plant diseases, and can threaten the health of both domestic animals and humans through the production of mycotoxins (Berek et al. 2001; McMullen et al. 1997). Many fusaria are transported through the atmosphere from one habitat to another (Schmale et al. 2012; Tallapragada et al. 2011). Previous work has shown that large-scale atmospheric features known as Lagrangian coherent structures (LCSs) or atmospheric transport barriers (ATBs) are associated with the long-distance transport of *Fusarium* in the lower atmosphere (Schmale et al., 2012; Tallapragada et al., 2011). ATBs are moving boundaries that effectively separate air masses of qualitatively different dynamics and may play a significant role in the movement of microbes among habitats (Senatore and Ross, 2011). Tallapragada et al. (2011) showed that LCSs (ATBs) were associated with changes in atmospheric counts of *Fusarium*. Though the work by Tallapragada et al. (2011) was the first to demonstrate that large fluctuations in atmospheric counts of *Fusarium* could be attributed to the passage of ATBs, it was unable to account for small-timescale fluctuations that might explain natural fluctuations among collections of *Fusarium.*

Recently, members of our research team have developed technologies with autonomous unmanned aerial vehicles (UAVs) to track the movement and structure of populations of microbes such as *Fusarium* in the lower atmosphere (Schmale et al. 2008). The UAVs were equipped with microbe-sampling devices that contained a total of four Petri plates that were opened and closed by remote control from the ground once the UAV was aloft (Schmale et al. 2008). In the present study, we used a new array of sampling devices that contained a total of eight Petri plates, with four 'inner' sampling arms and four 'outer' sampling arms that were used to collect consecutive aerobiological samples for periods of 10 minutes at 100 m above ground level. This method was used to test the null hypothesis that the recovery of fusaria would not vary across consecutive (a 10 min sample on the inner arms, immediately followed by a separate 10 min sample on the outer arms) aerobiological sampling intervals with UAVs 100 m above ground level. Thus, large fluctuations in the recovery of fusaria could be attributed to a suite of factors including the passage of LCSs (ATBs) and/or the contribution of local sources, and not random fluctuations in counts of *Fusarium* that would be representative of a ‘natural’ condition. The specific objective of this study was to determine if collections of fusaria vary between the inner and outer sampling arms of a UAV from consecutive sampling periods of 10 min. This work is prerequisite for understanding if changes in the recovery of fusaria in the lower atmosphere may be attributed to large-scale phenomena (e.g., LCSs) operating across varying temporal and spatial scales and may contribute to effective control measures for diseases causes by fusaria in the future.

2 Materials and methods

2.1 Autonomous unmanned aerial vehicles (UAVs) for sampling

Autonomous (self-controlling) UAVs were used to collect *Fusarium* from the atmosphere above Virginia Tech’s Kentland Farm in Blacksburg, VA, USA. The UAVs consisted of a Sig Rascal© airframe equipped with an autopilot computer and a suite of onboard telemetry devices (Schmale et al. 2008) and were programmed to fly a circular sampling pattern at a target altitude of 100 m above ground level and a nearly constant speed of 90km/h. Each UAV carried eight collection plates containing a *Fusarium* selective medium on the wings. The eight sampling plates were separated into ‘inner’ and ‘outer’ sampling arms (**Fig. 1**). For consecutive sampling flights, a 10 min sample was collected using the inner arms (4 plates were exposed during this sampling interval), immediately followed by a separate 10 min sample using the outer arms (4 plates exposed were exposed during this sampling interval) (**Fig. 1**). Sampling flights were also conducted with the inner and outer sampling devices open at the same time (8 plates exposed during the sampling interval).

2.2 Culturing and identification of *Fusarium*

A Fusarium selective medium (FSM) (Schmale et al. 2006) was used to bias our atmospheric collections for fungi in the genus *Fusarium*. Immediately following a sampling flight, the exposed plates were removed from the UAV and placed in small plastic containers for transport to the laboratory. The plates were incubated for 5 to 7 days at room temperature to allow white, fuzzy colonies of *Fusarium* to develop. Colonies of *Fusarium* were counted and subcultured to plates of ¼-strength potato dextrose agar (PDA) medium for further identification.

2.3 Statistical analyses.

We hypothesized that the recovery of fusaria would typically not vary significantly across consecutive aerobiological sampling intervals of short duration (a 10-min sample on the inner arms, immediately followed by a separate 10-min sample on the outer arms). If we fail to reject this hypothesis, then large fluctuations in the recovery of fusaria over short to intermediate timescales could be attributed to a suite of factors, such as the passage of LCSs (ATBs) and/or the contribution of a strong local source. By 'short' timescale, we mean short compared with the Lagrangian timescale, discussed below. It is also important to note that since the atmosphere is moving, short timescales are also related to short spatial scales. To test our hypothesis, colony counts of *Fusarium* obtained from different flights were assembled to perform statistical analyses (**Tables 1 and 2**). For flights with simultaneous inner and outer arm sampling (**Table 1**), we estimated the variability in sampled colony counts of *Fusarium*, yielding an estimate of error for colony counts. For flights with consecutive inner and outer arm sampling (plates exposed during consecutive sampling periods of 10 minutes) (**Table 2**), a simple linear regression was used to determine the relationship between colony counts of *Fusarium* collected for the inner and outer sampling arms. A scatter plot and a frequency plot were also used to show this relationship. Statistical analyses were performed using JMP 4.0. The correlation between colony counts from the inner and outer sampling arms was also explored as a function of time lag between sampling intervals (i.e., comparisons of colony counts between consecutive flights separated by 10 minutes, and between other flights separated by longer periods throughout a sampling day).

3 Results

3.1 Simultaneous sampling with eight plates

In order to compare samples collected from inner and outer arms during *different* time periods, it is essential to show that samples do not vary significantly between inner and outer arms during the *same* time period. In other words, we must examine the potential role (if any) that plate position on the UAV has on the recovery of fusaria. To do this, we conducted 21 simultaneous sampling flights in which all eight sampling devices (inner and outer sampling arms opened at the same time) were exposed during the same sampling interval (**Table 1**). For these 21 flights, 433 colonies were recovered across all 21 sampling intervals; 234 colonies were collected across the inner arms, and 199 colonies were collected across the outer arms.

Results of our correlation analysis for this sampling method showed that counts from the plates on the inner arms were positively correlated with counts from plates on the outer arms (r = 0.89, $P < 0.001$, n = 21). Thus, the location of the plates (inner versus outer sampling arms) did not impact the collection of fusaria.

We also used samples from this method to estimate the variation in colony counts for the inner and outer sampling arms. Considering only the 15-minute samples of **Table 1**, we calculated the total colony count, c, and the magnitude of the difference between the inner and outer plates, which is the variation in colony counts, δc. In **Fig. 2**, we plot the fractional variation, $\delta c/c$, versus c, and notice a trend. The curve corresponds to $1/\sqrt{c}$, the fractional standard deviation for a Poisson distribution. Thus, the probability of a viable airborne *Fusarium* spore impacting the samplers is well approximated as an inhomogenous Poisson process with an arrival rate varying on a timescale long compared to the sampling duration. Thus, when a colony count, c, is obtained, the margin of error can be approximated as $\pm\sqrt{c}$.

3.2 Consecutive sampling with four inner plates and four outer plates

To determine if collections of fusaria varied between consecutive sampling periods of 10 min, we conducted 102 consecutive sampling intervals (51 flights) 100 m above ground level in 2010 and 2011 (**Table 2**). Five hundred and ninety two colonies were recovered across all 102 sampling intervals; 275 colonies were collected across the inner arms, and 312 colonies were collected across the outer arms (excluding flights F207 and F208, which were clear outliers in the dataset). A significant positive correlation was observed for colony counts of *Fusarium* between the inner plates and the outer plates (r = 0.93, $P < 0.001$, n = 98). Scatter plots and a simple linear regression of consecutive sampling intervals are shown in **Fig. 3.** Two flights however, F207 and F208 (**Table 2**), were excluded from the scatter plot, since these flights were considered outliers and are the subject of additional discussion below. It should still be noted, however, that when these flights were included in the correlation analysis, a significant positive correlation was still observed (r = 0.38, $P < 0.01$, n = 102). A frequency plot showed that the distribution of colony counts was similar for the inner and outer sampling arms over the range of colony counts (**Fig. 4**).

The correlation between colony counts from the inner and outer sampling arms was also explored as a function of time lag, τ, between sampling intervals. This approach allowed us to examine the temporal variation of colony counts. From **Table 2** (excluding F207 and F208), pairwise comparisons of colony counts were determined for five time intervals: 0.17 h (n = 49 pairs), 0.5 h to 1.5 h (n = 83 pairs), 1.5 h to 3 h (n = 94 pairs), 3 h to 6 h (n = 84 pairs), and 6 h to 9 h (n = 16 pairs). An autocorrelation coefficient was determined as follows (autocorrelation coefficient for zero time-lag is defined as 1):

$$R(\tau) = \frac{E\left[(c_t - \mu)(c_{t+\tau} - \mu)\right]}{\sigma^2}$$

where c_t is the colony count at time t, $c_{t+\tau}$ is the colony count at time $t+\tau$, μ represents the mean value, σ represents the standard deviation of the colony counts, and $E[\bullet]$ represents expectation value. The results of this analysis are shown in **Fig. 5**; the similarity between collections of *Fusarium* decreases over time. Error bars were calculated using results from section 3.1 with the assumption that colony counts are Poisson distributed. A Gaussian distribution weighted method was used to obtain the error bars with sufficient number of simulations converging to a constant limit.

3.3 Anomalous punctuated changes in colony counts for two consecutive flights.

In flights F207 and F208, we observed a significant departure from the usual 10-minute time-lag correlation. Flight 207 started sampling at 12:00 PM on 25 October, 2011. Eighty colonies were recovered from the inner arms, but only 31 colonies were recovered from the outer arms. Flight 208 started sampling at 1:16 PM on the same day. Twelve colonies were recovered from the inner arms, but 120 colonies were recovered from the outer arms. The inner and outer samples from these flights were not correlated, and cannot be explained by the statistics of a slowly varying inhomogeneous Poisson process. We view these two flights as anomalies that are in need of further explanation. We hypothesized that an ATB could have contributed to the observed changes in colony counts (e.g., Tallapragada et al. 2011), but archived weather-based computations did not reveal the presence of any strong LCSs (data not shown). Furthermore, HYSPLIT back trajectories for these samples suggested that all of these samples originated from a similar location in West Virginia (within the scale of accuracy of the computations, on the order of 10-100km) (Fig. 6).

4 Discussion

Recent work has highlighted the role of Lagrangian coherent structures (LCSs) in the movement of fusaria in the lower atmosphere (Schmale et al. 2012; Tallapragada et al. 2011). Here, we extend this work by examining the relationship between the length of atmospheric sampling intervals with autonomous unmanned aerial vehicles (UAVs) and the recovery of fusaria. UAVs were equipped with an array of eight microbe-sampling devices with four ‘inner’ sampling arms and four ‘outer’ sampling arms. Each set of arms was used to collect consecutive aerobiological samples for periods of 10 minutes at 100 m above ground level at Kentland Farm in Blacksburg, Virginia. A total of 102 consecutive sampling intervals (51 flights) was conducted in 2010 and 2011. Results showed that counts of fusaria did not vary across consecutive aerobiological sampling intervals. This work supports the idea that atmospheric populations of fusaria are well-mixed, and large changes in the recovery of fusaria in the lower atmosphere may be attributed to large-scale phenomena (e.g., LCSs) operating across varying temporal and spatial scales.

Counts of *Fusarium* were not significantly different between plates located on inner and outer sampling arms in which all eight sampling devices were exposed during the same sampling interval. Thus, collections of *Fusarium* with UAVs were not influenced by the position of the plates. Random collections of *Fusarium* across all of the sampling surfaces is consistent with the idea that atmospheric populations of *Fusarium* are well-mixed (Schmale et al. 2006). The fractional variation in colony counts revealed that the statistical distribution of colony counts across the inner and outer sampling arms is well approximated by a slowly varying inhomogeneous Poisson process. Colony counts from consecutive sampling intervals separated by 10 minutes did not vary significantly, but the correlation drops to nearly zero for flights separated by 9 hours. The Lagrangian (autocorrelation) timescale,

$$T_L = \int_0^\infty R(\tau) d\tau,$$

is approximately 3 hours, which is on the order (~10,000s) estimated for velocity autocorrelations in atmospheric turbulence (Gifford 1987), and is also the Lagrangian timescale for layer (stratus) clouds. The time T_L provides the timescale for the variation of the arrival rate for the slowly varying inhomogeneous Poisson process assumption, and we note that this is indeed long compared with the sampling duration (10 minutes), further justifying the Poisson assumption. For purely stochastic motion, the autocorrelation is an exponential, $R(\tau) = \exp(-\tau / T_L)$ (Csanady 1973; Dosio et al. 2005). With horizontal winds on the scale of 2-

10 m/s, this timescale suggests that there are coherent ‘clouds’ of *Fusarium* with horizontal dimensions on the scale of 20-100 km. This idea is consistent with the observations of Tallapragada et al. (2011) based on mesoscale atmospheric simulations, who found that the typical size for a coherent air mass was on a similar scale (50-150 km), based on the average passage of an LCS over the sampling location every 5 to 7 hours.

Tallapragada et al. (2011) showed that LCSs (atmospheric transport barriers or ATBs) were correlated with changes in atmospheric counts of *Fusarium*. Schmale et al. (2012) suggested that LCSs were likely to influence the population structure of *F. graminearum*. With the exception of flights 207 and 208, we did not observe any significant variation in colony counts among consecutive sampling flights. Thus, we are now able to exclude fluctuations over short periods of time as potential contributors to changes in the atmospheric counts of *Fusarium*. Thus, large changes in populations of *Fusarium* in the lower atmosphere may be attributed in part to large-scale phenomena (such as LCSs) or strong local sources operating across varying temporal and spatial scales.

The inner and outer samples from flights F207 and F208 were not correlated, and represented a significant departure from the usual 10-minute time-lag correlation. Archived weather-based computations did not reveal the presence of any strong LCSs, and HYSPLIT back trajectories for these samples suggested that they both originated from a similar same location in West Virginia (Fig. 6). Less than 90 minutes separated the start of F207 and the end of F208, but there was significant variation over a timescale of 10 minutes during both flights. This suggests a patchy (heterogeneous) distribution of *Fusarium* in the atmosphere (Okubo and Levin 2001). With the horizontal wind speeds at that time being approximately 2 m/s at ground level, the patchiness spatial scale was at most 1 km over a cloud on the order of 10-20 km (bracketed by the more typical flights F206 and F209). It is possible that these high values were triggered by a local, and possibly temporally non-uniform, source. Future work aimed at identifying the species recovered in these flight populations may provide clues about the approximate origin and mixing of these populations.

Future work by our research team aims to examine meteorological events that might provide signatures for the life history of populations of *Fusarium* in the lower atmosphere. Such work may contribute to an increased understanding of the spread of plant diseases in the future (Aylor 2003).

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Table 1. Colony counts of *Fusarium* from simultaneous sampling (inner arms and outer arms were opened at the same time) with UAVs 100 m above ground level at Virginia Tech's Kentland Farm.

Flights	Date	Time Open (In & out)	Time Closed (In & out)	Counts In [a]	Counts Out [b]	Time Sampling (min)
F137	10-Mar-10	0929	0944	3	1	15
F138	10-Mar-10	1035	1042	1	8	7
F139	10-Mar-10	1130	1145	7	4	15
F140	10-Mar-10	1300	1315	5	2	15
F141	10-Mar-10	1400	1415	4	9	15
F142	11-Mar-10	1005	1020	3	3	15
F143	15-Jul-10	0950	1005	23	16	15
F144	15-Jul-10	1155	1210	35	37	15
F145	16-Jul-10	0925	0940	20	26	15
F146	16-Jul-10	1045	1100	27	23	15
F147	28-Sep-10	0959	1014	2	3	15
F148	28-Sep-10	1118	1133	6	2	15
F149	28-Sep-10	1412	1427	17	8	15
F150	28-Sep-10	1532	1540	9	6	8
F151	29-Sep-10	0915	0926	3	7	11
F152	29-Sep-10	1029	1044	4	1	15
F153	29-Sep-10	1323	1338	7	6	15
F154	01-Oct-10	0908	0923	8	3	15
F155	01-Oct-10	1203	1218	9	8	15
F156	01-Oct-10	1428	1443	31	20	15
F157	01-Oct-10	1700	1708	10	6	8

a Counts from plates on the inner sampling arms of the UAV

b Counts from plates on the outer sampling arms of the UAV

Table 2. Colony counts of *Fusarium* from consecutive (a 10 min sample on the inner arms, immediately followed by a separate 10 min sample on the outer arms) aerobiological sampling intervals with UAVs 100 m above ground level at Virginia Tech's Kentland Farm in 2010 and 2011.

Flights	Date	Open (In)	Closed (In)	Open (Out)	Closed (Out)	Counts In [a]	Counts Out [b]	Time Sampling Out (min)	Time Sampling In (min)
F158	06-Apr-11	0913	0923	0923	0933	6	10	10	10
F159	06-Apr-11	1027	1037	1037	1046	14	12	10	9
F160	06-Apr-11	1557	1607	1607	1616	18	26	10	9
F161	07-Apr-11	0952	1002	1002	1012	27	33	10	10
F162	07-Apr-11	1344	1354	1354	1404	16	13	10	10
F163	07-Apr-11	1514	1524	1524	1534	15	11	10	10
F164	07-Apr-11	1611	1621	1621	16:31	9	13	10	10
F167	08-Apr-11	1407	1422	1422	1435	5	9	15	13
F168	08-Apr-11	1510	1520	1520	1530	4	5	10	10
F169	11-Apr-11	0952	1002	1002	1012	22	21	10	10
F171	16-May-11	1449	1459	1459	1509	7	7	10	10
F173	18-May-11	1426	1436	1436	1446	2	1	10	10
F174	18-May-11	1600	1610	1610	1620	4	2	10	10
F175	19-May-11	0943	0953	0953	1003	4	5	10	10
F176	19-May-11	1045	1055	1055	1105	2	3	10	10
F177	19-May-11	1152	1202	1202	1212	1	2	10	10
F178	19-May-11	1312	1322	1322	1332	3	2	10	10
F179	19-May-11	1435	1445	1445	1455	6	3	10	10
F180	22-Aug-11	1000	1010	1010	1020	1	3	10	10
F181	22-Aug-11	1224	1234	1234	1244	3	2	10	10
F182	23-Aug-11	0942	0952	0952	1002	2	2	10	10
F183	23-Aug-11	1040	1050	1050	1100	2	2	10	10
F184	23-Aug-11	1149	1159	1159	1209	2	3	10	10
F185	23-Aug-11	1309	1319	1319	1329	4	5	10	10
F186	23-Aug-11	1424	1434	1434	1444	2	2	10	10
F187	23-Aug-11	1601	1611	1611	1621	4	5	10	10
F188	24-Aug-11	0915	0925	0925	0935	2	2	10	10
F189	24-Aug-11	1031	1041	1041	1051	4	5	10	10
F190	24-Aug-11	1159	1209	1209	1219	4	6	10	10
F191	24-Aug-11	1314	1324	1324	1334	4	5	10	10
F192	24-Aug-11	1426	1436	1436	1446	5	7	10	10
F193	25-Aug-11	0914	0924	0924	0934	1	2	10	10
F195	25-Aug-11	1200	1210	1210	1220	2	5	10	10
F197	26-Aug-11	1115	1125	1125	1135	3	2	10	10
F198	26-Aug-11	1313	1323	1323	1333	3	5	10	10
F199	26-Aug-11	1419	1429	1429	1439	7	12	10	10

F200	24-Oct-11	1018	1028	1028	1018	3	3	10	10
F201	24-Oct-11	1133	1143	1143	1153	4	5	10	10
F202	24-Oct-11	1303	1313	1313	1323	6	5	10	10
F203	24-Oct-11	1418	1428	1428	1438	5	4	10	10
F204	24-Oct-11	1530	1540	1540	1550	6	7	10	10
F205	25-Oct-11	0915	0925	0925	0935	1	2	10	10
F206	25-Oct-11	1031	1041	1041	1051	3	6	10	10
F207	25-Oct-11	1200	1210	1210	1220	80	31	10	10
F208	25-Oct-11	1316	1326	1326	1336	12	120	10	10
F210	25-Oct-11	1543	1553	1553	1603	8	6	10	10
F211	26-Oct-11	0956	1006	1006	1016	3	3	10	10
F212	26-Oct-11	1205	1215	1215	1225	1	2	10	10
F213	26-Oct-11	1316	1326	1326	1336	8	9	10	10
F214	26-Oct-11	1432	1442	1442	1452	4	4	10	10
F215	27-Oct-11	0858	0908	0908	0918	3	3	10	10

a Counts from plates on the inner sampling arms of the UAV

b Counts from plates on the outer sampling arms of the UAV

Fig. 1. An autonomous unmanned aerial vehicle (UAV) equipped with an array of eight microbe-sampling devices with four inner sampling arms and four outer sampling arms. Each arm carries two Petri plates containing a Fusarium selective medium. During takeoff and landing, the sampling devices are closed (a). After reaching the target altitude of 100 m, the inner sampling arms are opened for 10 minutes (b). These inner arms are closed, and the outer arms are opened for 10 minutes immediately following the first collection (c). Colonies of *Fusarium* are recovered in the laboratory and recorded for each of the plates (shown here from flight F189) (d).

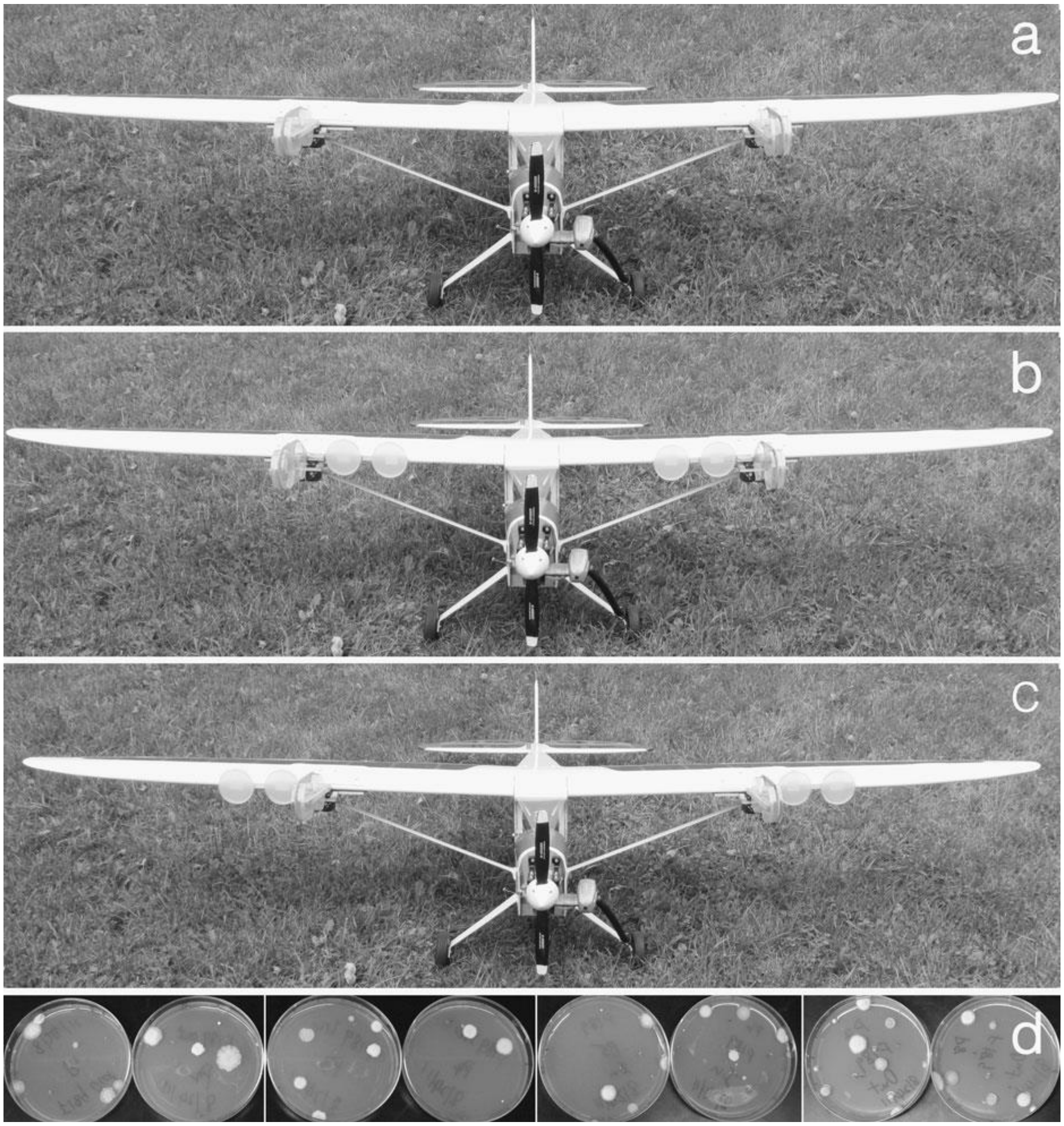


Fig. 2. Fractional variation in sampled colony counts of Fusarium (*c* is the total colony counts from inner and outer plates, and δc is the variation in colony counts) based on simultaneous sampling using inner (4 plates) and outer (4 plates) arms of a UAV during sampling periods of 15 minutes. Flights were conducted 100 m above ground level during 2010 and 2011. The probability of a viable airborne *Fusarium* spore impacting the samplers is approximated as a slowly varying inhomogenous Poisson process.

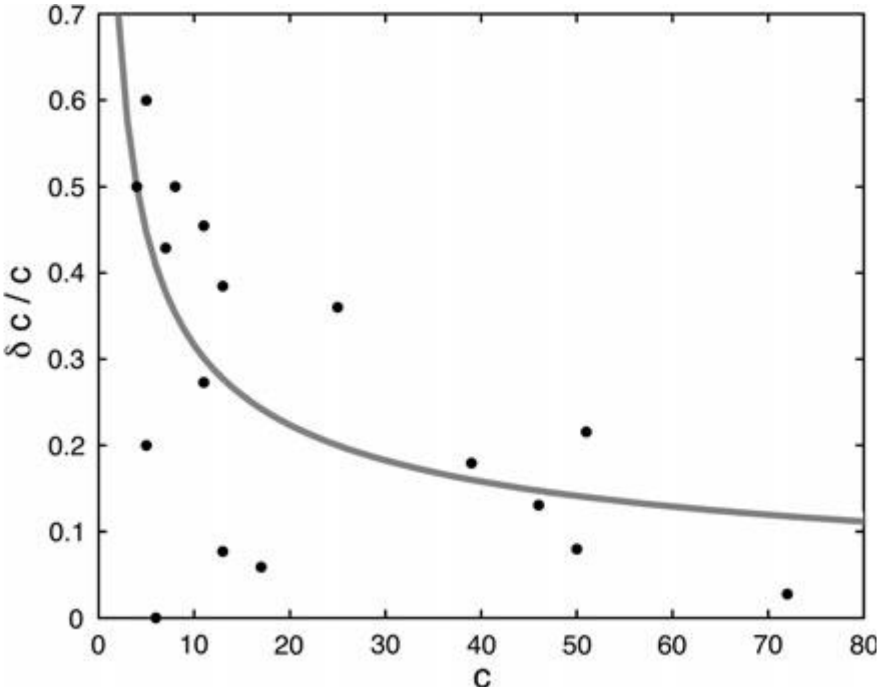


Fig. 3. Scatter plot and simple linear regression of consecutive sampling of *Fusarium* with inner (4 plates) and outer (4 plates) arms of a UAV. A significant correlation (r = 0.93, $P < 0.001$, n = 98) was observed between colony counts of *Fusarium* from the inner and outer arms. Flights were conducted 100 m above ground level during 2010 and 2011. Flights F207 and F208 were outliers and were removed from the analysis.

Fig. 4. Frequency plot of colony counts of *Fusarium* from consecutive sampling periods of 10 mins. Flights were conducted 100 m above ground level during 2010 and 2011. The plot shows that the distribution of colony counts was similar for the inner and outer sampling arms over the range of colony counts.

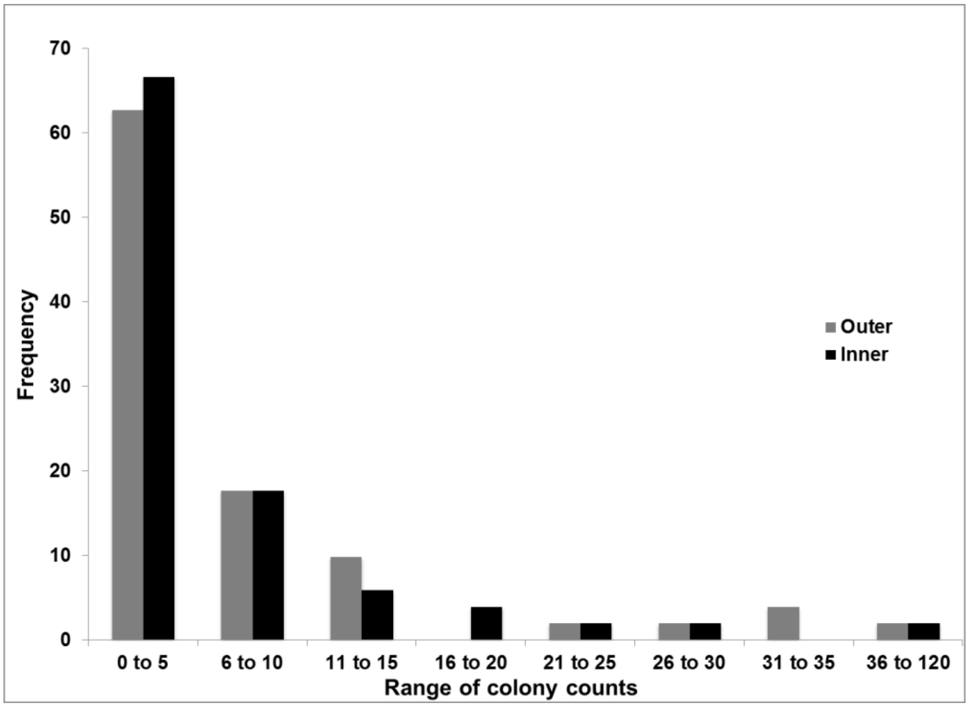


Fig. 5. The colony count autocorrelation coefficient $R(\tau)$ versus the time lag τ between sampling intervals. A high correlation is observed for a small time lag. The similarity between collections decreases over time; typical behavior for Lagrangian trajectories of particles (spores) in atmospheric turbulence.

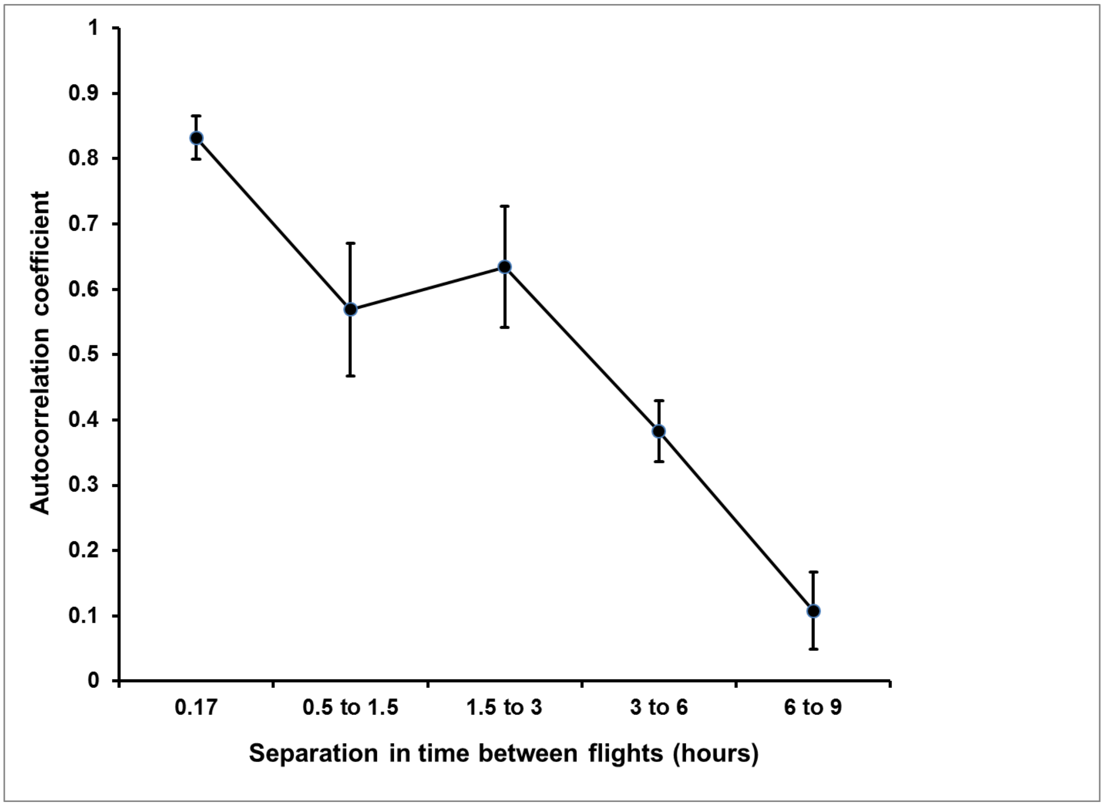
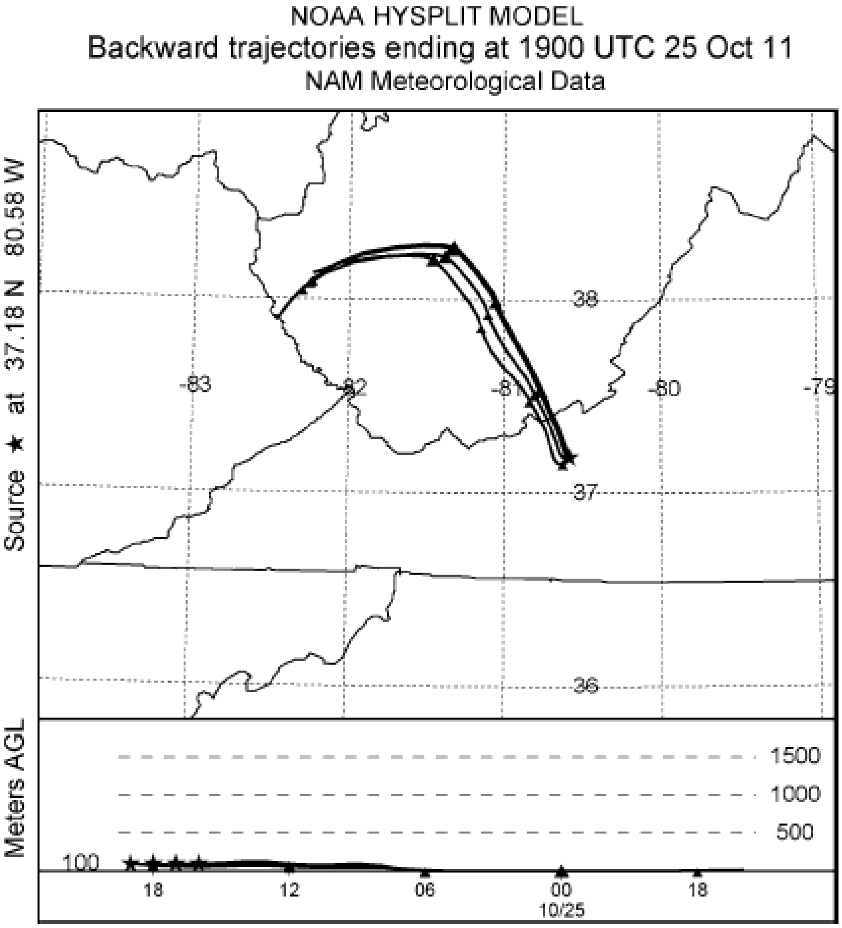


Fig. 6. HYSPLIT backward trajectories for flights 207 and 208 on based on 25 Oct 2011. Trajectories were calculated hourly for 1600-1900 UTC and suggest that trajectories suggest that all of the samples originated from a similar location in West Virginia (within the scale of accuracy of the computations, on the order of 10-100km).



CHAPTER 3

Diverse assemblages of fusaria collected with unmanned aircraft 100 m above ground level suggest contribution of multiple sources across broad geographical regions

Binbin LIN[a], Amir E. BOZORGMAGHAM[b], John G. JELESKO[a], Shane D. ROSS[b], David G. SCHMALE III[a],*.

[a]Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA 24061, USA;

[b]Department of Engineering Science and Mechanics, Virginia Tech, Blacksburg, VA 24061, USA;

*Corresponding author: David G. Schmale III
Email: dschmale@vt.edu;
Phone: (540) 231-6943;
Fax: (540) 231-7477

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ABSTRACT

Fungi in the genus *Fusarium* may be transported over long distances in the atmosphere. Little is known about the structure, composition, and potential origin of atmospheric populations of *Fusarium*. We hypothesized that (1) atmospheric populations of *Fusarium* are diverse and dynamic across large-scale temporal and spatial gradients and (2) potential sources of atmospheric populations of *Fusarium* extend across broad geographical regions. To test these hypotheses, autonomous unmanned aerial vehicles (UAVs) equipped with microbe-sampling devices were used to collect viable spores of *Fusarium* 100 m above the ground level at the Kentland Farm in Blacksburg, Virginia. One hundred and thirty five isolates of *Fusarium* were collected during 11 sampling flights on three days within a four day period in September and October, 2010. A portion of the translation elongation factor 1-alpha gene (TEF-1α) was used to assist in the identification of the *Fusarium* isolates to species. FusariumID and GenBank BLAST queries, coupled with model-based phylogenetic analyses, revealed at least 12 species of *Fusarium* in our atmospheric collections. Two of the reference *Fusarium* species together with many of the isolates collected with UAVs comprised a poorly resolved basal region of the *Fusarium* phylogeny. This poorly-resolved region may represent new species of *Fusarium*. Species richness, evenness, and diversity varied within and among our flight populations. Back trajectory analyses conducted 6 to 24 hours prior to our collections suggested the contribution of multiple sources of *Fusarium* across broad geographical regions. The actual contribution of these hypothesized source regions to the atmospheric populations of *Fusarium* remains unclear, but the diverse atmospheric populations of *Fusarium* suggest that inoculum may originate from multiple locations over large geographic distances. There was a positive correlation between trajectory distances over 24 hours and the number of species of *Fusarium* with the best fit given by a power law, analogous to the species-area relationship in ecology. This work contributes to an increased knowledge of the life history of *Fusarium* and how patterns in the species diversity depend on geographic scale.

Keywords: Fungi, Plant pathogen, Ascomycete, Genetic diversity, Inoculum source, Aerobiology, Aerobiological sampling, Unmanned aerial vehicles, UAV, Long-distance transport, Unresolved turbulence

Introduction

Fusarium is one of the most economically important genera of fungi worldwide (Leslie and Summerell 2006). Some species of *Fusarium* are important plant pathogens, causing significant crop losses and resulting mycotoxin contamination that may threaten human and domestic animal health (Berek et al. 2001; McMullen et al. 1997). The genus contains at least 80 biological species, and 100 or more proposed phylogenetic species (Leslie and Summerell 2006; O'Donnell 1996). Some of these species cause wilts, blights, root rots and cankers in agriculturally important crops worldwide (Leslie and Summerell 2006). Many species of *Fusarium* may be transported over long distances in the atmosphere from one habitat to another (Fernando et al. 2000; Katan et al. 1997; Maldonado-Ramirez et al. 2005; Schmale et al. 2005), posing a significant threat to crop and animal biosecurity with the potential to traverse county, state, and country borders.

There are a number of ways to identify unknown isolates of *Fusarium* to the level of species. First, isolates of *Fusarium* may be identified using morphological species concepts, in which species delimitation is based largely on the morphology of asexual and sexual spores produced on standard culture medium (Leslie et al. 2001). Second, unknown isolates of *Fusarium* may be identified by biological species concepts, in which species delimitation is based on reproductive assays that can define mating populations, such as within the *F. fujikuroi* complex (Kerényi et al. 1999). Third, unknown isolates of *Fusarium* may be identified to species using phylogenetic species concepts, based largely on DNA sequence similarity (Geiser et al. 2004; Nirenberg and O'Donnell 1998). This last approach has gained considerable traction in recent years because of the ease of DNA isolation and sequencing technologies.

Population genetic analyses may be used to develop predictions about potential sources of fungal populations (Bennett et al. 2005), and may contribute to develop strategies for disease management and control (Bissegger et al. 1997). To date, population genetic analyses have been applied to only a few species of *Fusarium*. Previous population genetic analyses have reported high levels of genetic diversity of *F. graminearum* (*G. zeae*) (Astolfi et al. 2012; Gale et al. 2007; Lee et al. 2010; Schmale et al. 2006; Talas et al. 2011; Zeller et al. 2004), *F. pseudograminearum* (Bentley et al. 2008), *F. verticillioides* (Reynoso et al. 2009), *F. solani* (Mohammadi and Mofrad 2009), *F. circinatum* (Wikler and Gordon 2000) and *F. oxysporum* (Bayraktar 2010). However, few studies have examined phylogenetic relationships among *Fusarium* species, particularly for those species that may be transported over long distances through the atmosphere.

Previous work has shown that atmospheric populations of *Fusarium* are influenced by large-scale atmospheric features known as Lagrangian coherent structures (LCSs) that may serve as atmospheric transport barriers (ATBs) (Schmale et al. 2012; Tallapragada et al. 2011). In these studies, LCSs/ATBs were associated with punctuated changes in colony forming units (CFUs) of *Fusarium* recovered from a series of collections with autonomous unmanned aerial vehicles (UAVs). Though these studies observed fluctuations in CFUs of *Fusarium* across varying temporal scales, they did not address the identity (i.e., species composition) or potential origin of atmospheric populations of *Fusarium*. We hypothesized that (1) atmospheric populations of *Fusarium* are diverse and dynamic across large-scale temporal and spatial gradients and (2) potential sources of *Fusarium* extend across broad geographical regions. To test these hypotheses, autonomous unmanned aerial vehicles (UAVs) equipped with microbe-sampling devices were used to collect viable spores of *Fusarium* 100 m above the ground level at the Kentland Farm in Blacksburg, Virginia. A portion of the translation elongation factor 1-alpha gene (TEF-1α) was used to assist in the identification of the *Fusarium* isolates to species. FusariumID (Geiser et al. 2004) and GenBank BLAST queries, coupled with phylogenetic analyses leveraging maximum likelihood and Bayesian methods, were used to identify isolates of *Fusarium* recovered from our collections. Back trajectory analyses were conducted for time periods prior to our collections to determine the potential geographic source areas of *Fusarium*. One could in principle geographically constrain the source regions for *Fusarium* species and determine correlations with species groupings and their probable geographic source regions. An increased understanding of the structure, composition, and potential source regions of atmospheric populations of *Fusarium* may aid in the development of disease management strategies in the future.

Materials and methods

Autonomous unmanned aerial vehicles (UAVs)

Autonomous (self-controlling) UAVs were used to collect *Fusarium* in the lower atmosphere 100 m above Virginia Tech's Kentland Farm in Blacksburg, VA, USA as described by Lin et al. (2013). Briefly, the UAVs flew defined sampling altitudes (100 m above ground level), sampling speeds (90km/h) and sampling patterns (circle), and carried eight collection plates containing a *Fusarium* selective medium on the wings. Once the UAV reached the target altitude of 100 m, the sampling devices were opened by remote control from the ground and exposed to the atmosphere for durations of 8-15 min (**Table 1**). Following each sampling mission, the exposed plates were removed from the UAV and stored in small plastic containers for transport to the laboratory.

Culturing and storage of Fusarium

Methods for culturing *Fusarium* were described by Lin et al. (2013). Briefly, colonies recovered from the sampling missions on the *Fusarium* selective medium were subcultured in the laboratory on new plates and single-spored. All single-spored cultures were transferred to plates of one quarter-strength potato dextrose agar (PDA) (BD Difco, Franklin Lakes, NJ, USA) medium containing a small piece of sterile filter paper (Fisher Scientific, Pittsburgh, PA, USA) cut to about half the size of the plate. Cultures were grown for 7 days at room temperature, and the colonized pieces of filter paper were removed and dried in a laminar flow hood (NuAire, Inc. Plymouth, MN, USA) overnight. Dried pieces of filter paper were placed in sterile coin envelopes and placed in refrigerated storage at 4°C. Spore suspensions were prepared from the other half of the plates (not containing the filter paper) by washing the plates with a sterile 20% glycerol aqueous (Fisher Scientific, Pittsburgh, PA, USA) solution for redundant long-term storage at minus 80°C (Leslie and Summerell 2006).

DNA extraction, PCR, and sequencing

Single-spored isolates of *Fusarium* were grown in 75 mL of potato dextrose broth (BD Difco, Franklin Lakes, NJ, USA) for 5 to 7 days on a rotating shaker at 100 rpm (Barnstead/Lab-Line MaxQ™ 3000, Champaign, IL, USA). The suspensions were filtered through four layers of cheesecloth and the resulting mycelium was lyophilized for 24 hr to remove water (FreeZone 2.5, Labconco, Kansas, MO, USA). The lyophilized mycelium was homogenized using 0.1-0.3 g

0.5 mm zirconia-silica beads with a Mini-Beadbeater (3110BX, BioSpec Products, Bartlesville, OK, USA) for1.5 min at 2,500 rpm. DNA was extracted from the homogenized mycelium using the Thermo/BioSprint15 workstation (Qiagen, Valencia, CA, USA) and the Biosprint 15 DNA Plant Kit (Qiagen, Valencia, CA, USA) following the manufacturer's protocols.

A portion of the translation elongation factor 1-alpha gene (TEF-1α) was amplified from each of the 135 isolates and from 69 vouchered *Fusarium* strains obtained from the Leslie laboratory. PCRs were conducted using the *Fusarium*-specific primers ef1 (forward primer; 5'-ATGGGTAAGGA(A/G)GACAAGAC-3') and ef2 (reverse primer; 5'-GGA(G/A)GTACCAGT(G/C)ATCATGTT-3') (O'Donnell et al. 1998) yielding a product of around 600-700 bp (Geiser et al. 2004). Reactions were performed using the following conditions: an initial long denaturation (94°C for 10 min), thermal cycler for 10 cycles (94°C for 30 s, 55°C for 45 s, 72°C for 1 min) and 20 cycles (94°C for 30 s, 52°C for 45 s, 72°C for 1 min), and a final extension (72°C for 10 min), followed by cooling at 4°C until recovery of the samples. The resulting amplification products were verified by electrophoresis in a 0.9% agarose gel containing ethidium bromide and visualized on a UV transilluminator (Universal hood II, BIO-RAD, Hercules, CA, USA). PCR products were sequenced directly in both directions at the University of Kentucky Advanced Genetic Technologies Center (UK-AGTC, Lexington, KY, USA). Sequences were trimmed and aligned using Lasergene 9.1 software (DNASTAR, Inc., Madison, WI, USA). Each consensus sequence served as an individual BLAST query against both FUSARIUM-ID (Geiser et al., 2004) and GenBank databases. Isolates with over 95% DNA sequence identity with vouchered *Fusarium* specimens were assigned to the respective known species (Geiser et al. 2004).

Phylogenetic analyses

Model-oriented phylogenetic analyses leveraging Maximum Likelihood (ML) and Bayesian methods were used to assist in the identification of specific *Fusarium* species and identify the phylogenetic relationships between the species. The *Fusarium* and fungal out group (GenBank accession number: HM626644.1, AB373728.1, HM626649.1, HM626647.1 and DQ247616.1) translation elongation factor DNA sequences were aligned using MAFFT (Katoh et al. 2005; Katoh et al. 2002). Modeltest v3.7 was used to identify the optimal evolutionary model (TrN+I+G) for use in the subsequent ML and Bayesian phylogenetic analyses. One hundred ML bootstrap replicates were performed using GARLI v1.0 (Zwickl 2006). The non-parametric bootstrap values were assigned using Consense from the PHYLIP package (Felsenstein 1989) enforcing consensus type Ml = 0.80. Thus, furcations showing less than 80% consensus non-parametric bootstrap support were collapsed into a polytomy. Six independent 10 million generation MrBayes v3.1.2 (Ronquist and Huelsenbeck 2003) runs, each with eight heated chains (temp=0.05), were performed. The parameter probability files from each of the MrBayes runs were analyzed using Tracer v1.5.0 (Rambaut and Drummond 2003). The resulting skyline plots did not show obvious signs of non-convergence. The ESS values for the LnL parameter ranged from 526-659 and the ESS values for the TL parameter ranged from 402-633. The ESS values for the other model parameters ranged in the thousands. The six independent Bayesian runs showed good evidence for both independent sampling and apparent convergence. Therefore, a single joint Bayesian analysis was generated using the sump and sumt commands using 25% burn in. The ML and Bayesian consensus trees were visualized using Figtree v1.3.1 (Rambaut 2009).

Analysis of species diversity

Species diversity was assessed using Simpson's Index, a composite measure of species richness and evenness (Magurran 2004; Simpson 1949):

$$\mathrm{Ds} = \frac{1}{\sum_{i=1}^{s} p_i^{\,2}}$$

where **P** is the proportion of number of individuals of one particular species found (n) divided by the total number of individuals found of all species (N) of each flight, **Σ** is the sum of the calculations, and **s** is the number of species of each flight. Simpson's index is heavily weighted towards the most abundant species in the sample while being less sensitive to species richness (Khan 2006).

Back trajectories and unresolved turbulence to identify potential source regions

Potential source regions were identified by calculating the back trajectories of the passive particles (spores) moving in the lower atmosphere. The trajectory of sampled particles was numerically integrated backward in time, using the available velocity data for past time steps:

$$\Delta \mathrm{x} = \int_{\mathrm{t}_0}^{\mathrm{t}_0 - \Delta \mathrm{T}} \mathrm{v}\,\mathrm{d}\mathrm{t}$$

Where t_0 is the time when sampled spores are collected and $\Delta \mathrm{T}$ is the integration duration. The result of this integration was used to generate hypotheses about the potential source region for each of the sample collections. The available velocity data were used for interpolation to find the unknown velocity at arbitrary points inside the domain of the field. If sub-grid scale turbulent velocity component is considered, then back-trajectories provide a single trajectory and the source "point" for sampled particles (spores). However, for the meteorological data which are available, the deterministic assumption is considered no longer valid, and the true motion of the particles could not be determined by this interpolation technique. Consequently, we incorporated unresolved (i.e., sub-grid scale) turbulent motion to assist in the calculations of the trajectories and the identification of potential source regions, which will in general no longer be single geographic points, but extended geographic regions. Unresolved turbulence is defined as the components of the velocity that cannot be described as a deterministic function of the grid point data; consequently, stochastic models must be used to obtain a reasonable estimate. This refers to the probabilistic motion of particles that could occur with respect to the constraints imposed from the existing velocity data at each node and at discrete time step. For the calculation of the *probabilistic source regions*, we used stochastic models suitable for atmospheric flows which describe the time varying unresolved velocity components as a random number based on available data on each grid point (background velocity data was based on the NAM-218 model which covers the North America and its spatiotemporal resolution is about 12 km and 3 hours, respectively):

$$v(x,t) = \bar{v}(x,t) + V_t(\bar{v},x,t)$$

Where $\bar{v}(x,t)$ shows the background deterministic velocity and $V_t(\bar{v},x,t)$ is the unresolved turbulent velocity which is a function of background velocity field as well as the position and time. The stochastic model for our simulation was based on Fay et al. (1995) and Draxler and Hess (1998). Due to the stochasticity of this model, we simulated the trajectories of many individual and independent particles (i.e., a Monte Carlo approach) to obtain an approximately converged probability distribution. The resulting position of those particles was considered the probabilistic source region, as integration was performed in the backward time direction. Ideally, one could determine the source region from where a back-trajectory intersects the ground. But the vertical wind component is difficult to resolve, and so three representative times are used: 6, 12, and 24 hours.

Trajectory distances were calculated as the arc length of the path traveled, approximated by summing all the 3-minute segments. Starting from the sampling point, a back-trajectory was calculated using a deterministic model similar to HYSPLIT. This trajectory is close to the mean location of the probability distribution when stochastic turbulent effects are included. The position of the trajectory was recorded every 3 minutes for a period of 24 hours.

Results

Collections of Fusarium

We collected a total of 135 isolates of *Fusarium* on 11 separate UAV flights 100 m above ground level in September and October, 2010 (**Table 1**). All eight sampling devices on the UAV were exposed to the atmosphere for durations of 8-15 min. The 11 flights were conducted on three different calendar dates: 28-Sep-2010 (flights F147-F150), 29-Sep-2010 (flights F151-F153), and 01-Oct-2010 (flights F154-F157) (**Table 1**). The fungal colony forming units (CFUs) from each of the collections across all eight plates ranged from 2 to 37 (**Table 1**).

Identification of Fusarium to the level of species

Two complementary approaches were used to assign the *Fusarium* isolates to previously characterized *Fusarium* species. The first approach queried the isolated Fusarium sequences against both the FusariumID and GenBank databases. The top BLAST pairwise hits were used to identify the closest *Fusarium* species. Based on this pairwise similarity approach at least 12 species of *Fusarium* were identified in our collections (**Table 2**). Pairwise DNA similarity matches are effective at identifying previously characterized genes; however, they do not reveal the inferred evolutionary relationships between the assigned Fusarium species. Therefore, phylogenetic analyses were also performed to understand the phylogenetic relationships between the *Fusarium* isolates and vouchered reference *Fusarium* species.

Complementary ML and Bayesian phylogenetic analyses revealed considerable phylogenetic diversity in the *Fusarium* isolated from the air over Kentland Farm. Sequences for the phylogenetic analyses included 69 voucher *Fusarium* specimens, five fungal outgroups, and 135 unknown isolates from 11 UAV flights (**Table S1**). Five fungal outgroups included Geejayessia cicatricum: HM626644.1, Cylindrocarpon sp. TBT-1: AB373728.1, Cyanonectria buxi: HM626649.1, Nectria cyanostoma: HM626647.1 and Neocosmospora sp. NRRL 22498: DQ247616.1, some randomly chose fungal species that belong to the same family as *Fusarium*, Nectriaceae, but represent different genera. And also these outgroups were identified using the same single DNA sequence marker, TEF-1α.). The overarching phylogenetic results from the ML and Bayesian analyses were largely concordant. Sixty five of 135 unknown isolates formed well supported clades with 66 of 69 vouchered *Fusarium* species. This is illustrated in Figure 1 and annotated as the “high density reference *Fusarium* region”. This region was typified by clades comprised of both *Fusarium* isolates from the air and vouchered *Fusarium* strains, showing strong bootstrap (ML analyses) and Bayesian posterior probability (Bayesian analyses) support for most nodes. Well supported clades of *Fusarium* isolates with a vouchered *Fusarium* species provided high-confidence species determination (Supplemental Fig S2 and S3). For example, isolates F156N1, F156N9, and F157N3 form a well-supported sister group with FIDN33 *F. lateritium* (100 bootstrap and 0.99 posterior probability supports). These species assignments were concordant with the pairwise similarity results obtained in the BLAST analyses (Table 2).

On the other hand, only three reference *Fusarium* strains (*F. babinda*, *F. equiseti*, and *F. scripi*) clustered with the remaining 70 *Fusarium* isolates. This region is described as the low density reference *Fusarium* region (Fig 1). The low density reference *Fusarium* region is typified by two characteristics. The first characteristic is that both the ML and Bayesian consensus analyses showed overall poor support for the relative branch order within this region. Not surprisingly, there was also inconsistent branch ordering within this region between the ML and Bayesian analyses (Supplemental Fig S1 and S2). Given the overall poorly supported topology in this region it was not possible to confidently assign these isolates to any one of the three reference *Fusarium* strains located in this region. Therefore, these *Fusarium* isolates were assigned the species designation of *F. babina/equiseti*-like. The second feature of this low density reference *Fusarium* region was that it comprised the basal region of the overall *Fusarium* phylogeny as evidenced by the proximity to the non-Fusarium fungal outgroup. The positioning of the outgroup was consistent in both the ML and the Bayesian consensus analyses, showing good bootstrap (100%) and posterior probability (1.0) support, respectively. Moreover, a phylogram of the Bayesian consensus analysis (Supplemental Fig 1) showed relatively short *F. babinda/equiseti-like* branch lengths proximal to the fungal outgroup. This argues against the hypothesis of a long branch artifact causing the inaccurate positioning of the fungal outgroup. Taken together, these phylogenetic results suggest that basal *F. babina/equiseti*-like isolates are closer to the inferred ancestral lineage that gave rise to the more derived high density reference *Fusarium* region.

Measurements of species richness and diversity

A detailed analysis of the species diversity across these flights was performed using Simpson's Index, which incorporates both species richness (the number of species in a flight) and evenness (the relative abundance of individuals per species within a flight) into a single measure (Tuomisto 2010). The results of this analysis are shown in Table 1; the relative abundance of individuals per species for each flight shown in Table 2. Species richness (the number of species) of an individual sampling mission varied from one to eight, and the species diversity across all of the flights ranged from 0 to 3.60 (**Table 1**). Flight populations with more species or greater evenness were considered to be more diverse. For example, flight F156 (8 species) was more diverse than flight F147 (1 species). Though the species richness of two flights may be equal (flights F148 and F155 had a species richness of 4 in each flight population), flight F155 was considered to be less diverse than F148, because all four species in F148 were more even, whereas there was greater variation in the abundance across the four species in F155 (**Table 2**).

Species distribution, back trajectories and potential source regions

We observed some variation in the distribution of *Fusarium* species among flight populations (**Fig 2**). This variability extended to flight populations collected during the same sampling date but at different times, and also between flights conducted on different sampling dates. For example, one species (*F. babina/equiseti-like*) was collected on F147, but on the next flight F148 we collected 4 different species (*F. fujikuroi*, *F. proliferatum*, *F. sporotrichioides*, *F. babinda/equiseti-like*). Some species were relatively abundant across most of the flights (e.g., *F. babinda/equiseti-like* was collected on 10/11 of the flights, *F. fujikuro*i (7/11), *F. sporotrichioides* (7/11), and *F. graminearum* (6/11)), and yet other species were only collected on certain sampling dates (e.g., *F. circinatum* was only collected on a single flight, F149 on 28-Sep-2010, *F. lactis* and *F. sambucinum* were collected only on 29-Sep-2010, and *F. armeniacum, F. avenaceum*, and *F. lateritium* were collected only on 01-Oct-2010) (**Fig 2**).

Numerical Monte Carlo simulations with 106 individual particles and based on stochastic models for unresolved turbulence revealed some important observations. First, the probabilistic potential source regions were not Gaussian distributions. Second, the distance between the centroid of the probabilistic source regions and the deterministic solution increased with time. Third, the stretch and spread of potential source regions depended on the background flow field and for different sampling times, different potential source configurations are expected. Figure 3 shows the potential source regions for 28, 29 Sep and 1 Oct 2010 respectively. The sampling location is shown by the green mark (Virginia Tech's Kentland Farm). For each figure, three backward integration times were considered (6, 12 and 24 hours), each represented by different shades of gray. Note that all the data corresponding to daily sampling flights are presented in these three figures (for the first and the last day we had four and for the second day we had three sampling flights).

Trajectory distances over 24h ranged from 394 km to 1,115 km (**Fig 4**). There was a positive correlation ($R^2 = 0.477$, $P = 0.027$) between trajectory distance, x, and number of species, S, with the best fit given by a power law with exponent 0.668 (**Fig 4**).

Discussion

Previous work has shown that Lagrangian coherent structures (LCSs), also known as atmospheric transport barriers (ATBs), were associated with punctuated changes in atmospheric populations of *Fusarium* (Schmale et al. 2012; Tallapragada et al. 2011). Little is known about the structure, composition, and potential origin of atmospheric populations of *Fusarium*. We used UAVs to collect viable spores of *Fusarium* 100 m above the ground level to test the hypotheses that (1) atmospheric populations of *Fusarium* are diverse and dynamic across large-scale temporal and spatial gradients and (2) potential sources of *Fusarium* extend across broad geographical regions. This study contributes to an increased understanding of the life history of *Fusarium*.

FusariumID and GenBank BLAST queries, coupled with model-oriented phylogenetic analyses leveraging maximum likelihood and Bayesian statistical methods, revealed at least 12 species of *Fusarium* in our collections. Two of these species *F. babinda* and *F. equiseti* formed a large poorly resolved (i.e. polytomy) with a large number of flight isolates that together comprised the more basal regions of the *Fusarium* phylogeny. These *F. babinda/equiseti*-like strains may represent the more ancestral state of the *Fusarium* species complex present in these analyses. This poorly resolved region was not an artifact of fast evolving species, but rather many closely related isolates that likely diverged very rapidly from one another. Additional phylogenetic analyses evaluating multiple loci will be required to resolve these *Fusarium* isolates into one or more distinct species in the future.

Some of the species recovered from our collections were expected (e.g., *F. avenaceum, F. graminearum, F. oxysporum*, *F. sporotrichioides*, etc.), since these species have been reported in agroecosystems (Fernando et al. 2000; Katan et al. 1997; Martin 1988; Schmale et al. 2005). Previous work by Schmale et al. (2012) reported that isolates of *F. graminearum* collected 40 to 320 m above ground level were pathogens on wheat and produced trichothecene mycotoxins. Other species recovered in our populations were unexpected (e.g., *F. lactis* and *F. circinatum*). Isolates of *F. lactis* have been reported from California, but to our knowledge have not been reported in the state of Virginia (Leslie and Summerell 2006). An isolate of *F. circinatum*, causal agent of pitch canker disease of pine, was collected on F149. Though the first report of *F. circinatum* in the U.S. was on *Pinus virginiana* in the state of North Carolina (Nirenberg and O'Donnell 1998), this fungus has not been reported previously in the state of Virginia. Recent greenhouse studies (Hill, Lin, and Schmale, unpublished observations) have demonstrated that the isolate of *F. circinatum* collected on F149 can cause pitch canker on a susceptible greenhouse-grown pine host (*Pinus echinata*). The potential source region for this isolate of *F. circinatum* is unknown, but modeling efforts conducted as part of this work suggest the contribution of multiple potential sources across broad geographical regions west and northwest of our sampling site, including Virginia, West Virginia, Kentucky, Ohio, and Indiana (see **Fig 3(a)**).

Species richness, evenness, and diversity varied within and among our flight populations, supporting our hypothesis that atmospheric populations of *Fusarium* are diverse and dynamic. We used an index combining both species richness and abundance to provide an indication of *Fusarium* species diversity for each individual sampling flight. This diversity is likely influenced by many factors, including potential inoculum sources and source regions (Bennett et al. 2005; Leslie and Summerell 2006; Ma et al. 2004; Schmale et al. 2006). Based on the information reviewed in Leslie and Summerell (2006), some *Fusarium* species have specific plant hosts (e.g., *F. lactis* and fig) while other have broad host ranges (e.g., *F. oxysporum*). Some species appears to be associated with specific geographic areas (e.g., *F. lactis* has mostly been observed in California, USA) (Leslie and Summerell 2006), while others are ubiquitous (e.g., *F. graminearum, F. fujikuroi, F. oxysporum*, etc.). It is interesting that we collected species of *Fusarium* which represent so many different variations of the life history of *Fusarium*; species representing both broad and narrow host ranges, and species representing both broad and narrow source regions worldwide.

Back trajectory analyses conducted 6 to 24 hours prior to our collections suggested the contribution of multiple sources of *Fusarium* across broad geographical regions. Fortuitously, the wind was coming from a significantly different direction each day, which provides a means to geographically constrain the corresponding source regions for the *Fusarium* species sampled: *F. circinatum, F. proliferatum,* and *F. verticillioides* were only collected on 28-Sep-2010, which came primarily from west-northwest of the sampling site; *F. lactis* and *F. sambucinum* were only collected on 29-Sep-2010, primarily from east-southeast of the sampling site; and *F. armeniacum, F. avenaceum,* and *F. lateritium* were only collected on 01-Oct-2010, primarily from north of the sampling site. *F. babina/equiseti-like, F. fujikuroi,* and *F. sporotrichioides* were collected in large numbers on 28-Sep-2010 and 01-Oct-2010, but not 29-Sep-2010, suggesting source regions to the west and north of the sampling site. Similarly, the collection pattern for *F. oxysporum* suggests source regions to the east, north, and south, but not from the west. The most ubiquitous species are those categorized as *F. babinda/equiseti-like*, which was collected in large numbers on each day, suggesting a large geographic range including the eastern U.S. Interestingly, the geographic pattern for *F. babinda/equiseti-like* matched *F. equiseti*, which 75% of the spores coming on 01-Oct-2010, from the north (similar to 70% for *F. equiseti*), suggesting host plants with a common geographic range. Overall, we notice that the fewest spores were collected on 29-Sep-2010, where back-trajectory analysis indicates that at 24 hours, the source region includes a significant fraction in the Atlantic Ocean. As no host plants are present in the ocean, this may provide an explanation for the smaller spore numbers on 29-

Sep-2010, i.e., the spores contributing to the sample would be limited to only the potential source area over dry land.

Based on the assumptions of back trajectory analyses, the area of the potential source region increases with time. On 28-Sep-2010, source regions were as follows: at 6 hours the west of Virginia, at 12 hours the central part of Kentucky, at 24 hours the eastern part of Indiana, south and western portions of Ohio, and the southwest of West Virginia. On 29-Sep-2010, source regions were as follows: at 6 hours the central part of Virginia, at 12 hours Virginia and North Carolina, and at 24 hours the South-West of Virginia and West Virginia, central part of North Carolina, East of South Carolina, and the Atlantic Ocean. On 01-Oct-2010, source regions were as follows: at 6 hours the central part of West Virginia, at 12 hours the North-West Pennsylvania, North-East Ohio, and Lake Erie, at 24 hours the North Michigan, Lake Huron, and North of Lake Michigan. Thus, as the potential source region expands over time, there may be additional opportunity for differential source contributions from distinct geographic areas (Bowers et al. 2011). However, we found no correlation of species richness with potential source region area, which was consistent with the previous research demonstrating no strong influence of spatial structure on species richness (Harrison et al. 2006). The size of the potential source region area may be more a reflection of modeling uncertainty than an estimate of the size of the actual contributing region, i.e., the actual source area is a small subset of the potential source region, but is hard to pinpoint using the currently limited spatiotemporal resolution of meteorological models. Association analyses of species and/or genotypes from the potential source regions with our flight collections could be one of the direct results of this study. Though the actual contribution of these hypothesized source regions to the atmospheric populations of *Fusarium* remains unclear, the diverse atmospheric populations of *Fusarium* suggest that inoculum may originate from multiple locations over large geographic distances.

An increased understanding of the structure, composition, and potential source regions of atmospheric assemblages of *Fusarium* may aid in the development of disease management strategies in the future. Future research aims to link to local (collected near the ground) and regional (collected in the lower atmosphere with UAVs) collections of *Fusarium* across different sampling times, dates, and seasons. The careful dissection of these linkages may provide additional clues about the life history of the *Fusarium* and how patterns in the species diversity depend on geographic scale.

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Supplemental Table 1. Comparisons of GenBank, Fusarium-ID, and phylogenetic analyses for all of the isolates collected 100 m above ground level during September and October, 2010.

Isolate	Flight	Date	Genbank Accession Number	Identification based on Fusarium-ID Query	Fusarium-ID (%)	Identification based on GenBank Query	Genbank (%)	Identification using Garli method	Identification using Bayesian method
F147N1	F147	28-Sep-10	KC874683	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	610 / 612 (99%)	Fusarium sp. NRRL 5537	627/632 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F147N5	F147	28-Sep-10	KC874684	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	609 / 610 (99%)	Fusarium sp. NRRL 45996	632/637 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F148N2	F148	28-Sep-10	KC874685	FD_01857_EF-1a [*Fusarium sp.*]	608 / 608 (100%)	Gibberella fujikuroi isolate V95	619/621 (99%)	F. fujikuroi	F. fujikuroi
F148N3	F148	28-Sep-10	KC874686	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	609 / 610 (99%)	Fusarium proliferatum isolate 2-91	626/630 (99%)	F. proliferatum	F. proliferatum
F148N4	F148	28-Sep-10	KC874687	FD_01857_EF-1a [Fusarium sp.]	619 / 625 (99%)	Gibberella fujikuroi partial tef-1 gene	639/645 (99%)	F. fujikuroi	F. fujikuroi
F148N6	F148	28-Sep-10	KC874688	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	607 / 621 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	636/640 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F148N7	F148	28-Sep-10	KC874689	FD_01304_EF-1a [Fusarium sp.]	615 / 617 (99%)	Fusarium sporotrichioides strain NRRL 29977	628/632 (99%)	F. sporotrichioides	F. sporotrichioides
F148N8	F148	28-Sep-10	KC874690	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	596 / 604 (99%)	Fusarium sp. NRRL 32997	621/635 (98%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F149N3	F149	28-Sep-10	KC874691	FD_01304_EF-1a [Fusarium sp.]	626 / 632 (99%)	Fusarium sporotrichioides strain NRRL 52928	643/648 (99%)	F. sporotrichioides	F. sporotrichioides
F149N6	F149	28-Sep-10	KC874692	FD_01857_EF-1a [Fusarium sp.]	601 / 602 (99%)	Gibberella fujikuroi partial tef-1 gene	622/627 (99%)	F. fujikuroi	F. fujikuroi
F149N7	F149	28-Sep-10	KC874693	GFSC isolate NRRL 25331, MLSTGibberella fujikuroi species complex	615 / 624 (99%)	Gibberella circinata strain NRRL25331	620/630 (99%)	F. circinatum	F. circinatum
F149N8	F149	28-Sep-10	KC874694	FD_01388_EF-1a [Fusarium verticillioides]	642 / 645 (99%)	Gibberella moniliformis strain PUMCH10XB00173	651/656 (99%)	F. verticillioides	F. verticillioides
F149N9	F149	28-Sep-10	KC874695	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	672 / 678 (99%)	Fusarium sp. NRRL 5537	672/678 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F149N11	F149	28-Sep-10	KC874696	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	635 / 651 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	654/657 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F149N12	F149	28-Sep-10	KC874697	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	609 / 624 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	628/630 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F149N13	F149	28-Sep-10	KC874698	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	633 / 649 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	652/655 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like

F149N17	F149	28-Sep-10	KC874699	FD_01857_EF-1a [Fusarium sp.]	602 / 604 (99%)	Gibberella fujikuroi isolate V95	608/611 (99%)	F. fujikuroi	F. fujikuroi
F149N19	F149	28-Sep-10	KC874700	FD_01119_EF-1a [Fusarium graminearum]	625 / 629 (99%)	Gibberella zeae strain LMSA 1.09.107	614/615 (99%)	F. graminearum	F. graminearum
F149N20	F149	28-Sep-10	KC874701	FD_01304_EF-1a [Fusarium sp.]	628 / 631 (99%)	Fusarium sporotrichioides strain NRRL 52928	651/655 (99%)	F. sporotrichioides	F. sporotrichioides
F149N21	F149	28-Sep-10	KC874702	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	576 / 612 (94%)	Fusarium cf. incarnatum H04-707S-4 PCNB	626/631 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F149N23	F149	28-Sep-10	KC874703	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	614 / 614 (100%)	Fusarium sp. NRRL 5537	629/632 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F149N24	F149	28-Sep-10	KC874704	FD_01304_EF-1a [Fusarium sp.]	618 / 621 (99%)	Fusarium sporotrichioides strain NRRL 29977	624/627 (99%)	F. sporotrichioides	F. sporotrichioides
F149N25	F149	28-Sep-10	KC874705	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	637/642 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N1	F150	28-Sep-10	KC874706	FD_01858_EF-1a [Fusarium sp.]	609 / 611 (99%)	F. proliferatum isolate NL131-2	626/630 (99%)	F. proliferatum	F. proliferatum
F150N2	F150	28-Sep-10	KC874707	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	608 / 611 (99%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	617/619 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N3	F150	28-Sep-10	KC874708	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	607 / 609 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	613/616 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N5	F150	28-Sep-10	KC874709	FD_01304_EF-1a [Fusarium sp.]	614 / 617 (99%)	Fusarium sporotrichioides strain NRRL 29977	623/627 (99%)	F. sporotrichioides	F. sporotrichioides
F150N6	F150	28-Sep-10	KC874710	FD_01857_EF-1a [Fusarium sp.]	596 / 597 (99%)	Gibberella fujikuroi isolate V22	610/613 (99%)	F. fujikuroi	F. fujikuroi
F150N7	F150	28-Sep-10	KC874711	FD_01857_EF-1a [Fusarium sp.]	604 / 606 (99%)	Gibberella fujikuroi isolate V22	607/609 (99%)	F. fujikuroi	F. fujikuroi
F150N8	F150	28-Sep-10	KC874712	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	610 / 613 (99%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	626/630 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N9	F150	28-Sep-10	KC874713	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	602 / 618 (97%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	626/630 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N10	F150	28-Sep-10	KC874714	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	628/631 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N11	F150	28-Sep-10	KC874715	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	610 / 625 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	627/629 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N13	F150	28-Sep-10	KC874716	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	591 / 605 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	627/632 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F150N14	F150	28-Sep-10	KC874717	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 620 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	633/636 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like

F150N15	F150	28-Sep-10	KC874718	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	591 / 605 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	610/611 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F151N1	F151	29-Sep-10	KC874719	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	604 / 619 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	623/625 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F151N3	F151	29-Sep-10	KC874720	FD_00986_EF-1a [Fusarium graminearum]	618 / 619 (99%)	Gibberella zeae strain NRRL 31084	622/624 (99%)	F. graminearum	F. graminearum
F151N4	F151	29-Sep-10	KC874721	FD_01857_EF-1a [Fusarium sp.]	587 / 588 (99%)	Gibberella fujikuroi isolate V22	607/611 (99%)	F. fujikuroi	F. fujikuroi
F151N5	F151	29-Sep-10	KC874722	FD_00986_EF-1a [Fusarium graminearum]	511 / 535 (96%)	Gibberella zeae isolate CS3005	531/555 (96%)	F. graminearum	F. graminearum
F151N6	F151	29-Sep-10	KC874723	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	610/612 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F151N8	F151	29-Sep-10	KC874724	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	611 / 612 (99%)	Fusarium sp. NRRL 32522	618/621 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F151N9	F151	29-Sep-10	KC874725	FD_01119_EF-1a [Fusarium graminearum]	546 / 554 (99%)	Gibberella zeae isolate CS3005	622/668 (94%)	F. graminearum	F. graminearum
F151N10	F151	29-Sep-10	KC874726	FD_01119_EF-1a [Fusarium graminearum]	625 / 628 (99%)	Gibberella zeae isolate G5S	611/612 (99%)	F. graminearum	F. graminearum
F152N2	F152	29-Sep-10	KC874727	F. oxysporum species complex isolate NRRL 28391, MLST103	618 / 619 (99%)	Fusarium oxysporum strain NRRL 43431	618/619 (99%)	F. oxysporum	F. oxysporum
F152N4	F152	29-Sep-10	KC874728	GFSC isolate NRRL 25200, MLSTGibberella fujikuroi species complex	620 / 634 (98%)	Fusarium lactis strain NRRL25200	620/634 (98%)	F. lactis	F. lactis
F152N5	F152	29-Sep-10	KC874729	F. oxysporum species complex isolate NRRL 28391, MLST103	604 / 605 (99%)	Fusarium oxysporum strain NRRL 26404	615/618 (99%)	F. oxysporum	F. oxysporum
F153N1	F153	29-Sep-10	KC874730	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	580 / 605 (96%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	604/617 (98%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F153N2	F153	29-Sep-10	KC874731	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	601 / 616 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	614/615 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F153N3	F153	29-Sep-10	KC874732	GFSC isolate NRRL 25200, MLSTGibberella fujikuroi species complex	605 / 618 (98%)	Fusarium lactis strain NRRL25200	613/628 (98%)	F. lactis	F. lactis
F153N4	F153	29-Sep-10	KC874733	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	589 / 605 (97%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	608/611 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F153N5	F153	29-Sep-10	KC874734	FD_01853_EF-1a [Fusarium sp.]	630 / 633 (99%)	Fusarium sporotrichioides strain F95	655/658 (99%)	F. sporotrichioides	F. sporotrichioides
F153N6	F153	29-Sep-10	KC874735	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	602 / 603 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	609/610 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F153N8	F153	29-Sep-10	KC874736	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	553 / 564 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	579/582 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like

F153N9	F153	29-Sep-10	KC874737	FD_01119_EF-1a [Fusarium graminearum]	647 / 650 (99%)	Gibberella zeae isolate G5S	613/613 (100%)	F. graminearum	F. graminearum
F153N10	F153	29-Sep-10	KC874738	FD_01307_EF-1a [Fusarium sp.]	531 / 554 (96%)	Fusarium sambucinum partial tef-1alpha gene	532/554 (97%)	F. sambucinum	F. sambucinum
F153N11	F153	29-Sep-10	KC874739	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	569 / 604 (94%)	Fusarium cf. incarnatum H04-707S-4 PCNB	622/625 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F153N12	F153	29-Sep-10	KC874740	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	609 / 610 (99%)	Fusarium sp. NRRL 5537	624/628 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F153N13	F153	29-Sep-10	KC874741	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	634 / 651 (97%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	651/654 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F154N1	F154	1-Oct-10	KC874742	FD_01114_EF-1a [Fusarium graminearum]	613 / 616 (99%)	Gibberella zeae strain LMSA 1.09.129	644/649 (99%)	F. graminearum	F. graminearum
F154N2	F154	1-Oct-10	KC874743	FD_00986_EF-1a [Fusarium graminearum]	608 / 609 (99%)	Gibberella zeae strain NRRL 31084	617/621 (99%)	F. graminearum	F. graminearum
F154N3	F154	1-Oct-10	KC874744	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	598 / 598 (100%)	Fusarium sp. NRRL 32522	604/605 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F154N4	F154	1-Oct-10	KC874745	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	616/619 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F154N5	F154	1-Oct-10	KC874746	FD_01119_EF-1a [Fusarium graminearum]	604 / 618 (98%)	Gibberella zeae isolate CS3005	623/637 (98%)	F. graminearum	F. graminearum
F154N6	F154	1-Oct-10	KC874747	F. oxysporum species complex isolate NRRL 40182, MLST99	629 / 629 (100%)	Fusarium oxysporum strain NRRL28359	628/629 (99%)	F. oxysporum	F. oxysporum
F154N7	F154	1-Oct-10	KC874748	FD_01304_EF-1a [Fusarium sp.]	605 / 606 (99%)	Fusarium sporotrichioides EF-1alpha gene, strain: CBS 119839	624/624 (100%)	F. sporotrichioides	F. sporotrichioides
F154N8	F154	1-Oct-10	KC874749	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	507 / 540 (94%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	533/554 (97%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F154N11	F154	1-Oct-10	KC874750	FD_01853_EF-1a [Fusarium sp.]	607 / 609 (99%)	Fusarium sporotrichioides strain NRRL 53434	613/615 (99%)	F. sporotrichioides	F. sporotrichioides
F155N1	F155	1-Oct-10	KC874751	F. incarnatum-equiseti species complex isolate NRRL 34039, MLST1-b	603 / 605 (99%)	Fusarium sp. NRRL 34039	618/623 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N2	F155	1-Oct-10	KC874752	FD_01857_EF-1a [Fusarium sp.]	584 / 587 (99%)	Gibberella fujikuroi isolate V95	598/604 (99%)	F. fujikuroi	F. fujikuroi
F155N3	F155	1-Oct-10	KC874753	FD_01119_EF-1a [Fusarium graminearum]	628 / 629 (99%)	Gibberella zeae isolate CS3005	649/652 (99%)	F. graminearum	F. graminearum
F155N4	F155	1-Oct-10	KC874754	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	594 / 604 (98%)	Fusarium sp. NRRL 32997	599/610 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N5	F155	1-Oct-10	KC874755	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	597 / 606 (98%)	Fusarium sp. NRRL 32997	604/615 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like

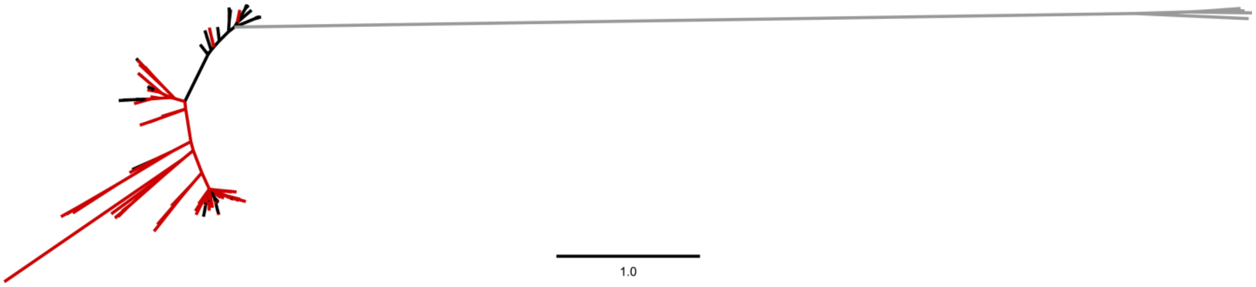
F155N6	F155	1-Oct-10	KC874756	F. oxysporum species complex isolate NRRL 26962, MLST89	623 / 625 (99%)	Fusarium oxysporum, strain ISPaVe1018	626/628 (99%)	F. oxysporum	F. oxysporum
F155N7	F155	1-Oct-10	KC874757	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	610/612 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N8	F155	1-Oct-10	KC874758	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	598 / 599 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	610/612 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N10	F155	1-Oct-10	KC874759	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	610/612 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N11	F155	1-Oct-10	KC874760	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	600 / 601 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	612/614 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N12	F155	1-Oct-10	KC874761	FD_01119_EF-1a [Fusarium graminearum]	573 / 580 (99%)	Gibberella zeae strain LMSA 1.09.107	579/587 (99%)	F. graminearum	F. graminearum
F155N13	F155	1-Oct-10	KC874762	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	654 / 655 (99%)	Fusarium sp. NRRL 5537	654/655 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N14	F155	1-Oct-10	KC874763	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	556 / 556 (100%)	Fusarium sp. NRRL 5537	574/577 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F155N15	F155	1-Oct-10	KC874764	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	590 / 594 (99%)	Fusarium sp. NRRL 45996	609/617 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N1	F156	1-Oct-10	KC874765	FD_01345_EF-1a [Fusarium lateritium]	610 / 635 (96%)	Fusarium lateritium isolate F0104	630/645 (98%)	F. lateritium	F. lateritium
F156N2	F156	1-Oct-10	KC874766	F. oxysporum species complex isolate NRRL 40182, MLST99	605 / 606 (99%)	Fusarium oxysporum strain NRRL 38361	619/623 (99%)	F. oxysporum	F. oxysporum
F156N3	F156	1-Oct-10	KC874767	FD_01857_EF-1a [Fusarium sp.]	596 / 600 (99%)	Gibberella fujikuroi isolate V95	599/604 (99%)	F. fujikuroi	F. fujikuroi
F156N4	F156	1-Oct-10	KC874768	FD_01857_EF-1a [Fusarium sp.]	545 / 546 (99%)	Gibberella fujikuroi isolate V22	561/564 (99%)	F. fujikuroi	F. fujikuroi
F156N5	F156	1-Oct-10	KC874769	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	595 / 603 (99%)	Fusarium equiseti EF-1alpha gene, strain: MAFF 236723	611/615 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N6	F156	1-Oct-10	KC874770	FD_01304_EF-1a [Fusarium sp.]	615 / 617 (99%)	Fusarium sporotrichioides strain NRRL 29977	625/628 (99%)	F. sporotrichioides	F. sporotrichioides
F156N9	F156	1-Oct-10	KC874771	FD_01345_EF-1a [Fusarium lateritium]	626 / 652 (96%)	Fusarium lateritium isolate F0104	650/664 (98%)	F. lateritium	F. lateritium
F156N10	F156	1-Oct-10	KC874772	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	597 / 600 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	608/611 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N11	F156	1-Oct-10	KC874773	FD_01843_EF-1a [Fusarium armeniacum]	594 / 597 (99%)	Fusarium armeniacum strain NRRL 6227	603/604 (99%)	F. armeniacum	F. armeniacum
F156N13	F156	1-Oct-10	KC874774	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	576 / 611 (94%)	Fusarium cf. incarnatum H04-707S-4 PCNB	629/633 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like

F156N 14	F156	1-Oct-10	KC874775	FD_01857_EF-1a [Fusarium sp.]	602 / 604 (99%)	Gibberella fujikuroi isolate V95	617/622 (99%)	F. fujikuroi	F. fujikuroi
F156N 15	F156	1-Oct-10	KC874776	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	615 / 619 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	628/632 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 16	F156	1-Oct-10	KC874777	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	600 / 601 (99%)	Gibberella fujikuroi partial tef-1 gene	598/599 (99%)	F. fujikuroi	F. fujikuroi
F156N 18	F156	1-Oct-10	KC874778	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	601 / 621 (97%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	628/637 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 19	F156	1-Oct-10	KC874779	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	614 / 615 (99%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	624/627 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 20	F156	1-Oct-10	KC874780	FD_01853_EF-1a [Fusarium sp.]	591 / 623 (95%)	Fusarium sporotrichioides strain NRRL 53434	596/628 (95%)	F. sporotrichioides	F. sporotrichioides
F156N 21	F156	1-Oct-10	KC874781	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	618 / 628 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	631/635 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 22	F156	1-Oct-10	KC874782	FD_00986_EF-1a [Fusarium graminearum]	619 / 620 (99%)	Gibberella zeae strain NRRL 31084	623/625 (99%)	F. graminearum	F. graminearum
F156N 24	F156	1-Oct-10	KC874783	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	612 / 612 (100%)	Fusarium cf. incarnatum NRRL 43498	624/626 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 27	F156	1-Oct-10	KC874784	FD_01857_EF-1a [*Fusarium sp.*]	603 / 604 (99%)	Gibberella fujikuroi isolate V95	613/616 (99%)	F. fujikuroi	F. fujikuroi
F156N 28	F156	1-Oct-10	KC874785	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	614 / 615 (99%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	620/622 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 29	F156	1-Oct-10	KC874786	FD_01857_EF-1a [Fusarium sp.]	608 / 611 (99%)	Gibberella fujikuroi isolate V22	614/617 (99%)	F. fujikuroi	F. fujikuroi
F156N 30	F156	1-Oct-10	KC874787	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	641 / 643 (99%)	Fusarium cf. incarnatum NRRL 43498	632/635 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 32	F156	1-Oct-10	KC874788	FD_01857_EF-1a [*Fusarium sp.*]	614 / 616 (99%)	Gibberella fujikuroi isolate V22	618/620 (99%)	F. fujikuroi	F. fujikuroi
F156N 33	F156	1-Oct-10	KC874789	FD_01317_EF-1a [*Fusarium sp.*]	607 / 623 (97%)	Gibberella avenacea voucher FRC R-9369	618/622 (99%)	F. avenaceaum	F. avenaceaum
F156N 35	F156	1-Oct-10	KC874790	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	610 / 626 (97%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	636/641 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 36	F156	1-Oct-10	KC874791	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	620 / 622 (99%)	Fusarium cf. incarnatum MLST 3-b clone spt072	627/630 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N 37	F156	1-Oct-10	KC874792	FD_01304_EF-1a [*Fusarium sp.*]	614 / 617 (99%)	Fusarium sporotrichioides strain NRRL 29977	618/621 (99%)	F. sporotrichioides	F. sporotrichioides
F156N 39	F156	1-Oct-10	KC874793	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	614 / 615 (99%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	619/622 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like

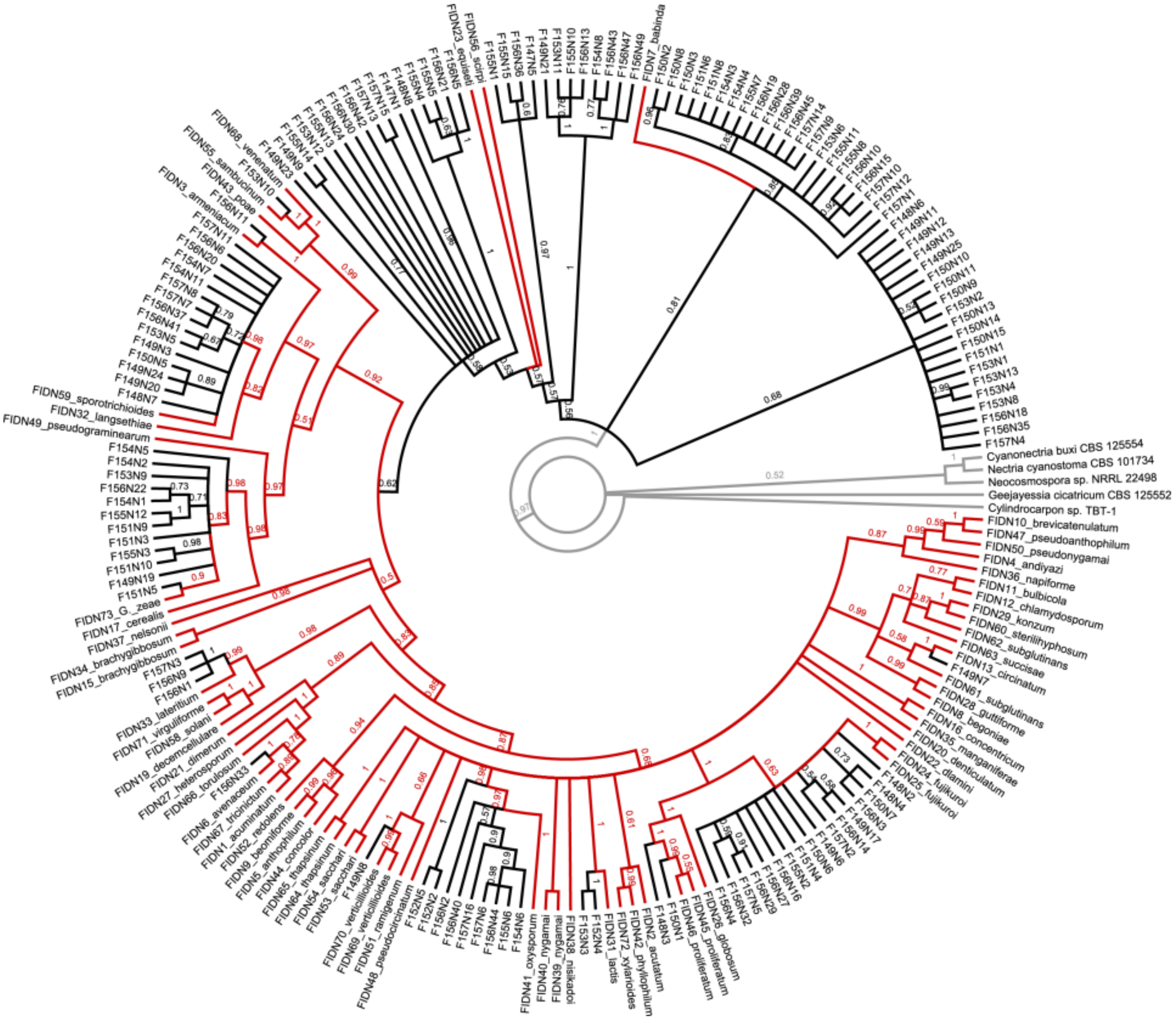
F156N40	F156	1-Oct-10	KC874794	FD_01376_EF-1a [*Fusarium oxysporum*]	618 / 619 (99%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	623/625 (99%)	F. oxysporum	F. oxysporum
F156N41	F156	1-Oct-10	KC874795	FD_01304_EF-1a [*Fusarium sp.*]	628 / 631 (99%)	Fusarium sporotrichioides strain NRRL 29977	633/636 (99%)	F. sporotrichioides	F. sporotrichioides
F156N42	F156	1-Oct-10	KC874796	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	625 / 626 (99%)	Fusarium cf. incarnatum NRRL 43498	629/631 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N43	F156	1-Oct-10	KC874797	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	574 / 609 (94%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	609/631 (97%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N44	F156	1-Oct-10	KC874798	F. oxysporum species complex isolate NRRL 26962, MLST89	619 / 620 (99%)	Fusarium oxysporum,strain ISPaVe1018	623/625 (99%)	F. oxysporum	F. oxysporum
F156N45	F156	1-Oct-10	KC874799	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 615 (97%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	612/631 (97%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N47	F156	1-Oct-10	KC874800	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	577 / 612 (94%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	615/640 (96%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F156N49	F156	1-Oct-10	KC874801	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	569 / 606 (94%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	597/621 (96%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N1	F157	1-Oct-10	KC874802	F. incarnatum-equiseti species complex isolate NRRL 34005, MLST24-a	604 / 605 (99%)	Fusarium cf. incarnatum M03-11345S-1 DCPA	604/605 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N2	F157	1-Oct-10	KC874803	FD_01857_EF-1a [*Fusarium sp.*]	584 / 594 (98%)	Gibberella fujikuroi isolate V95	595/607 (98%)	F. fujikuroi	F. fujikuroi
F157N3	F157	1-Oct-10	KC874804	FD_01345_EF-1a [*Fusarium lateritium*]	624 / 651 (96%)	Fusarium lateritium isolate F0104	635/650 (98%)	F. lateritium	F. lateritium
F157N4	F157	1-Oct-10	KC874805	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	610 / 624 (98%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	629/630 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N5	F157	1-Oct-10	KC874806	FD_01857_EF-1a [*Fusarium sp.*]	611 / 614 (99%)	Gibberella fujikuroi isolate V22	614/617 (99%)	F. fujikuroi	F. fujikuroi
F157N6	F157	1-Oct-10	KC874807	F. oxysporum species complex isolate NRRL 26962, MLST89	577 / 577 (100%)	Fusarium oxysporum	580/580 (100%)	F. oxysporum	F. oxysporum
F157N7	F157	1-Oct-10	KC874808	FD_01304_EF-1a [*Fusarium sp.*]	620 / 623 (99%)	Fusarium sporotrichioides strain NRRL 29977	621/623 (99%)	F. sporotrichioides	F. sporotrichioides
F157N8	F157	1-Oct-10	KC874809	FD_00929_EF-1a [*Fusarium sp.*]	535 / 539 (99%)	Fusarium sporotrichioides strain NRRL 29977	541/544 (99%)	F. sporotrichioides	F. sporotrichioides
F157N9	F157	1-Oct-10	KC874810	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	499 / 500 (99%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	503/505 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N10	F157	1-Oct-10	KC874811	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	475 / 480 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	477/480 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N11	F157	1-Oct-10	KC874812	FD_01853_EF-1a [*Fusarium sp.*]	600 / 602 (99%)	Fusarium sporotrichioides strain NRRL 29977	600/602 (99%)	F. sporotrichioides	F. sporotrichioides

F157N12	F157	1-Oct-10	KC874813	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	612 / 613 (99%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	628/631 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N13	F157	1-Oct-10	KC874814	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	602 / 604 (99%)	Fusarium cf. incarnatum NRRL 43498	606/609 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N14	F157	1-Oct-10	KC874815	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	336 / 336 (100%)	Fusarium sp. NRRL 32522	339/340 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N15	F157	1-Oct-10	KC874816	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	534 / 536 (99%)	Fusarium cf. incarnatum NRRL 43498	540/543 (99%)	F. babinda/equiseti-like	F. babinda/equiseti-like
F157N16	F157	1-Oct-10	KC874817	FD_01376_EF-1a [*Fusarium oxysporum*]	623 / 624 (99%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	630/633 (99%)	F. oxysporum	F. oxysporum

Supplemental Fig S1. Phylogram of Bayesian phylogenetic analysis. Red branches are reference *Fusarium* strains, and black branches are *Fusarium* strains sampled during the flights. Grey branches indicate non-Fusarium fungal strains used as an out group to root the tree. Branch lengths indicate the posterior nucleotide substitution rate.



Supplemental Fig S2. Cladogram of Bayesian phylogenetic analysis. Branch colors are described in Supplemental Fig S1. Node labels indicate posterior probabilities for each node.



Supplemental Fig S3. Maximum Likelihood phylogenetic analysis cladogram. Branch colors are described in Supplemental Fig S1. Node labels indicate non-parametric bootstrap support values.

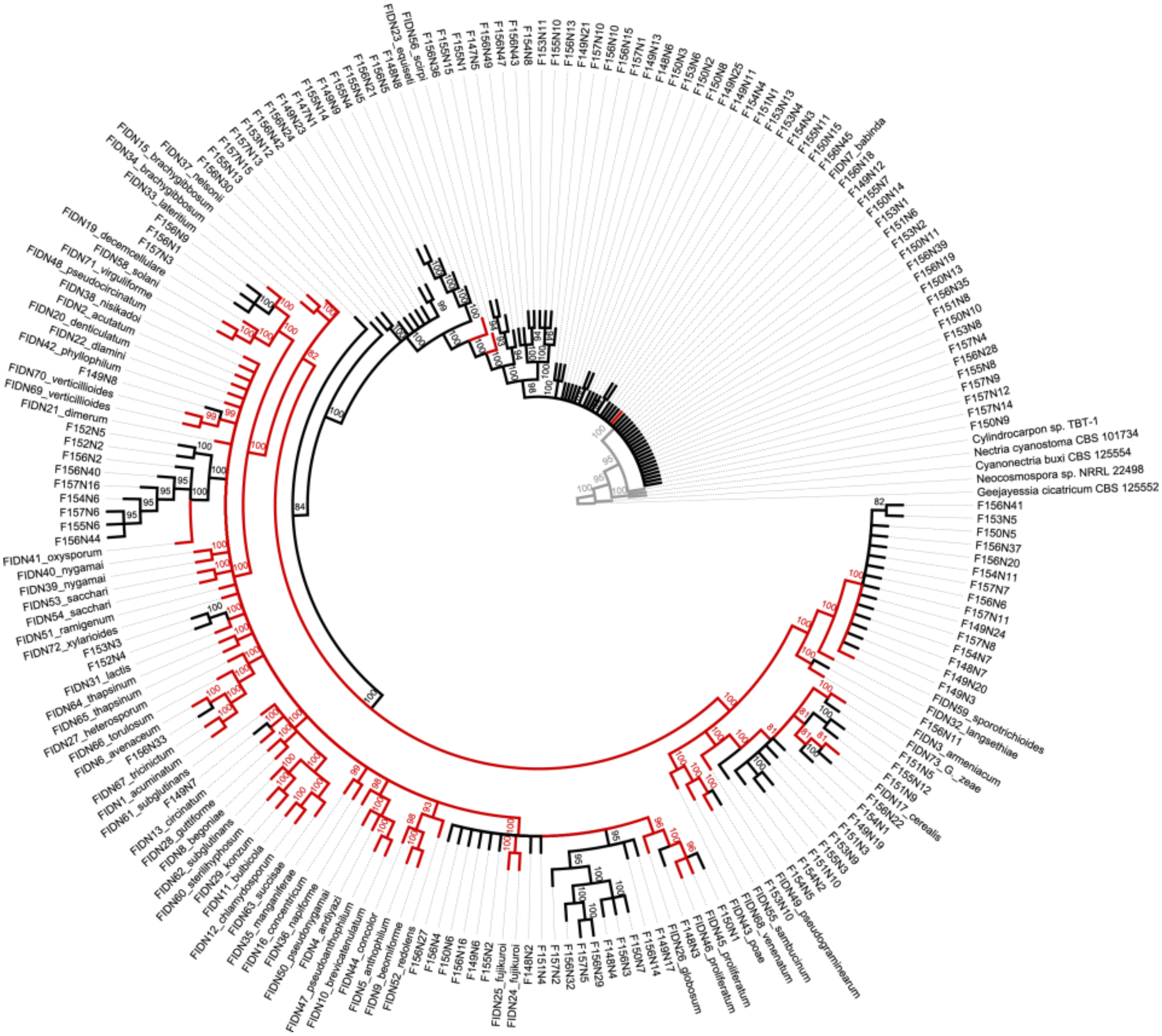


Table 1: Colony forming units (CFUs) of *Fusarium* collected with UAVs 100 m above ground level at Virginia Tech's Kentland Farm during September and October, 2010. The UAVs were equipped with eight microbe-sampling devices that were opened by remote control from the ground once the UAV reached its target altitude of 100 m, and exposed to the atmosphere for durations of 8-15 min. A portion of the translation elongation factor 1-alpha gene (TEF-1α) was amplified and sequenced to assist in the identification of the isolates to species. The Simpson index was used to provide a measure of species richness, evenness, and diversity within and among our flight populations.

Flights	**Dates**	**Start Time**	**Stop Time**	**Sampling Time (min)**	**Number of isolates (N)**	**Number of species (s)**	**Simpson Index (Ds)***
Flight147	28-Sep-10	0959	1014	15	2	1	0
Flight148	28-Sep-10	1118	1133	15	6	4	3.60
Flight149	28-Sep-10	1412	1427	15	15	6	3.46
Flight150	28-Sep-10	1532	1540	8	13	4	1.94
Flight151	29-Sep-10	0915	0926	11	8	3	2.46
Flight152	29-Sep-10	1029	1044	15	3	2	1.80
Flight153	29-Sep-10	1323	1338	15	12	5	2.12
Flight154	01-Oct-10	0908	0923	15	9	4	3.52
Flight155	01-Oct-10	1203	1218	15	14	4	1.85
Flight156	01-Oct-10	1428	1443	15	37	8	3.38
Flight157	01-Oct-10	1700	1708	8	16	5	3.12

* Species diversity: $Ds = \frac{1}{\sum_{i=1}^{s} p_i^2}$

Where $P_i = n_i/N$

N = the total number of individuals found of all species of each flight

n_i = number of individuals of one particular species found (Table 2)

s = the number of species of each flight

Table 2: Relative abundance of different species of *Fusarium* collected during 11 UAV sampling flights 100 m above ground level in September and October, 2010. At least 12 species of *Fusarium* were recovered during these sampling flights. Two of these species may represent new species of *Fusarium*, and are referred to as '*F. babinda-like'* and '*F. equiseti-like',* since these fungi appear to be phylogenetically close to the known species *F. babinda* and *F. equiseti*. Information for potential plant hosts and geographic distribution is included as reviewed by Leslie and Summerell (2006).

***Fusarium* species**	**Plant host**	**Continent**	**Number of isolates (n_i)**										
			28-Sep-2010				**29-Sep-2010**			**01-Oct-2010**			
			F147	**F148**	**F149**	**F150**	**F151**	**F152**	**F153**	**F154**	**F155**	**F156**	**F157**
F. armeniacum	Soybean	South America	0	0	0	0	0	0	0	0	0	1	0
F. avenaceum	Legumes, carnations, cereals	North and South America, Europe, Africa, Asia, and Australia	0	0	0	0	0	0	0	0	0	1	0
F. babinda	Wheat, corn, barley, and oat	Australia, South Africa, Asia, and Europe	0	0	0	0	0	0	0	0	0	0	0
F. circinatum	Pinus species and other coniferous genera	North and South America, South Africa, and Asia	0	0	1	0	0	0	0	0	0	0	0
F. equiseti	Cereal grains, especially maize and barley	Europe, North America, Africa and Australia	0	0	0	0	0	0	0	0	0	0	0
F. fujikuroi	Maize, rice, sorghum	Europe, North and South America, Africa and Asia	0	2	2	2	1	0	0	0	1	7	2
F. graminearum	Maize, wheat and barley	Europe, North and South America, Africa and Asia	0	0	1	0	4	0	1	3	2	1	0
F. lactis	Fig	South America	0	0	0	0	0	1	1	0	0	0	0
F. lateritium	Hazelnut	North and South America, Africa, Australia, and Asia	0	0	0	0	0	0	0	0	0	2	1
F. oxysporum	Tomato, tobacco, legumes, cucurbits, sweet potatoes and banana	North and South America, Europe, Africa, Asia, and Australia	0	0	0	0	0	2	0	1	1	3	2
F. proliferatum	Maize, sorghum, mango, asparagus	North America, Africa, Asia and Australia	0	1	0	1	0	0	0	0	0	0	0
F. sambucinum	potato and corn	North and South America, Europe, Africa, Asia, and Australia	0	0	0	0	0	0	1	0	0	0	0
F. sporotrichioides	Wheat, barley, rice, and oat	North and South America, Europe, Africa, Asia, and Australia	0	1	3	1	0	0	1	2	0	4	3
F. verticillioides	Maize	Throughout the world wherever maize is cultivated	0	0	1	0	0	0	0	0	0	0	0
F. babinda/equiseti-like	unknown		2	2	7	9	3	0	8	3	10	18	8

Fig 1. Cladogram of Bayesian phylogenetic analysis of *Fusarium* strains. Red branches are reference *Fusarium* strains, and black branches are *Fusarium* strains sampled during the flights. Grey indicates non-Fusarium fungal strains used as an out group to root the tree. Flights were conducted 100 m above ground level during September and October, 2010. Node labels are posterior probabilities of the basal nodes. For more detailed visualizations of this phylogenetic analysis see Supplemental Figures S1 and S2.

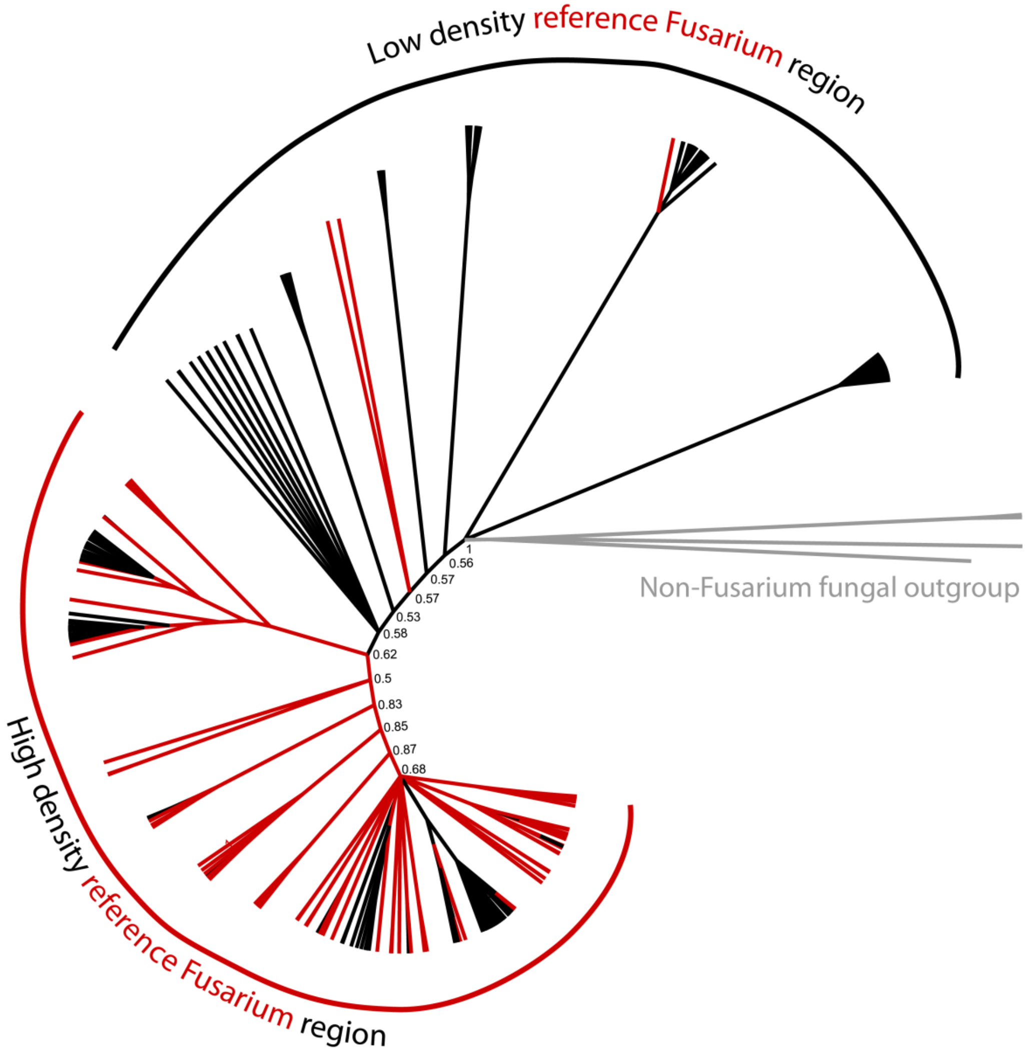


Fig 2. Comparison of different species of *Fusarium* collected during 11 UAV sampling flights 100 m above ground level in September and October, 2010. Different shades of grey represent different species of *Fusarium*. The number of species was normalized as a function of sampling time (individuals of one particular species from an individual sampling mission (n) divided by the sampling interval (min), N/min).

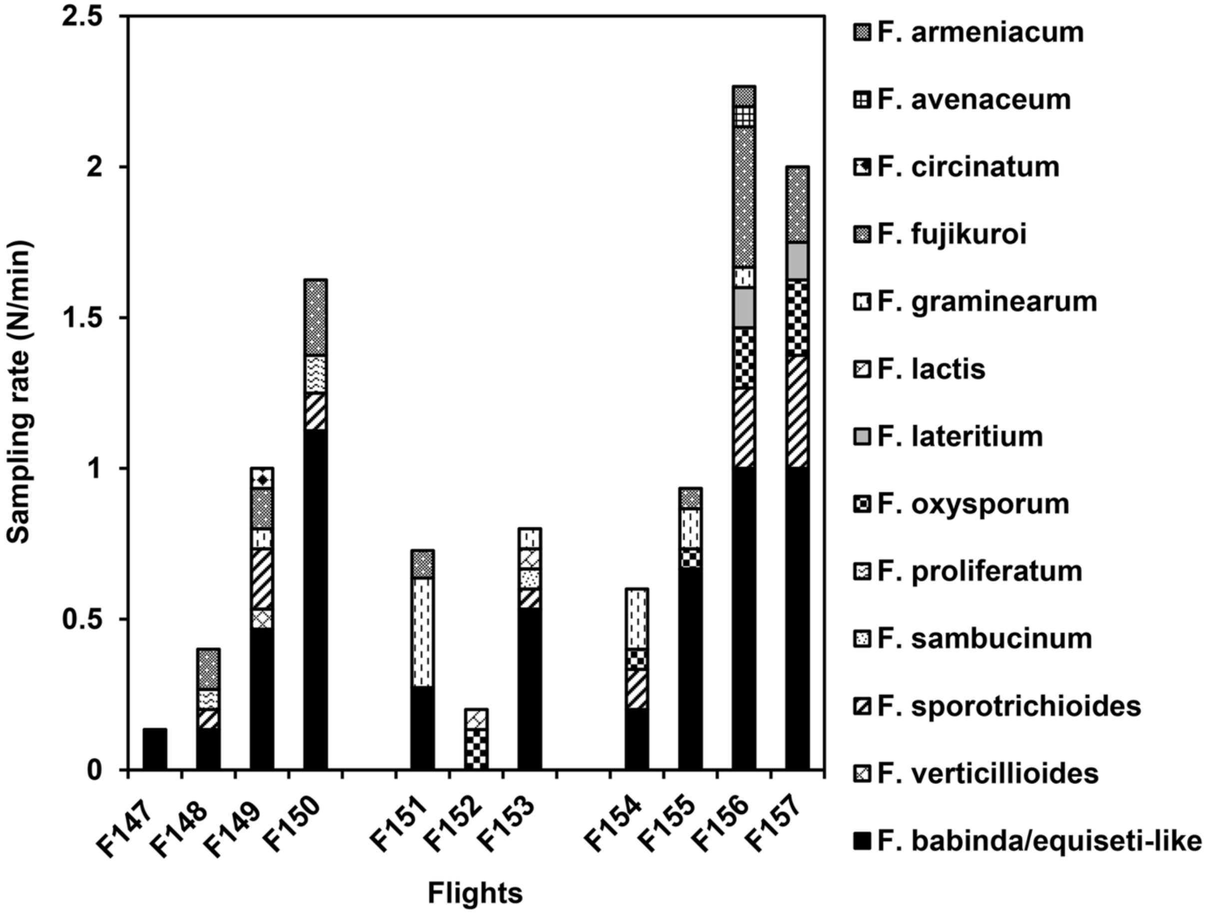
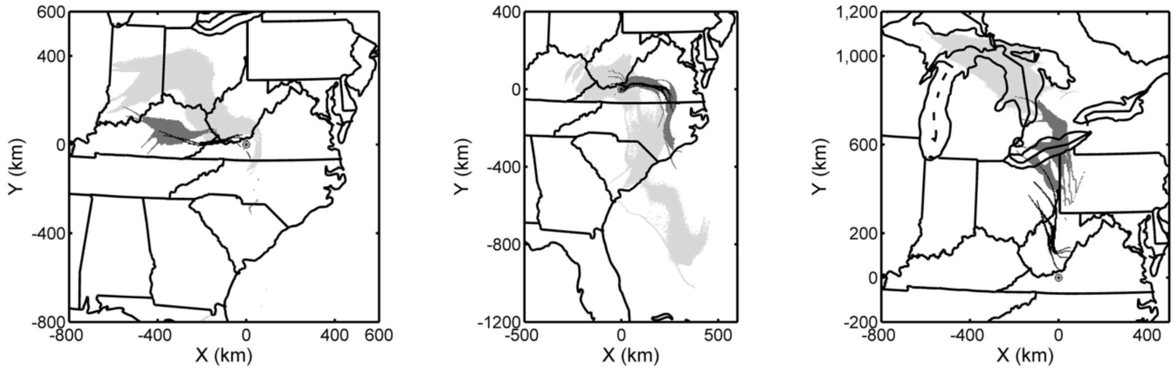
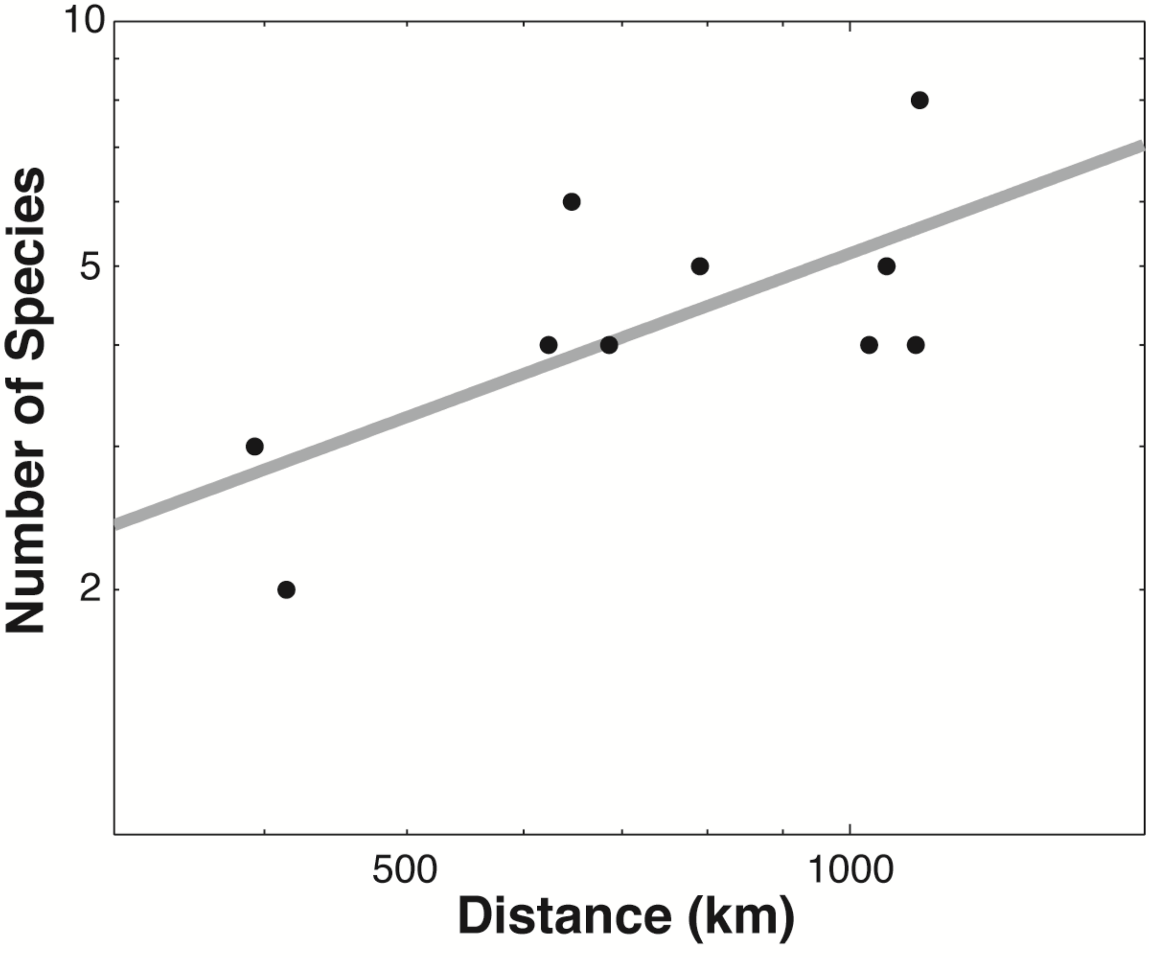


Fig 3. Identification of potential source areas through back trajectory analyses conducted 6 to 24 hours prior to our 11 UAV sampling flights for *Fusarium*. (a) Flights conducted on 28-Sep-2010 (F147-F150), (b) flights conducted on 29-Sep-2010 (flights F151-F153), and (c) flights conducted on 01-Oct-2010 (flights F154-F157). The 6 hour back-trajectory source region is shown as the darkest region, the 12 hour is medium gray, and 24 hour is the lightest gray. The source regions were mostly to the west-northwest on 28-Sep-2010, the east-southeast on 29-Sep-2010, and the north on 01-Oct-2010. Notice the source region grows with time, representing greater uncertainty over long periods of time. The x and y axes give the distances east and north in km with respect to the sampling location at Kentland Farm in Blacksburg, VA.



(a) (b) (c)

Fig 4. Trajectory distance (24 h), *x*, and the number of species of *Fusarium*, *S*, were positively correlated ($R^2 = 0.477$, $P = 0.027$) with the best fit regression line given by a power law, $\boldsymbol{S = 0.0512x^{0.668}}$, which appears as a straight line on log-log axes. Trajectory distances were calculated as the arc length of the path traveled, approximated by summing all the 3-minute segments. Starting from the sampling point, a back-trajectory was calculated using a deterministic model similar to HYSPLIT. This trajectory is very close to the mean location of the probability distribution when stochastic turbulent effects are included. The position of the trajectory was recorded every 3 minutes for a period of 24 hours. F147 is not included in the figure, since only one species was recovered on this flight.



CHAPTER 4

Seasonal associations between atmospheric assemblages of *Fusarium* collected 1 meter and 100 meters above crop fields

Binbin Lin[1], Shane D. Ross[2], Aaron J. Prussin, II[1], David G. Schmale III[1*],

[1]Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA;

[2]Department of Engineering Science and Mechanics, Virginia Tech, Blacksburg, VA;

*Corresponding author: David G. Schmale III

Email: dschmale@vt.edu;

Phone: (540) 231-6943;

Fax: (540) 231-7477

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Abstract

Spores of fungi in the genus *Fusarium* may be transported through the atmosphere over long distances. We hypothesized that assemblages of *Fusarium* collected 1 m and 100 m above crop fields would vary with height and season. To test this hypothesis, *Fusarium* was collected from the atmosphere using a Burkard volumetric sampler (BVS) 1 m above ground level and autonomous unmanned aerial vehicles (UAVs) 100 m above ground level. A total of 2,218 colony forming units (CFUs) of *Fusarium* (615 CFUs from 104 BVS sampling periods, and 1603 CFUs from 112 UAV flights) were collected over crop fields in Blacksburg, VA over four calendar years (2009-2012). Spore concentrations ranged from 0 to 13.48 and 0 to 6.41 for the BVS and the UAVs, respectively. Spore concentrations were generally higher in the fall, spring, and summer, and lower in the winter. Spore concentrations from the BVS were generally higher than those from the UAVs for both seasonal and hourly collections. A Gaussian plume transport model used to estimate the distance to the sampled source during the seasons suggested that the most distant sources (> 4 km) were sampled during winter. This work engenders hypotheses about the contribution of inoculum sources across local (farm) and regional (state) scales. An increased understanding of the aerobiology of *Fusarium* may contribute to new and improved control strategies for crop diseases causes by fusaria in the future.

Keywords: fungi, plant pathogen, inoculum source, aerobiology, aerobiological sampling, Burkard volumetric sampler, BVS, unmanned aerial vehicle, UAV, long-distance transport

1 Introduction

Fungi in the genus *Fusarium* cause devastating diseases in humans, animals, and plants (Berek et al., 2001; Bush et al., 2004; Leslie and Summerell, 2006; McMullen et al., 1997). These fungi produce asexual (conidia) and sexual (ascospores) spores that may be transported through the atmosphere from one location to another (Fernando et al., 2000; Katan et al., 1997; Maldonado-Ramirez et al., 2005; Schmale et al., 2005). The atmospheric transport of *Fusarium* is governed by processes of liberation, horizontal transport, and deposition (Isard and Gage, 2001). This transport is linked to different boundary layers in the atmosphere, including the surface boundary layer (SBL) and planetary boundary layer (PBL) (Isard and Gage, 2001). Liberation and deposition take place in the SBL, which is characterized by strong vertical gradients in wind speed, temperature, and humidity (Balsley et al., 2003). Horizontal transport takes place in the PBL, where biota can be transported long distances due to well mixed turbulence (Isard and Gage, 2001; Maldonado-Ramirez et al., 2005; Schmale et al., 2005).

The atmospheric transport distances of fungal spores range from millimeters to hundreds of kilometers (Aylor, 1998, 1999). Long distance transport has been investigated for some pathogens, for example sporangia of *Pseudoperonospora cubensis*, causal agent of tobacco blue mold, may be transported across states and even oceans (Aylor, 1986; Aylor et al., 1982). Though many fungi (and some oomycetes) of relevance to plants, domestic animals, and humans may be transported over long distances in the atmosphere, it is often difficult to pinpoint the source(s) of inoculum at both local (farm) and regional (state or country) scales.

Little is known about the aerobiological linkages between populations of *Fusarium* transported in the SBL and the PBL. Such knowledge could assist in predicting the movement of these fungi and prevent the spread of those individuals that can cause disease (Strange and Scott, 2005). Recently, an autonomous unmanned aerial vehicle (UAV) platform was developed to collect populations of *Fusarium* in the lower atmosphere (Schmale et al., 2008; Techy et al., 2010). These UAVs were used to characterize fluctuations in populations of Fusarium over short time intervals (Lin et al., 2013), and to establish that isolates of single species of *Fusarium* (*F. graminearum*) collected 40 to 320 meters above ground level cause disease and produce mycotoxins (Schmale et al., 2012). Ground-based technologies have also been developed to collected microbes near the surface of the earth, such as the Burkard volumetric sampler (BVS) (Kennedy et al., 2000). Here, we leverage technologies with UAVs and a BVS to examine associations between colony forming units (CFUs) of *Fusarium* collected 1 m and 100 m above crop fields. Previous work suggests that spore concentrations generally decrease with increasing height above ground level (Aylor, 1998; Dasgupta, 1988; de Jong et al., 2002; Khattab and Levetin, 2008). We hypothesized that CFUs of *Fusarium* collected 1 m and 100 m above crop fields would vary with height and season. To test this hypothesis, *Fusarium* was collected from the atmosphere using a Burkard volumetric sampler (BVS) 1 m above ground level and autonomous unmanned aerial vehicles (UAVs) 100 m above ground level. These collections were performed across multiple seasons over four calendar years. An increased understanding of the aerobiology of *Fusarium* may contribute to new and improved control strategies for crop diseases causes by fusaria in the future.

2 Materials and methods

2.1 Sample collection procedures

Two sampling devices were used in this study: an autonomous (self-controlling) unmanned aerial vehicle (UAV) (Schmale et al., 2008) and a Burkard volumetric sampler (BVS) (Burkard

Manufacturing Co. Ltd., Rickmansworth, Hertfordshire, England) (Kennedy et al., 2000). The BVS was used to collect *Fusarium* 1 m above ground level (AGL) for sampling intervals of 60-120 min and the UAVs were used to collect *Fusarium* 100 m AGL for sampling intervals of 10-20 min (**Figure 1**). Most of the UAV samples were collected within a Burkard sampling interval, such that both samplers were operating simultaneously and thus the resulting collections could be compared. Each sampling device contained large (9 cm diameter) plates of *Fusarium* selective medium (FSM) as described by Schmale et al. 2006 and Lin et al. 2013. All samples were collected at Virginia Tech's Kentland Farm in Blacksburg, VA across multiple seasons over four calendar years (2009, 2010, 2011, and 2012) (**Figure 2 and Table 3**).

2.2 Culturing and identification of *Fusarium*

Colonies of *Fusarium* were cultured and identified as described by Lin et al. (2013). Following each sampling mission, sampling plates were returned to the laboratory and incubated for 7-15 days at ambient room temperature. White, fluffy colonies of *Fusarium* were counted on each of the sampling plates. Each individual colony of *Fusarium* was subcultured onto new plates of FSM and single-spored into small plates of ¼ potato dextrose agar to assist in downstream identification and to prepare for cryogenic storage.

2.3 Collection efficiencies of UAVs and BVS

Spore concentrations were divided by collection efficiencies of UAVs and the BVS to get corrected aerial spore concentrations. Collection efficiencies were calculated using published methods (Aylor, 1993; Aylor et al., 2006; Chamberlain, 1975; McCartney et al., 1993). Spore sizes were determined for *Fusarium* species previously reported to be present in the atmospheric assemblages (Lin et al. unpublished observations) by measuring the length and width of three randomly selected spores as reported by Leslie and Summerell (2006) (**Table 1**). This information was used to calculate the aerodynamical diameter, d_a, of each spore described as (Chamberlain, 1975; McCartney et al., 1993),

$$d_a = 1.145\left(\frac{1}{\alpha}\right)^{\frac{1}{2}} s_d^{\frac{2}{3}} s_l^{\frac{1}{3}} \tag{1}$$

$$\alpha = 0.087\left(\frac{s_l}{s_d}\right) + 0.97 \tag{2}$$

where s_d is the spore diameter and s_l is the spore length. The d_a of each spore can be used to estimate the settling velocity, v_s, and is calculated as a function of Stokes' drag defined by (Chamberlain, 1975; McCartney et al., 1993),

$$v_s = \frac{g {d_a}^2 (\rho - \rho_a)}{18\mu} \tag{3}$$

where g is the gravitational acceleration (9.8 m s^{-2}), μ is the dynamic viscosity of the air (1.81×10^{-5} kg m^{-1} s^{-1} at STP), ρ is the density of the spore (assumed to be 1000 kg m^{-3}), and ρ_a is density of the air (assumed to be 1.2 kg m^{-3}).

Finally, sampling efficiency of the UAV, E_{pp}^{UAV}, can be calculated as previously described (Aylor et al., 2006),

$$E_{pp}^{UAV} = \frac{0.99}{1 + 0.268 {S_{UAV}}^{-1.527}} \tag{4}$$

where the Stokes number relevant for UAV sampling, S_{UAV}, is given by:

$$S_{UAV} = \frac{U_0 \tau_R}{D_p}$$

(5)

where U_0 is the flight speed (**Table 2)**, D_P is the diameter of the petri plate sampler, and τ_R is the particle relaxation time described by,

$$\tau_R = \frac{v_s}{g}$$

(6)

Sampling efficiency of the BVS was calculated as previously described (Aylor, 1993),

$$E_{pp}{}^{BVS} = 1 + \left[\left(\frac{U_a}{U_s}\right) - 1\right] f(s)$$

(7)

where U_a is the undisturbed airflow upwind of spore sampler (estimated to be ~0.1 m s^{-1} (Aylor, 1993)), U_s is the flow speed of the BVS (12 m s^{-1}), and $f(s)$ is given by,

$$f(s) = \frac{2S_{BVS}}{(1 + 2S_{BVS})}$$

(8)

where the Stokes number relevant for BVS sampling, S_{BVS}, is given by,

$$S_{BVS} = \frac{v_s U_a}{gL}$$

(9)

where L is the width of the sample entrance on the BVS (estimated to be 9 cm). **Table 1** shows the s_l, s_d, d_a, v_s, $E_{pp}{}^{UAV}$, and $E_{pp}{}^{BVS}$ for each *Fusarium spp.* we collected during sampling.

2.4 Calculations of spore concentrations

The number of colonies (spores) collected was converted to counts per unit volume of air sampled (spores/m^3). *Fusarium* spore concentrations, C (spores/m^3) were calculated as previously described (Aylor et al., 2011) from the number of spore deposited on the samplers, N_P (colony forming units or CFUs), the volumetric flow rate of air sampling, V_R ($m^3 min^{-1}$), the efficiency of spore collection by the samplers, E_{pp}, and the duration of the sampling period, T_D (min) using,

$$C = \frac{C_{raw}}{E_{pp}} \tag{10}$$

where $C_{raw} = \frac{N_P}{V_R T_D}$ is the raw (uncorrected) concentration. The V_R of the sampling device is 0.02 m^3min^{-1} for the BVS and 9.6 m^3min^{-1} per petri plate for the UAV (up to 8 plates were used per flight), and T_D was 10-205 min for the BVS and 5-28 min for the UAV (**Table 2**).

2.5 Gaussian Plume Model

For the case of a steady, continuous release of spores from a point source at a height z_s above ground level, C can be represented by an equation for a Gaussian plume (Aylor, 1999), which varies with the height of the sampler, z according to

$$C \propto \exp\left(\frac{-(z-z_s)^2}{2\sigma_z^2}\right) \tag{11}$$

where $\sigma_z = ax^b$ is the effective height of the plume (in m) which changes with the horizontal downwind distance, x, of the sampler from the source and parameters a and b are a function of meteorological conditions (Prussin et al. unpublished observations). From relationship (11), we can obtain an approximation to the horizontal distance of the sampled sources. If we assume that the BVS (at a height z_{BVS} = 1 m AGL) and the UAV (at a height z_{UAV} = 100 m AGL) samplers are simultaneously sampling from a common source, then the ratio in concentration, C_{UAV}/C_{BVS}, which would be sampled is approximately,

$$\frac{C_{UAV}}{C_{BVS}} = \exp\left(\frac{1}{2\sigma_z^2}\left[-(z_{UAV}-z_s)^2+(z_{BVS}-z_s)^2\right]\right) \tag{12}$$

This equation can be used to estimate the distance, x, to the source using C_{UAV}/C_{BVS} and an assumed height for the source, z_s. In fact, only the relative height between the source and each sampler is important. Since z_s is unknown, we can assume it is close to ground level, in which case, $z_{BVS} \approx z_s$, and (12) simplifies further.

2.6 Data analysis methods

JMP Pro 10 (SAS Institute Inc.) was used to conduct statistical analyses. Linear regression analyses were performed with sampling time intervals (0900-1100, 1100-1300, 1300-1500, 1500-1700), altitude (1 m and 100 m), and season (spring, summer, fall, and winter), with the response variable as corrected spore concentrations. ANOVA was used to analyze the differences between species and spore types that were associated with the calculations of UAV collection efficiencies.

3 Results

Collection efficiencies for UAV and BVS samplers are shown in **Table 1**. Results indicated that the collection efficiency of the BVS (99.97%) was much higher than the UAVs (1.34%), when considering macroconidia. UAV collection efficiencies were significantly different for different species ($P = 0.02$) and spore types ($P < 0.01$) of *Fusarium*. Since sample *Fusarium* populations obtained via both the UAVs and BVS are not further resolved down to the species level, it is necessary to determine an effective average efficiency for each method, E_{eff}^{UAV} and E_{eff}^{BVS}. Using 11 UAV flight populations (Lin et al., unpublished observations) which were resolved down to the species level, we were able to divide the uncorrected concentration C_{raw} for each flight population by the corrected concentration C (see eq. (10)), and obtain an effective efficiency for each flight population. Taking the average efficiency fore these 11 species-resolved flights, we obtain an average effective efficiency, essentially a weighted average of the UAV efficiencies given in **Table 1**. The effective efficiencies range from 0.16% to 4.06%, with a mean of 1.34% and a standard error of the mean of ±0.39%. For BVS sampling, the efficiencies are all 99.9% or above (**Table 1**), with an unweighted average of 99.97%, very close to perfect efficiency. Thus, we used E_{eff}^{UAV} = 1.34% and E_{eff}^{BVS} = 100%.

A total of 2,218 CFUs of *Fusarium* (615 CFUs from 104 BVS sampling periods, and 1603 CFUs from 112 UAV flights) were collected over crop fields in Blacksburg, VA over four calendar years (2009-2012) (**Table 3**). Corrected spore concentrations will be given in what follows. Spore concentrations ranged from 0 to 13.48 and 0 to 6.41 spores m^{-3} for the BVS and the UAVs, respectively. Multiple linear regression analyses indicated that there were significant differences in season ($P < 0.01$) and height ($P < 0.01$), but not time of day ($P = 0.54$). There were 30 BVS sampling intervals during which two UAV samples were obtained, in order to check for consistency in the BVS/UAV comparisons. These thirty pairs of UAV samples, which were separated in time by between 0.83 and 2.92 hours (average 1.27 h and standard deviation 0.38 h) showed a high correlation (r=0.798) in spore concentrations, consistent with earlier results which considered spore concentration correlations as a function of the time between sample flights (Lin et al. 2013).

Seasonal trends in spore concentrations are shown in Figure 2. Spore concentrations were generally higher in the fall, spring, and summer, and lower in the winter (**Figure 2**). For 104 BVS sampling periods, mean spore concentrations ranged from 0.11 to 2.93 spores m-3 across all seasons (sampling intervals: spring 35, summer 16, fall 44, and winter 9). For 112 UAV flights, mean spore concentrations ranged from 0.19 to 1.13 spores m-3 for all seasons (sampling intervals: spring 33, summer 24, fall 43, and winter 12). The lowest spore concentrations were observed in BVS samples in the winter. The highest spore concentrations were observed in BVS samples in the spring. Moreover, spore concentrations were generally higher with BVSs than those with UAVs for both seasonal and hourly data (**Table 3**, **Figure 2**, and **Figure 3**).

For BVS sampling, there were 30 sampling periods with zero collections across all seasons (no data sampling intervals: spring 9/35, summer 1/16, fall 14/44, and winter 6/9). For UAV flights, there were 9 sampling periods with zero collections across all seasons (no data sampling intervals: spring 3/33, summer 1/24, fall 2/43, and winter 3/12). In spring, there were 30 simultaneous BVS-UAV sampling intervals, during which 1 or more CFU was collected by the UAV. Of those simultaneous sample intervals, 83% (25/30) included times during which 1 or more CFU was collected by the BVS. The ratios for the other seasons are: summer 96% (22/23), fall 80% (33/41), and winter 22% (2/9). Only twice were zero CFUs collected with both the BVS and UAV.

For those times when both BVS and UAV had non-zero collections, we formed the ratio C_{UAV}/C_{BVS}, and used a Gaussian plume transport model, eq. (12), to estimate the average distance to the sampled source during the seasons, which are as follows: spring (2.1 km), summer (1.6 km), fall (1.2 km), and winter (4.1 km).

4 Discussion

Though many fungi (and some oomycetes) of relevance to plants, domestic animals, and humans may be transported over long distances in the atmosphere, it is often difficult to pinpoint the source(s) of inoculum at both local (farm) and regional (state or country) scales. We leveraged technologies with autonomous unmanned aerial vehicles (UAVs) and a Burkard volumetric sampler (BVS) to examine associations between assemblages of *Fusarium* collected 1 m and 100 m above crop fields. A total of 2,218 colony forming units (CFUs) of *Fusarium* (615 CFUs from 104 BVS sampling periods, and 1603 CFUs from 112 UAV flights) was collected over crop fields in Blacksburg, VA over four calendar years (2009-2012). This is the first multiyear study reporting the simultaneous collection of *Fusarium* at multiple heights in the atmosphere over crop fields, and extends the work of others that have examined spore concentrations of different biological agents at different heights in the atmosphere (Aylor, 1998; Dasgupta, 1988; De Jong et al., 2002; Khattab and Levetin, 2008).

Many factors need to be considered when trying to determine how spore collections varies with height (1 m vs. 100 m AGL), including changes in local source strengths of *Fusarium*, variations due to weather patterns, and the biophysical processes that control disease spread (Aylor, 1999, 2003; Isard and Gage, 2001). To collect such complete information may never be feasible, so it is important to consider how to interpret the recovered data from simpler measurements. Therefore, the number of spores counted was converted to spore concentrations (spores/m^3) by dividing the spore count by the amount of air sampled in cubic meters and the collection efficiency (related to inertial effects of spores relative to the air), which were then related to variations in environmental and biological data obtained in the sampling field (Morris et al., 2011). Measurements of spore concentration near the earth's surface (1 m AGL) and in the lower atmosphere (100 m AGL) can be made complementary. The BVS was able to show something of the extent and movement of spore clouds in the SBL, while the UAVs were able to sample horizontal spore profiles quickly in the PBL (Hirst and Stedman, 1967; Jones and Harrison, 2004).

The average collection efficiency of the BVS sampler (99.97%) is much higher than UAV samplers (1.34%), when considering different sizes of macroconidia, which is consistent with previous reports demonstrating UAVs have a much lower sampling efficiency than BVSs (Aylor, 1993; Aylor et al., 2006). In order to get an accurate estimate of aerial spore concentrations, it is important to consider sampling efficiency, as approximately 99% of the spores in the atmosphere are not collected by the UAV samplers used in this study. Additionally, in order to have a fair comparison between spore concentrations at 1 m AGL and 100 m AGL, one must consider collection efficiency due to the large differences between the two types of samplers. Sampling efficiencies varied with spore size. This is due to differences in spore sizes and shapes, which ultimately affect collection efficiencies (Aylor, 1993; Aylor et al., 2006; Leslie and Summerell, 2006). If collection efficiency was not considered, it is possible to get false results indicating one species is more prevalent when in actuality it could just have a higher collection efficiency. Collection efficiency is defined as the number of spores collected by the sampling device compared to the total number of spores present in the same unit area of the sampler. Additionally, since collection efficiency is a function of settling velocity and spore size, collection efficiency is dependent on *Fusarium spp.* with each species having unique collection efficiency (Aylor, 1993; Aylor et al., 2006). Unfortunately, the methods we presented here did not allow us to differentiate the type of spore that was collected, and thus we can only speculate on the potential spore type that was recovered for each CFU recovered. Future work should address the development of a method to determine the fraction of each spore type being collected, which will ultimately increase estimates of spore concentrations.

Spore concentrations ranged from 0 to 13.48 and 0 to 6.41 spores m^{-3} for the BVS and the UAVs, respectively. Spore concentrations were generally higher in the fall, spring, and summer, and lower in the winter. The seasonal patterns in the spore concentrations of *Fusarium* are diverse with BVSs and UAVs. Seasonal climate changes, such as temperature, rainfall, humidity, ultraviolet (UV) light and wind, are thought to play an important role in spore release, survival, and dispersal (Dill-Macky and Jones, 2000; Jones and Harrison, 2004; Lyon et al., 1984). These are dictated in part by favorable environmental conditions (Dill-Macky and Jones, 2000; Schmale et al., 2005). Overall, we observed dramatic decreases (95% for BVS and 78% for the UAVs) in the winter. Environmental conditions in Blacksburg, VA are considered to be unfavorable for spore production, and might explain the decreased number of spores observed in the winter.

Spore concentrations from the BVS were generally higher than those from the UAVs for both seasonal and hourly collections. This is consistent with previous reports demonstrating a general decrease in spore concentrations with increasing height from ground level (Bergamini et al., 2004; Chakraborty et al., 2001; Hirst and Stedman, 1967; Khattab and Levetin, 2008). However, in the winter, spore concentrations of *Fusarium* with BVSs were lower than those with UAVs. Since the atmospheric transport processes were performed in different boundary layers (Isard and Gage, 2001; Maldonado-Ramirez et al., 2005), we speculate that BVS samples are more likely to come from local sources, while the UAV samples are more likely to come from distance sources. So, perhaps local inoculum sources were inoperative in Blacksburg in the winter and thus were unable to contribute to local collections. Though the actual contribution of local and more distant sources to atmospheric assemblages of *Fusarium* remains unclear, ground level (1m AGL) had significantly higher concentrations of *Fusarium* than 100 m AGL, suggesting that sampling height is one of the many variables that influence bioaerosol levels (Khattab and Levetin, 2008).

However, from the ratio in concentration, C_{UAV}/C_{BVS}, we can use a Gaussian plume transport model to approximately determine whether what is sampled is from a distant or local source. The estimated average distance to a ground-level source during the seasons, based on the concentrations from the 1 m AGL and 100 m AGL samplers, is as follows: spring (2.1 km), summer (1.6 km), fall (1.2 km), and winter (4.1 km). In addition, winter was the season with the highest percentage of simultaneous sampling periods, 78%, during which something was collected with the UAV but nothing was collected by the BVS. Thus, there is good evidence that the samples collected during the winter are coming from more distant sources than during the other seasons, and in addition, the UAV samples are more likely to come from distant sources.

This work engenders hypotheses about the contribution of inoculum sources across local (farm) and regional (state) scales. An increased understanding of the aerobiology of *Fusarium* may contribute to new and improved control strategies for crop diseases caused by fusaria in the future.

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Table 1. Estimates of collection efficiencies with unmanned aerial vehicles (UAVs) and a Burkard volumetric sampler (BVS) for different spore types (macroconidia, mesoconidia, microconidia, and ascospores) from 14 species of *Fusarium*. The species listed were identified from flight collections reported in Lin et al., unpublished observations.

Species	Spore type	Spore Diameter (μm) [A]	Spore Length (μm) [A]	d_a (μm) [B]	v_s (mm/s) [C]	E_{pp}^{UAV} [D]	E_{pp}^{BVS} [E]
F. armeniacum	Macroconidium	2.9	56	5.47	0.90	1.34%	99.98%
F. avenaceaum	Macroconidium	2.9	59	5.48	0.90	1.35%	99.98%
	Ascospore	4.5	16	6.95	1.45	2.75%	99.97%
F. babinda	Macroconidium	3.7	38	6.75	1.37	2.52%	99.97%
	Microconidium	2.9	15	4.82	0.70	0.92%	99.98%
F. circinatum	Macroconidium	2.9	29	5.27	0.84	1.20%	99.98%
	Microconidium	2.9	9	4.35	0.57	0.67%	99.99%
	Ascospore	5	14	7.32	1.61	3.21%	99.96%
F. equiseti	Macroconidium	1.5	85	2.72	0.22	0.16%	99.99%
	Ascospore	5	27	8.37	2.11	4.75%	99.95%
F. fujikuroi	Macroconidium	2.9	41	5.41	0.88	1.30%	99.98%
	Microconidium	2.9	15	4.82	0.70	0.92%	99.98%
	Ascospore	5	15	7.44	1.67	3.37%	99.96%
F. graminearum	Macroconidium	4.4	56	8.16	2.00	4.41%	99.95%
	Ascospore	3.5	21	5.96	1.07	1.74%	99.98%
F. lactis	Macroconidium	2.9	38	5.39	0.87	1.28%	99.98%
	Microconidium	2.9	9	4.35	0.57	0.67%	99.99%
F. lateritium	Macroconidium	4.4	56	8.16	2.00	4.41%	99.95%
	Ascospore	7	17	9.91	2.96	7.71%	99.93%
F. oxysporum	Macroconidium	3.7	44	6.83	1.40	2.61%	99.97%
	Microconidium	2.9	9	4.35	0.57	0.67%	99.99%
F. proliferatum	Macroconidium	2.9	41	5.41	0.88	1.30%	99.98%
	Microconidium	2.2	6	3.2	0.31	0.26%	99.99%
	Ascospore	5	16	7.55	1.71	3.51%	99.96%
F. sambucinum	Macroconidium	5.1	44	9.13	2.51	6.10%	99.94%
	Ascospore	8	24	11.91	4.26	12.75%	99.90%
F. sporotrichioides	Macroconidium	2.9	32	5.32	0.85	1.24%	99.98%
	Mesoconidium	2.9	25	5.19	0.81	1.15%	99.98%
	Microconidium	4.4	7	5.59	0.94	1.43%	99.98%
F. verticillioides	Macroconidium	2.9	62	5.48	0.90	1.35%	99.98%
	Microconidium	2.9	10	4.45	0.60	0.72%	99.99%

[A] Spore dimensions (length and width) were estimated by measuring three spores for each species as listed in Leslie and Summerell (2006).

[B] Calculated using **eq. 1**.

[C] Calculated using **eq. 3**.

[D] Calculated using **eq. 4**. The flight speed of the UAVs was 90 km hr^{-1} and each sampling plate was 90 mm wide.

[E] Calculated using **eq. 7**. The flow rate of the BVS was 20 L/min with an opening of 9 cm.

Table 2. Parameters involved in estimating the aerial concentration and collection efficiency of *Fusarium* spores.

Parameter	Value	Source
g	9.8 m s^{-2}	Physical constant
μ	1.81 x 10^{-5} kg $m^{-1}s^{-1}$	Physical constant
ρ	1000 kg m^{-3}	(Chamberlain, 1975)
ρ_a	1.2 kg m^{-3}	Physical constant
U_0	90 km hr^{-1}	UAV onboard measurement
D_P	9 cm	Diameter of petri dish
L	9 cm	Length of BVS opening
U_a	0.1 m s^{-1}	(Aylor, 1993)
U_s	12 m s^{-1}	(Aylor, 1993)
BVS flow rate	0.02 $m^3 min^{-1}$	(Kennedy et al., 2000)
UAV flow rate	9.6 m^3 min^{-1}	(Aylor et al., 2011)
E_{eff}^{UAV}	$\approx$1.34 %	Derived parameter

Table 3. Colony forming units (CFUs) of *Fusarium* collected with a Burkard volumetric sampler (BVS) 1 m above ground level and an unmanned aerial vehicle (UAV) 100 m above ground level. Samples were collected at Virginia Tech's Kentland Farm in Blacksburg, VA over four calendar years (2009, 2010, 2011, & 2012). CFUs were converted to concentrations (number of viable spores/m^3 of air sampled).

Year	Number of UAV flights	CFUs from UAV flights	Number of BVS intervals	CFUs from BVS	Mean spore concentrations from UAVs (spores/m^3)*	Mean spore concentrations from BVS (spores/m^3)*
2009	14	70	10	87	0.52	1.81
2010	24	441	18	163	1.28	2.56
2011	60	1028	62	354	0.86	2.43
2012	14	64	14	11	0.23	0.27

*Spore concentrations from UAVs and BVSs were calculated using **eq. 10** in the text.

Figure 1: Illustration of sampling plan for *Fusarium* using a Burkard volumetric sampler (BVS) 1 m above ground level (right) and an unmanned aerial vehicle (UAV) 100 m above ground level (left). The BVS collected samples for 120 minutes, and the UAVs collected samples for 20 minutes. Both samplers were operated concurrently.

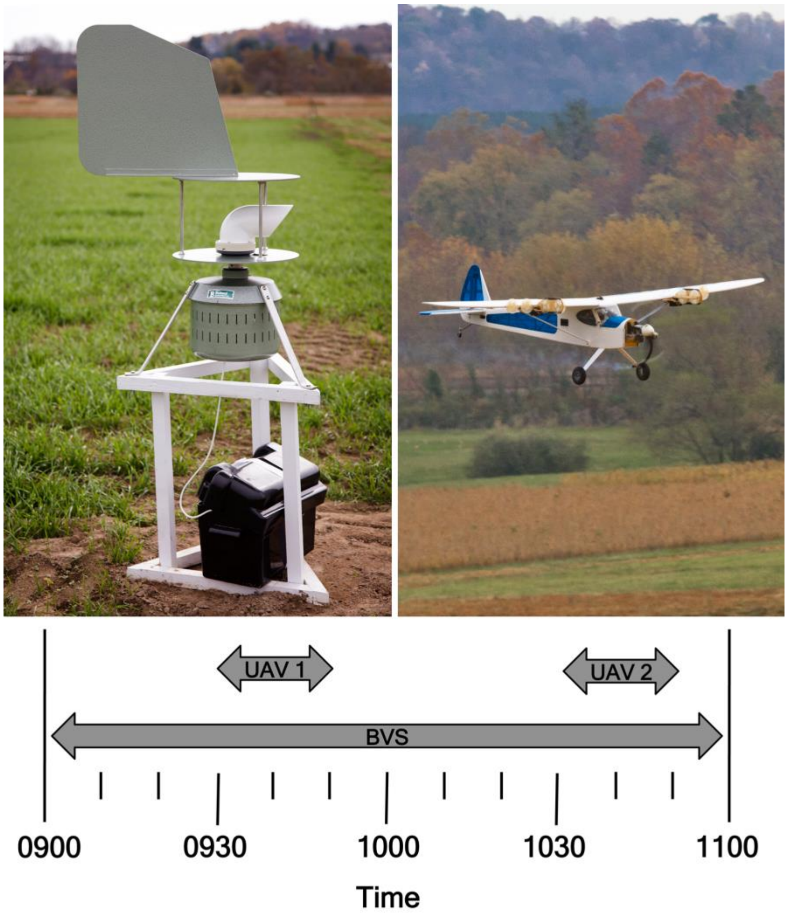


Figure 2: Seasonal collections of *Fusarium* with a Burkard volumetric sampler (BVS) 1 m above ground level and an unmanned aerial vehicle (UAV) 100 m above ground level. Samples were collected at Virginia Tech's Kentland Farm in Blacksburg, VA over four calendar years (2009, 2010, 2011, & 2012). CFUs were converted to concentrations (number of viable spores/m^3 of air sampled). Mean spore concentrations (spores/m^3) across seasons between UAV and BVS are reported. Error bars represent the standard error of the mean. The number of collections contributing to each mean is denoted above each bar.

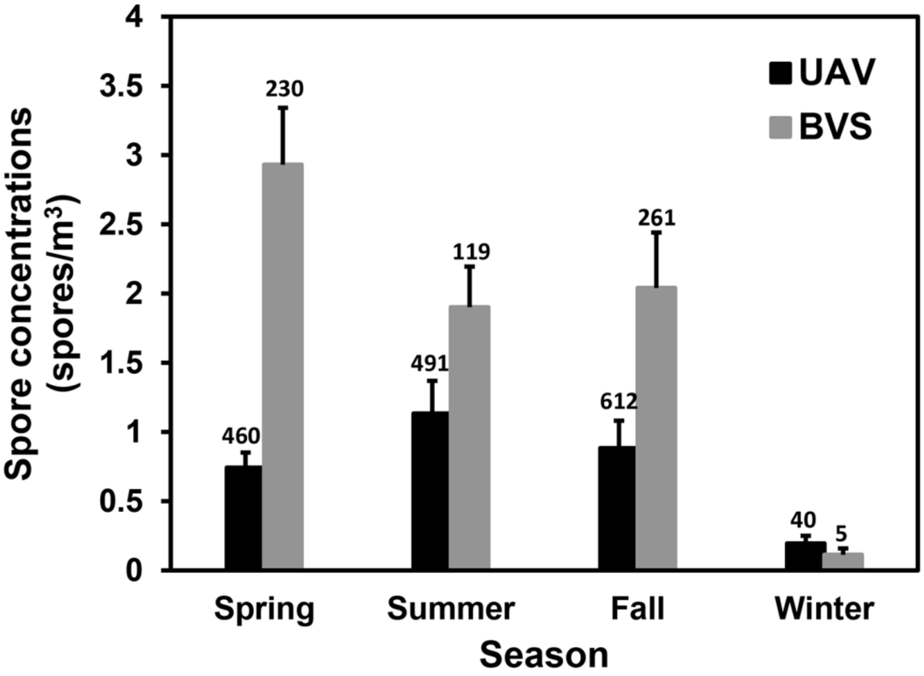
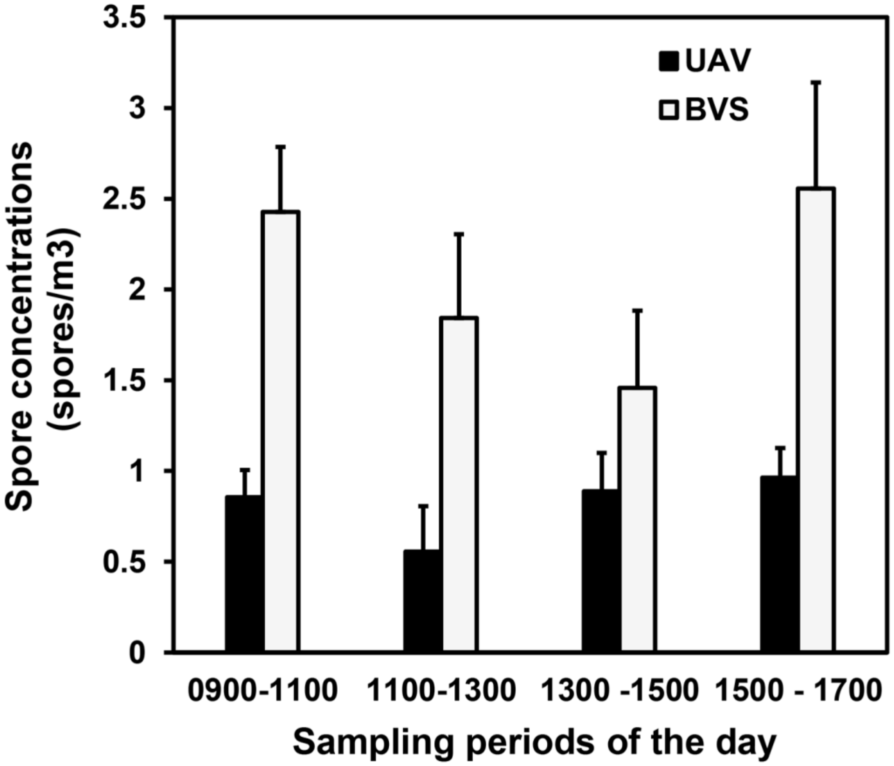


Figure 3. Mean spore concentrations (number of viable spores/m^3 of air sampled) of *Fusarium* collected with a Burkard volumetric sampler (BVS) 1 m above ground level and an unmanned aerial vehicle (UAV) 100 m above ground level across four different sampling intervals (0900-1100, 1100-1300, 1300-1500, and 1500-1700). Samples were collected at Virginia Tech's Kentland Farm in Blacksburg, VA over four calendar years (2009, 2010, 2011, & 2012).



CHAPTER 5

Conclusions and Future Directions

This work has expanded our knowledge on the movement and structure of atmospheric populations of *Fusarium*. The main results of this work indicated that (1) consecutive collections of *Fusarium* at 100 m demonstrated small variations in counts, and the similarity between collections decreased as the time between sampling intervals increased, (2) diverse atmospheric populations of *Fusarium* appeared to be associated with multiple source regions, and the number of *Fusarium* species collected with UAVs increased back-trajectory distance of the sampled air, (3) the distribution of spore concentrations was similar for both samplers over different times of the day, spore concentrations for both samplers varied with season, and spore concentrations were generally higher with BVS samplers than those with UAVs for both hourly and seasonal data, and (4) the three different isolates tested were able to cause plant diseases in three different hosts (wheat, corn, and pine), confirming that these were potential agents of disease.

Future studies should systematically investigate the influence of various factors contributing to the atmospheric collections: (1) sampling *Fusarium* with UAVs from multiple geographic locations at the same time, (2) investigating the relationship of the host ranges and structure of atmospheric populations of *Fusarium*, (3) assessing the source regions of *Fusarium* and its transport distances in the atmosphere, (4) determining the seasonal pattern of the structure of atmospheric populations of *Fusarium*, and (5) examining the association of atmospheric transport barriers (ATBs) and populations of specific *Fusarium* species.

Our research has demonstrated that collections of *Fusarium* in the lower atmosphere that are sampled over small time scales are likely to be more similar, in terms of bulk concentration, than those sampled over large time scales (Lin et al., 2013) dropping to nearly zero correlation after ~9 hours. In other words, the correlation in concentration decreases with increasing time between flights. This work supports the idea that atmospheric populations of *Fusaria* are well mixed, and large changes in the recovery of *Fusaria* in the lower atmosphere may be attributed to large-scale phenomena (e.g., ATBs) operating across varying temporal and spatial scales (Lin et al., 2013; Miedaner et al., 2001; Tallapragada et al., 2011). Future work may include sampling *Fusarium* with UAVs at multiple geographic locations, which may help resolve the spatial variations in the punctuated changes. UAVs can be flown at well-spaced, distinct geographic locations simultaneously. *Fusarium* samples collected with UAVs from multiple locations at the same time will provide opportunities to investigate the geographic origin of *Fusarium* species using the methods based on population genetics, coalescence, and phylogenetic analysis (Stukenbrock and McDonald, 2008). These future studies will increase our understanding of the ecological processes leading to the emergence of new pathogens that may be potential risks in future agricultural systems (Stukenbrock and McDonald, 2008).

Results from Chapter 3 suggested that diverse atmospheric populations of *Fusarium* appeared to be associated with multiple sources from different regions. We collected species of *Fusarium* with UAVs which represent so many different elements of the life history of *Fusarium*; species representing both broad and narrow host ranges, and species representing both broad and narrow source regions worldwide. This work offered a promising hypothesis to the relationship of the host ranges and structure of atmospheric populations of *Fusarium,* which can be tested using molecular technologies coupled with phylogenetic analysis (Morris et al., 2008). The atmospheric transport processes of *Fusarium* may be similar to the water cycle, which plays an important role in the dissemination of the plant pathogen *Pseudomonas syringae* (Morris et al., 2007; Morris et al., 2008). This future work may provide a thorough understanding of the ecology and life history of pathogens by evaluating the importance of non-agricultural habitats (e.g., soil, cloud, wild plant, and animal) in the evolution of a plant pathogen and the emergence of virulence (Morris et al., 2009).

Differences between *Fusarium* samples collected with BVSs 1 m and UAVs 100 m AGL are currently focused on spore concentrations. Significant differences in the concentrations of *Fusarium* spores with both samplers were observed for both hourly and seasonal data (Lin and Schmale, unpublished observations). We speculate that spores collected with UAVs (100 m AGL), have been transported long distances in the planetary boundary, where spores can be transported long distances due to well mixed turbulence (Isard and Gage, 2001; Maldonado-Ramirez et al., 2005), and are more likely to come from regional sources. However, it is currently unknown whether the sources of *Fusarium* for BVSs (1 m AGL) are from either local or distant sources or both, since spore release (local sources) and deposition (distant sources) take place in the surface boundary layer (Isard and Gage, 2001). Future studies should be focused on the development of ways to assess the sources regions of *Fusarium* and to identify realistic transport distances in the lower atmosphere. One approach would be to combine sequence and structure information of atmospheric populations of *Fusarium* with effective transport Models to assess and validate spread (Bowers et al., 2011; Knights et al., 2011).

It is also important for future work to focus on the seasonal motion and structure of atmospheric populations of *Fusarium*. Understanding seasonal patterns can assist with understanding the impact of climate change on disease dynamics (Doohan et al., 2003; Fernando et al., 2000; Inch et al., 2005). Future work should be focused on further investigating trends in species composition/diversity and trying to determine what kind of species can be carried in the atmosphere throughout all of the seasons and which are only common in a specific season.

Previous research has demonstrated that large-scale atmospheric features (e.g., ATBs) are associated with the long-distance transport of *Fusarium* in the lower atmosphere (Schmale et al., 2012; Tallapragada et al., 2011). However, they were unable to account for the fluctuations that have taken place in the structure of atmospheric populations of *Fusarium*. These fluctuations likely occur on a spatial scale smaller than the large-scale atmospheric features, something more on the scale (< 10 km) of a Gaussian plume (Aylor, 1999). Further analyses should be focused on identifying the population structure of the *Fusarium* collected on both sides of ATBs. Moreover, the future work can examine patterns of genetic diversity within and between species of atmospheric populations of *Fusarium* associated with ATBs.

Understanding the biota that inhabits our atmosphere enhances our ability to predict its influence on agricultural crops, the water cycle, weather patterns, and climate. On-going research is attempting to answer some of the many questions that still remain on the importance of microbial communities in the atmosphere (DeLeon-Rodriguez et al., 2013; Després et al., 2012; Giongo et al., 2013). Our research contributes to the overall knowledge of the role the genus *Fusarium* plays in these microbial communities.

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APPENDIX A

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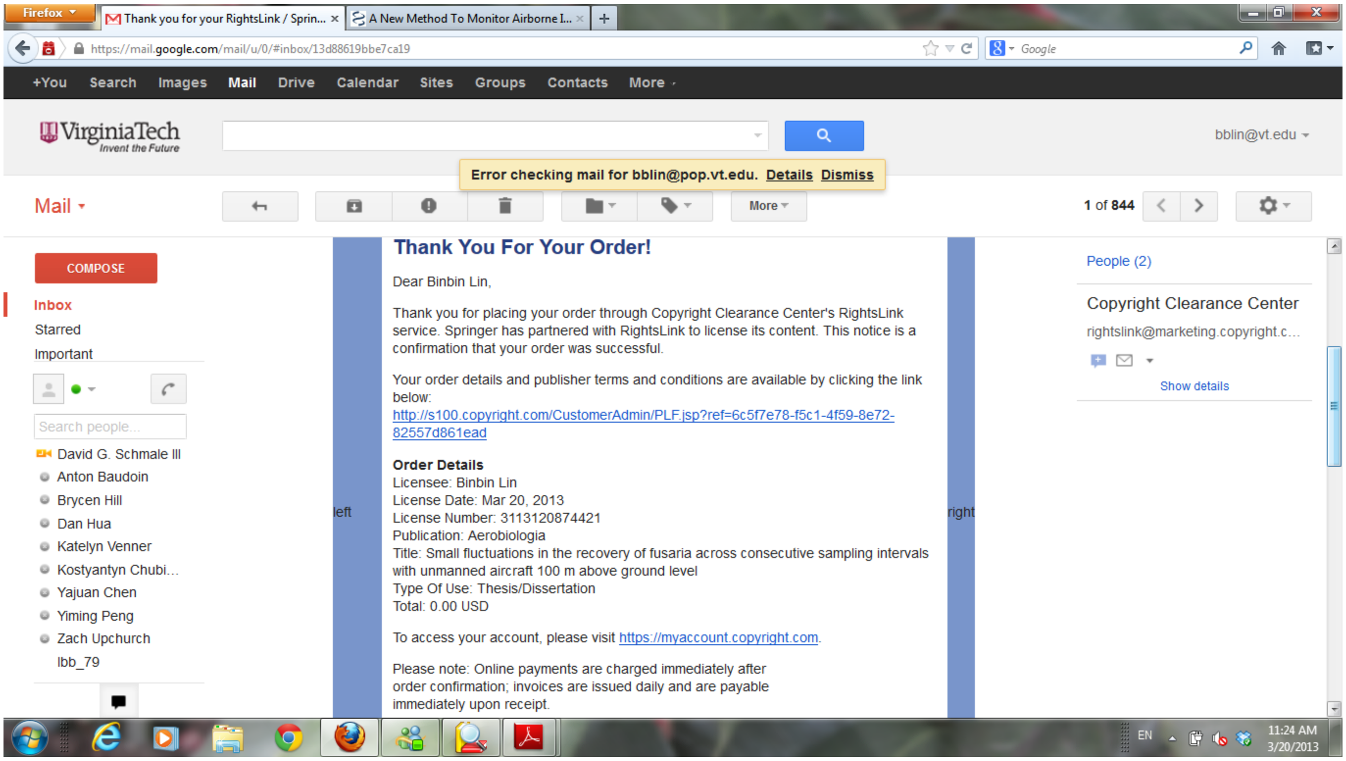

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APPENDIX B
BVS and UAV sampling information

Table 1. Sampling intervals with a Burkard volumetric sampler (BVS) 1 m above ground level across all seasons over four calendar years (2009, 2010, 2011, & 2012).

Burk#	Date	Season	Start time	Stop time	Time (min)
B1	09-Nov-09	Fall 2009	9:10 AM	12:00 PM	170.0
B2	09-Nov-09	Fall 2009	12:02 PM	3:00 PM	178.0
B3	10-Nov-09	Fall 2009	9:00 AM	12:00 PM	180.0
B4	10-Nov-09	Fall 2009	12:02 PM	1:00 PM	58.0
B5	13-Nov-09	Fall 2009	9:00 AM	12:00 PM	180.0
B6	13-Nov-09	Fall 2009	12:02 PM	3:00 PM	178.0
B7	16-Nov-09	Fall 2009	9:02 AM	12:00 PM	178.0
B8	16-Nov-09	Fall 2009	12:02 PM	3:05 PM	183.0
B9	17-Nov-09	Fall 2009	9:00 AM	12:05 PM	185.0
B10	17-Nov-09	Fall 2009	12:07 PM	3:01 PM	174.0
B11	14-Jan-10	Winter2010	9:25 AM	12:00 PM	155.0
B12	14-Jan-10	Winter2010	12:01 PM	3:02 PM	181.0
B13	15-Jan-10	Winter2010	9:50 AM	12:10 PM	140.0
B14	09-Mar-10	Spring 2010	9:15 AM	11:55 AM	160.0
B15	09-Mar-10	Spring 2010	11:57 AM	3:00 PM	183.0
B16	10-Mar-10	Spring 2010	9:00 AM	11:58 AM	178.0
B17	10-Mar-10	Spring 2010	12:00 PM	3:00 PM	180.0
B18	11-Mar-10	Spring 2010	8:58 AM	11:00 AM	122.0
B19	15-Jul-10	Summer 2010	8:59 AM	12:20 PM	201.0
B20	16-Jul-10	Summer 2010	9:03 AM	12:05 PM	182.0
B21	28-Sep-10	Fall 2010	9:20 AM	12:03 PM	163.0
B22	28-Sep-10	Fall 2010	12:04 PM	3:02 PM	178.0
B23	28-Sep-10	Fall 2010	3:04 PM	4:00 PM	56.0
B24	29-Sep-10	Fall 2010	9:00 AM	12:01 PM	181.0
B25	29-Sep-10	Fall 2010	12:02 PM	2:00 PM	118.0
B26	01-Oct-10	Fall 2010	9:00 AM	12:25 PM	205.0
B27	01-Oct-10	Fall 2010	12:25 PM	2:57PM	152.0
B28	01-Oct-10	Fall 2010	2:58 PM	6:15 PM	197.0
B29	04-Apr-11	Spring 2011	9:30 AM	11:53 AM	143.0
B30	06-Apr-11	Spring 2011	9:00 AM	10:57 AM	57.0
B31	06-Apr-11	Spring 2011	11:00 AM	12:28 PM	88.0
B32	06-Apr-11	Spring 2011	3:00 PM	5:00 PM	120.0
B33	07-Apr-11	Spring 2011	9:00 AM	10:58 AM	118.0
B34	07-Apr-11	Spring 2011	11:00 AM	12:58 PM	118.0
B35	07-Apr-11	Spring 2011	1:00 PM	2:58 PM	118.0
B36	07-Apr-11	Spring 2011	3:00 PM	5:00 PM	120.0

B37	08-Apr-11	Spring 2011	8:30 AM	10:27 AM	117.0
B38	08-Apr-11	Spring 2011	10:30 AM	12:43 PM	133.0
B39	08-Apr-11	Spring 2011	12:45 PM	2:47 PM	122.0
B40	08-Apr-11	Spring 2011	2:49 PM	3:58 PM	69.0
B41	11-Apr-11	Spring 2011	9:00 AM	10:59 AM	119.0
B42	16-May-11	Spring 2011	9:07 AM	11:12 AM	125.0
B43	16-May-11	Spring 2011	11:15 AM	1:11 PM	116.0
B44	16-May-11	Spring 2011	1:11 PM	3:16 PM	125.0
B45	17-May-11	Spring 2011	9:08 AM	11:06 AM	118.0
B46	17-May-11	Spring 2011	11:08 AM	11:56 AM	48.0
B47	18-May-11	Spring 2011	9:03 AM	10:59 AM	116.0
B48	18-May-11	Spring 2011	11:00 AM	1:02 PM	122.0
B49	18-May-11	Spring 2011	1:05 PM	3:10 PM	125.0
B50	18-May-11	Spring 2011	3:12PM	4:56 PM	104.0
B51	19-May-11	Spring 2011	9:18 AM	11:15 AM	117.0
B52	19-May-11	Spring 2011	11:18 AM	1:40 PM	142.0
B53	19-May-11	Spring 2011	1:42 PM	3:24 PM	102.0
B54	22-Aug-11	Summer 2011	9:00 AM	11:00 AM	120.0
B55	22-Aug-11	Summer 2011	11:01 AM	2:00 PM	119.0
B56	23-Aug-11	Summer 2011	9:15 AM	11:00 AM	105.0
B57	23-Aug-11	Summer 2011	11:01 AM	1:00PM	119.0
B58	23-Aug-11	Summer 2011	1:00 PM	3:00 PM	120.0
B59	23-Aug-11	Summer 2011	3:00 AM	5:00 AM	120.0
B60	24-Aug-11	Summer 2011	9:00 AM	11:00 AM	120.0
B61	24-Aug-11	Summer 2011	11:05 AM	1:00 PM	115.0
B62	24-Aug-11	Summer 2011	1:00PM	3:00 PM	120.0
B63	25-Aug-11	Summer 2011	8:55 AM	11:00 AM	125.0
B64	25-Aug-11	Summer 2011	11:01 AM	1:00 PM	119.0
B65	26-Aug-11	Summer 2011	9:05 AM	11:00 AM	115.0
B66	26-Aug-11	Summer 2011	11:01 AM	1:00 PM	119.0
B67	26-Aug-11	Summer 2011	1:01 PM	3:00 PM	119.0
B68	24-Oct-11	Fall 2011	9:15 AM	11:00 AM	105.0
B69	24-Oct-11	Fall 2011	11:01 AM	1:00 PM	119.0
B70	24-Oct-11	Fall 2011	1:01 PM	3:05 PM	124.0
B71	24-Oct-11	Fall 2011	3:06 PM	4:35PM	89.0
B72	25-Oct-11	Fall 2011	9:15 AM	9:35 AM	20.0
B73	25-Oct-11	Fall 2011	9:36 AM	10:30 AM	54.0
B74	25-Oct-11	Fall 2011	10:31 AM	10:51 AM	20.0
B75	25-Oct-11	Fall 2011	10:52 AM	12:00 PM	68.0
B76	25-Oct-11	Fall 2011	12:01PM	12:21 PM	20.0
B77	25-Oct-11	Fall 2011	12:22 PM	1:15 PM	53.0

B78	25-Oct-11	Fall 2011	1:16 PM	1:36 PM	20.0
B79	25-Oct-11	Fall 2011	1:37 PM	2:30 PM	53.0
B80	25-Oct-11	Fall 2011	2:31 PM	2:41 PM	10.0
B81	25-Oct-11	Fall 2011	2:42 PM	3:42 PM	60.0
B82	25-Oct-11	Fall 2011	3:43 PM	4:03 PM	20.0
B83	26-Oct-11	Fall 2011	9:00 AM	9:55 AM	55.0
B84	26-Oct-11	Fall 2011	9:56 AM	10:16 AM	20.0
B85	26-Oct-11	Fall 2011	10:16 AM	12:05PM	109.0
B86	26-Oct-11	Fall 2011	12:05 PM	12:25 AM	20.0
B87	26-Oct-11	Fall 2011	12:26 PM	1:15 PM	49.0
B88	26-Oct-11	Fall 2011	1:16 PM	1:36 PM	20.0
B89	26-Oct-11	Fall 2011	1:36 PM	2:30 PM	54.0
B90	26-Oct-11	Fall 2011	2:32PM	2:52 PM	20.0
B91	26-Oct-11	Fall 2011	2:52 PM	3:30 PM	38.0
B92	27-Oct-11	Fall 2011	9:00 AM	9:30 AM	30.0
B93	28-Oct-11	Fall 2011	9:00 AM	11:00 AM	120.0
B94	10-Jan-12	Winter 2012	9:00 AM	11:00 AM	120.0
B95	10-Jan-12	Winter 2012	11:00 AM	1:00 PM	120.0
B96	10-Jan-12	Winter 2012	1:00 PM	3:00 PM	120.0
B97	10-Jan-12	Winter 2012	3:00 PM	4:30 PM	90.0
B98	12-Jan-12	Winter 2012	9:00 AM	11:00 AM	120.0
B99	12-Jan-12	Winter 2012	11:00 AM	1:00 PM	120.0
B100	02-Apr-12	Spring 2012	9:15 AM	11:00 AM	105.0
B101	02-Apr-12	Spring 2012	11:00 AM	1:00 PM	120.0
B102	02-Apr-12	Spring 2012	1:00 PM	3:00 PM	120.0
B103	03-Apr-12	Spring 2012	9:00 AM	11:00 AM	120.0
B104	03-Apr-12	Spring 2012	11:00 AM	1:00 PM	120.0
B105	03-Apr-12	Spring 2012	1:00 PM	3:00 PM	120.0
B106	03-Apr-12	Spring 2012	3:00 PM	4:15 PM	75.0
B107	04-Apr-12	Spring 2012	9:00 AM	11:00 AM	120.0

Table 2. Sampling intervals with an unmanned aerial vehicle (UAV) 100 m above ground level across all seasons over four calendar years (2009, 2010, 2011, & 2012).

Flight#	Date	Season	Start time	Stop time	Time (min)
F116	09-Nov-09	Fall 2009	10:30 AM	10:38 AM	8.0
F117	09-Nov-09	Fall 2009	12:35 PM	12:43 PM	8.0
F118	10-Nov-09	Fall 2009	9:45 AM	9:50 AM	5.0
F119	13-Nov-09	Fall 2009	9:46 AM	9:55 AM	9.0
F120	13-Nov-09	Fall 2009	10:57 AM	11:07 AM	10.0
F121	13-Nov-09	Fall 2009	12:46 PM	12:56 PM	10.0
F122	13-Nov-09	Fall 2009	2:09 PM	2:29 PM	10.0
F123	16-Nov-09	Fall 2009	9:41 AM	9:56 AM	15.0
F124	16-Nov-09	Fall 2009	10:45 AM	11:00 AM	15.0
F125	16-Nov-09	Fall 2009	1:23 PM	1:38 PM	15.0
F126	16-Nov-09	Fall 2009	2:45 PM	3:00 PM	15.0
F127	17-Nov-09	Fall 2009	10:50 AM	11:05 AM	15.0
F128	17-Nov-09	Fall 2009	11:45 AM	12:00 PM	15.0
F129	17-Nov-09	Fall 2009	12:45 PM	1:00 PM	15.0
F130	14-Jan-10	Winter2010	1:30 PM	1:45 PM	15.0
F131	14-Jan-10	Winter2010	2:45 PM	3:00 PM	15.0
F132	15-Jan-10	Winter2010	10:35 AM	10:50 AM	15.0
F133	15-Jan-10	Winter2010	11:40 AM	11:55 PM	15.0
F134	09-Mar-10	Spring 2010	11:11 AM	11:26 AM	15.0
F135	09-Mar-10	Spring 2010	12:53 PM	1:06 PM	13.0
F136	09-Mar-10	Spring 2010	2:06 PM	2:21 PM	15.0
F137	10-Mar-10	Spring 2010	9:29 AM	9:44 AM	15.0
F138	10-Mar-10	Spring 2010	10:35 AM	10:42 AM	7.0
F143	15-Jul-10	Summer 2010	9:50 AM	10:05 AM	15.0
F144	15-Jul-10	Summer 2010	11:55 AM	12:10 PM	15.0
F145	16-Jul-10	Summer 2010	9:25 AM	9:40 AM	15.0
F146	16-Jul-10	Summer 2010	10:45 AM	11:00 AM	15.0
F147	28-Sep-10	Fall 2010	9:59AM	10:14AM	15.0
F148	28-Sep-10	Fall 2010	11:18AM	11:33AM	15.0
F149	28-Sep-10	Fall 2010	2:12PM	2:27PM	15.0
F150	28-Sep-10	Fall 2010	3:32PM	3:47PM	15.0
F151	29-Sep-10	Fall 2010	9:15AM	9:26AM	11.0
F152	29-Sep-10	Fall 2010	10:29AM	10:44AM	15.0
F153	29-Sep-10	Fall 2010	1:23PM	1:38PM	15.0

F154	01-Oct-10	Fall 2010	9:08AM	9:23AM	15.0
F155	01-Oct-10	Fall 2010	12:03PM	12:18PM	15.0
F156	01-Oct-10	Fall 2010	2:28PM	2:43PM	15.0
F157	01-Oct-10	Fall 2010	5:00PM	5:08PM	8.0
F158	06-Apr-11	Spring 2011	9:13AM	9:33AM	20.0
F159	06-Apr-11	Spring 2011	10:27AM	10:47AM	20.0
F160	06-Apr-11	Spring 2011	3:57PM	4:17PM	20.0
F161	07-Apr-11	Spring 2011	9:52AM	10:12AM	20.0
F162	07-Apr-11	Spring 2011	1:44PM	2:04PM	20.0
F163	07-Apr-11	Spring 2011	3:14PM	3:34PM	20.0
F164	07-Apr-11	Spring 2011	4:11PM	4:31PM	20.0
F165	08-Apr-11	Spring 2011	9:00AM	9:10AM	10.0
F166	08-Apr-11	Spring 2011	9:41AM	9:51AM	10.0
F167	08-Apr-11	Spring 2011	2:07PM	2:35PM	28.0
F168	08-Apr-11	Spring 2011	3:10PM	3:30PM	20.0
F169	11-Apr-11	Spring 2011	9:52AM	10:12AM	20.0
F170	16-May-11	Spring 2011	1:26PM	1:46PM	20.0
F171	16-May-11	Spring 2011	2:49PM	3:09PM	20.0
F172	18-May-11	Spring 2011	12:45PM	1:05PM	20.0
F173	18-May-11	Spring 2011	2:26PM	2:46PM	20.0
F174	18-May-11	Spring 2011	4:00PM	4:20PM	20.0
F175	19-May-11	Spring 2011	9:43AM	10:03AM	20.0
F176	19-May-11	Spring 2011	10:45AM	11:05AM	20.0
F177	19-May-11	Spring 2011	11:52AM	12:12PM	20.0
F178	19-May-11	Spring 2011	1:12PM	1:32PM	20.0
F179	19-May-11	Spring 2011	2:35PM	2:55PM	20.0
F180	22-Aug-11	Summer 2011	10:00AM	10:20AM	20.0
F181	22-Aug-11	Summer 2011	12:24PM	12:44PM	20.0
F182	23-Aug-11	Summer 2011	9:42AM	10:02AM	20.0
F183	23-Aug-11	Summer 2011	10:40AM	11:00AM	20.0
F184	23-Aug-11	Summer 2011	11:49AM	12:09PM	20.0
F185	23-Aug-11	Summer 2011	1:09PM	1:29PM	20.0
F186	23-Aug-11	Summer 2011	2:24PM	2:44PM	20.0
F187	23-Aug-11	Summer 2011	4:01PM	4:21PM	20.0
F188	24-Aug-11	Summer 2011	9:15AM	9:35AM	20.0
F189	24-Aug-11	Summer 2011	10:31AM	10:51AM	20.0
F190	24-Aug-11	Summer 2011	11:59AM	12:19PM	20.0
F191	24-Aug-11	Summer 2011	1:14PM	1:34PM	20.0
F192	24-Aug-11	Summer 2011	2:26PM	2:46PM	20.0

F193	25-Aug-11	Summer 2011	9:14AM	9:34AM	20.0
F194	25-Aug-11	Summer 2011	10:28AM	10:48AM	20.0
F195	25-Aug-11	Summer 2011	12:00PM	12:20PM	20.0
F196	26-Aug-11	Summer 2011	10:05AM	10:25AM	20.0
F197	26-Aug-11	Summer 2011	11:15AM	11:35AM	20.0
F198	26-Aug-11	Summer 2011	1:13PM	1:33PM	20.0
F199	26-Aug-11	Summer 2011	2:19PM	2:39PM	20.0
F200	24-Oct-11	Fall 2011	10:08AM	10:28AM	20.0
F201	24-Oct-11	Fall 2011	11:33AM	11:53AM	20.0
F202	24-Oct-11	Fall 2011	1:03PM	1:23PM	20.0
F203	24-Oct-11	Fall 2011	2:18PM	2:38PM	20.0
F204	24-Oct-11	Fall 2011	3:30PM	3:50PM	20.0
F205	25-Oct-11	Fall 2011	9:15AM	9:35AM	20.0
F206	25-Oct-11	Fall 2011	10:31AM	10:51AM	20.0
F207	25-Oct-11	Fall 2011	12:00PM	12:20PM	20.0
F208	25-Oct-11	Fall 2011	1:16PM	1:36PM	20.0
F209	25-Oct-11	Fall 2011	2:31PM	2:41PM	10.0
F210	25-Oct-11	Fall 2011	3:43PM	4:03PM	20.0
F211	26-Oct-11	Fall 2011	9:56AM	10:16AM	20.0
F212	26-Oct-11	Fall 2011	12:05PM	12:25PM	20.0
F213	26-Oct-11	Fall 2011	1:16PM	1:36PM	20.0
F214	26-Oct-11	Fall 2011	2:32PM	2:52PM	20.0
F215	27-Oct-11	Fall 2011	8:58AM	9:18AM	20.0
F216	28-Oct-11	Fall 2011	9:15AM	9:35AM	20.0
F217	28-Oct-11	Fall 2011	10:29AM	10:39AM	10.0
F218	10-Jan-12	Winter 2012	9:19AM	9:39AM	20.0
F219	10-Jan-12	Winter 2012	10:16AM	10:36AM	20.0
F220	10-Jan-12	Winter 2012	11:14AM	11:34AM	20.0
F221	10-Jan-12	Winter 2012	12:28PM	12:48PM	20.0
F222	10-Jan-12	Winter 2012	1:29PM	1:49PM	20.0
F223	10-Jan-12	Winter 2012	2:30PM	2:50PM	20.0
F224	12-Jan-12	Winter 2012	11:36AM	11:56AM	20.0
F225	12-Jan-12	Winter 2012	12:26PM	12:46PM	20.0
F226	02-Apr-12	Spring 2012	12:25PM	12:35PM	10.0
F227	03-Apr-12	Spring 2012	9:22AM	9:32AM	10.0
F228	03-Apr-12	Spring 2012	1:30PM	1:50PM	20.0
F229	03-Apr-12	Spring 2012	2:35PM	2:55PM	20.0
F230	03-Apr-12	Spring 2012	3:38PM	3:58PM	20.0
F231	04-Apr-12	Spring 2012	9:47AM	10:07AM	20.0

Table 3. Comparisons of Fusarium-ID and GenBank for the isolates of *Fusarium* collected with a Burkard volumetric sampler (BVS) 1 m above ground level across all seasons over four calendar years (2009, 2010, 2011, & 2012).

Season	Isolate	Identification based on Fusarium-ID Query	Fusarium-ID (%)	Identification based on GenBank Query	Genbank (%)
Spring	B30N1	FD_01317_EF-1a [*Fusarium sp.*]	643 / 644 (99.84%)	Fusarium avenaceum strain CC39	647/649 (99%)
Spring	B34N1	FD_01276_EF-1a [*Fusarium commune*]	636 / 637 (99.84%)	Fusarium commune strain NRRL 22903	652/654 (99%)
Spring	B36N1	FD_00805_EF-1a [*Fusarium sp.*]	648 / 650 (99.69%)	Fusarium oxysporum strain LYF025	650/655 (99%)
Spring	B38N1	FD_01315_EF-1a [*Fusarium sp.*]	618 / 633 (97.63%)	Fusarium acuminatum strain NRRL 54218	642/642 (100%)
Spring	B38N5	FD_01317_EF-1a [*Fusarium sp.*]	643 / 647 (99.38%)	Fusarium avenaceum strain LMSA 1.09.142	650/652 (99%)
Spring	B42N2	FD_01119_EF-1a [*Fusarium graminearum*]	627 / 630 (99.52%)	Gibberella zeae isolate G5S	638/640 (99%)
Spring	B42N1	FD_01304_EF-1a [*Fusarium sp.*]	628 / 631 (99.52%)	Fusarium sporotrichioides strain NRRL 53434/2616/11	642/644 (99%)
Spring	B42N3	FD_01317_EF-1a [*Fusarium sp.*]	612 / 617 (99.18%)	Fusarium avenaceum isolate 9.7	618/621 (99%)
Spring	B43N1	FD_01304_EF-1a [*Fusarium sp.*]	627 / 630 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	643/646 (99%)
Spring	B43N2	FD_01304_EF-1a [*Fusarium sp.*]	628 / 630 (99.68%)	Fusarium sporotrichioides strain LMSA 1.09.114	641/643 (99%)
Spring	B43N3	FD_01304_EF-1a [*Fusarium sp.*]	627 / 630 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	640/643 (99%)
Spring	B43N4	FD_01304_EF-1a [*Fusarium sp.*]	628 / 631 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	641/644 (99%)
Spring	B43N5	FD_01304_EF-1a [*Fusarium sp.*]	630 / 633 (99.52%)	Fusarium sporotrichioides strain NRRL 53434/2616/11	642/644 (99%)
Spring	B43N6	FD_01304_EF-1a [*Fusarium sp.*]	630 / 633 (99.52%)	Fusarium sporotrichioides strain NRRL 53434/2616/11	643/645 (99%)
Spring	B44N1	FD_01304_EF-1a [*Fusarium sp.*]	631 / 634 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	642/645 (99%)
Spring	B44N2	FD_01304_EF-1a [*Fusarium sp.*]	629 / 632 (99.52%)	Fusarium langsethiae strain NRRL 53422/2321/2	644/648 (99%)
Spring	B44N3	FD_01304_EF-1a [*Fusarium sp.*]	629 / 632 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	641/644 (99%)
Spring	B44N4	FD_01304_EF-1a [*Fusarium sp.*]	630 / 632 (99.68%)	Fusarium sporotrichioides strain LMSA 1.09.114	644/646 (99%)
Spring	B44N7	FD_01304_EF-1a [*Fusarium sp.*]	630 / 632 (99.68%)	Fusarium sporotrichioides strain LMSA 1.09.114	640/642 (99%)
Spring	B44N5	FD_01321_EF-1a [*Fusarium sp.*]	567 / 612 (92.64%)	Fusarium cf. incarnatum H04-707S-4 PCNB	625/630 (99%)
Spring	B44N6	FD_01321_EF-1a [*Fusarium sp.*]	600 / 649 (92.44%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	648/650 (99%)
Spring	B46N2	FD_01119_EF-1a [*Fusarium graminearum*]	612 / 615 (99.51%)	Gibberella zeae strain ATCC 60309	619/621 (99%)
Spring	B47N2	FD_00986_EF-1a [*Fusarium graminearum*]	638 / 638 (100%)	Gibberella zeae isolate M02-7035S-2 DCPA	654/654 (100%)
Spring	B47N4	FD_00986_EF-1a [*Fusarium graminearum*]	617 / 618 (99.83%)	Gibberella zeae strain NRRL 31084	617/618 (99%)
Spring	B47N5	FD_00986_EF-1a [*Fusarium graminearum*]	635 / 636 (99.84%)	Gibberella zeae isolate M02-7035S-2 DCPA	647/648 (99%)
Spring	B47N6	FD_00986_EF-1a [*Fusarium graminearum*]	628 / 629 (99.84%)	Gibberella zeae isolate M02-7035S-2 DCPA	645/647 (99%)

Spring	B47N1	FD_01119_EF-1a [*Fusarium graminearum*]	628 / 630 (99.68%)	Gibberella zeae isolate G5S	643/644 (99%)
Spring	B47N3	FD_01119_EF-1a [*Fusarium graminearum*]	629 / 630 (99.84%)	Gibberella zeae isolate G5S	643/643 (100%)
Spring	B47N7	FD_01119_EF-1a [*Fusarium graminearum*]	614 / 615 (99.83%)	Gibberella zeae isolate G5S	615/615 (100%)
Spring	B47N8	FD_01119_EF-1a [*Fusarium graminearum*]	611 / 613 (99.67%)	Gibberella zeae isolate G5S	612/613 (99%)
Spring	B48N1	FD_00986_EF-1a [*Fusarium graminearum*]	629 / 632 (99.52%)	Gibberella zeae isolate CS3005	648/652 (99%)
Spring	B48N2	FD_00986_EF-1a [*Fusarium graminearum*]	633 / 638 (99.21%)	Gibberella zeae isolate M02-7035S-2 DCPA	647/652 (99%)
Spring	B49N1	FD_01304_EF-1a [*Fusarium sp.*]	634 / 637 (99.52%)	Fusarium langsethiae strain NRRL 53422/2321/2	671/677 (99%)
Spring	B50N1	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	625 / 626 (99.84%)	Gibberella intermedia isolate C33	651/655 (99%)
Spring	B50N2	FD_01304_EF-1a [*Fusarium sp.*]	630 / 631 (99.84%)	Fusarium langsethiae strain NRRL 53422/2321/2	657/661 (99%)
Spring	B50N3	F. incarnatum-equiseti species complex isolate NRRL 28714, MLST26-b	589 / 613 (96.08%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	608/623 (98%)
Spring	B50N4	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	649 / 663 (97.88%)	Gibberella intermedia isolate C33	656/669 (98%)
Spring	B51N1	FD_00986_EF-1a [*Fusarium graminearum*]	623 / 623 (100%)	Gibberella zeae strain NRRL 31084	633/636 (99%)
Spring	B51N2	FD_01119_EF-1a [*Fusarium graminearum*]	618 / 619 (99.83%)	Gibberella zeae strain LMSA 1.09.106	646/649 (99%
Spring	B51N3	FD_00986_EF-1a [*Fusarium graminearum*]	627 / 643 (97.51%)	Gibberella zeae isolate CS3005	650/668 (97%)
Spring	B51N4	FD_00986_EF-1a [*Fusarium graminearum*]	626 / 628 (99.68%)	Gibberella zeae strain NRRL 31084	642/645 (99%)
Spring	B51N5	FD_01119_EF-1a [*Fusarium graminearum*]	627 / 630 (99.52%)	Gibberella zeae isolate G5S	641/643 (99%)
Spring	B51N6	FD_00986_EF-1a [*Fusarium graminearum*]	607 / 611 (99.34%)	Gibberella zeae isolate M02-7035S-2 DCPA	644/651 (99%)
Spring	B51N7	FD_01119_EF-1a [*Fusarium graminearum*]	618 / 621 (99.51%)	Gibberella zeae isolate G5S	639/644 (99%)
Spring	B51N8	FD_00986_EF-1a [*Fusarium graminearum*]	641 / 646 (99.22%)	Gibberella zeae isolate CS3005	669/675 (99%)
Spring	B51N9	FD_01119_EF-1a [*Fusarium graminearum*]	627 / 629 (99.68%)	Gibberella zeae isolate CS3005	645/648 (99%)
Spring	B51N10	FD_00986_EF-1a [*Fusarium graminearum*]	626 / 628 (99.68%)	Gibberella zeae isolate CS3005	652/658 (99%)
Spring	B51N11	FD_00986_EF-1a [*Fusarium graminearum*]	640 / 643 (99.53%)	Gibberella zeae isolate CS3005	674/678 (99%)
Spring	B51N12	FD_01119_EF-1a [*Fusarium graminearum*]	627 / 629 (99.68%)	Gibberella zeae strain LMSA 1.09.105	636/638 (99%)
Spring	B51N13	FD_01119_EF-1a [*Fusarium graminearum*]	627 / 629 (99.68%)	Gibberella zeae isolate CS3005	654/659 (99%)
Spring	B51N14	FD_00986_EF-1a [*Fusarium graminearum*]	642 / 646 (99.38%)	Gibberella zeae isolate CS3005	676/680 (99%)
Spring	B51N15	FD_00986_EF-1a [*Fusarium graminearum*]	642 / 643 (99.84%)	Gibberella zeae isolate CS3005	678/680 (99%)

Spring	B52N1	FD_01304_EF-1a [*Fusarium sp.*]	630 / 631 (99.84%)	Fusarium langsethiae strain NRRL 53422/2321/2	657/661 (99%)
Spring	B52N2	FD_01119_EF-1a [*Fusarium graminearum*]	640 / 644 (99.37%)	Gibberella zeae isolate 152	662/665 (99%)
Spring	B52N3	FD_01304_EF-1a [*Fusarium sp.*]	627 / 631 (99.36%)	Fusarium sporotrichioides strain NRRL 29977	649/655 (99%)
Spring	B53N1	FD_01304_EF-1a [*Fusarium sp.*]	641 / 646 (99.22%)	Fusarium langsethiae strain NRRL 53422/2321/2	670/675 (99%)
Spring	B53N2	FD_01857_EF-1a [*Fusarium sp.*]	615 / 618 (99.51%)	Gibberella fujikuroi isolate PRC	642/648 (99%)
Spring	B53N3	FD_01857_EF-1a [*Fusarium sp.*]	632 / 635 (99.52%)	Gibberella fujikuroi isolate PRC	648/652 (99%)
Spring	B53N4	FD_01304_EF-1a [*Fusarium sp.*]	644 / 646 (99.69%)	Fusarium langsethiae strain NRRL 53422/2321/2	678/680 (99%)
Spring	B53N5	FD_01304_EF-1a [*Fusarium sp.*]	643 / 646 (99.53%)	Fusarium langsethiae strain NRRL 53422/2321/2	671/674 (99%)
Spring	B53N6	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	612 / 615 (99.51%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	628/632 (99%)
Spring	B102N1	FD_01647_EF-1a| F. incarnatum-equiseti species complex 7-a	607 / 616 (98.53%)	Fusarium equiseti	619/622(99%)
Spring	B104N1	FD_01635_EF-1a | F. incarnatum-equiseti species complex 18-b	594 / 597 (99.49%)	Fusarium sp. NRRL 31167	594/597(99%)
Spring	B104N2	FD_01857_EF-1a [Fusarium sp.]	587 / 588 (99.82%)	Fusarium sp. S112	594/595(99%)
Spring	B106N1	FD_01858_EF-1a [Fusarium sp.]	557 / 558 (99.82%)	Gibberella fujikuroi	558/558(100%)
Spring	B106N2	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a	597 / 635 (94.01%)	Fusarium cf. incarnatum	642/642(100%)
Summer	B19N1	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	672 / 676 (99.4%)	Fusarium sp. NRRL 5537	672/676 (99%)
Summer	B19N2	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	674 / 676 (99.7%)	Fusarium sp. NRRL 5537	674/676 (99%)
Summer	B19N3	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	664 / 683 (97.21%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	685/691 (99%)
Summer	B19N4	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	640 / 646 (99.07%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	659/665 (99%)
Summer	B19N9	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	669 / 677 (98.81%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7097S-1 DCPA	683/690 (99%)
Summer	B19N10	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	584 / 602 (97%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	608/615 (99%)
Summer	B20N2	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	641 / 645 (99.37%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	652/657 (99%)
Summer	B55N2	FD_01320_EF-1a [*Fusarium pallidoroseum*]	363 / 398 (91.2%)	Fusarium cf. incarnatum	394/406 (97%)
Summer	B55N1	FD_01321_EF-1a [*Fusarium sp.*]	595 / 619 (96.12%)	Fusarium sp. NRRL 43637	619/621 (99%)
Summer	B60N1	FD_01162_EF-1a NRRL26794 GFSC Gibberella fujikuroi species complex	504 / 588 (85.71%)	Fusarium cf. incarnatum MLST 1-c clone spt113	557/640 (87%)
Summer	B60N2	FD_01320_EF-1a [*Fusarium pallidoroseum*]	504 / 588 (85.71%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	586/628 (93%)
Summer	B60N7	FD_01320_EF-1a [*Fusarium pallidoroseum*]	465 / 507 (91.71%)	Fusarium cf. incarnatum	498/510 (98%)
Summer	B61N8	FD_01322_EF-1a [*Fusarium sp.*]	537 / 576 (93.22%)	Fusarium cf. incarnatum MLSTs 1-a and 1-c clone spt110	558/576 (97%)
Fall	B2N3	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	660 / 675 (97.77%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	673/674 (99%)
Fall	B2N8	FD_01160_EF-1a	627 / 628 (99.84%)	Fusarium subglutinans strain NRRL 22016	655/658 (99%)

Fall	B2N9	FD_01379_EF-1a [Fusarium proliferatum]	655 / 668 (98.05%)	Gibberella intermedia isolate V217	659/665 (99%)
Fall	B2N17	FD_01388_EF-1a [Fusarium verticillioides]	672 / 677 (99.26%)	Gibberella moniliformis isolate 8.3	686/692 (99%)
Fall	B2N21	FD_01388_EF-1a [Fusarium verticillioides]	669 / 673 (99.4%)	Gibberella moniliformis isolate 8.3	683/688 (99%)
Fall	B2N19	FD_01388_EF-1a [Fusarium verticillioides]	645 / 645 (100%)	Gibberella moniliformis isolate 8.3	661/664 (99%)
Fall	B2N38	FD_01388_EF-1a [Fusarium verticillioides]	669 / 675 (99.11%)	Gibberella moniliformis isolate 8.3	680/687 (99%)
Fall	B3N3	FD_00986_EF-1a [Fusarium graminearum]	640 / 642 (99.68%)	Gibberella zeae isolate CS3005	674/679 (99%)
Fall	B3N4	FD_00986_EF-1a [Fusarium graminearum]	628 / 628 (100%)	Gibberella zeae isolate CS3005	647/648 (99%)
Fall	B3N2	FD_00986_EF-1a [Fusarium graminearum]	641 / 642 (99.84%)	Gibberella zeae isolate CS3005	677/681 (99%)
Fall	B3N7	FD_00986_EF-1a [Fusarium graminearum]	641 / 644 (99.53%)	Gibberella zeae isolate CS3005	672/678 (99%)
Fall	B3N10	FD_00986_EF-1a [Fusarium graminearum]	641 / 642 (99.84%)	Gibberella zeae isolate CS3005	674/680 (99%)
Fall	B3N5	FD_01119_EF-1a [Fusarium graminearum]	629 / 629 (100%)	Gibberella zeae isolate CS3005	658/661 (99%)
Fall	B3N6	FD_01119_EF-1a [Fusarium graminearum]	630 / 631 (99.84%)	Gibberella zeae isolate CS3005	679/685 (99%)
Fall	B3N9	FD_01160_EF-1a	643 / 643 (100%)	Fusarium subglutinans strain NRRL 22016	676/678 (99%)
Fall	B3N8	FD_01378_EF-1a [Fusarium proliferatum]	628 / 634 (99.05%)	Fusarium proliferatum MUCL 31970	665/674 (99%)
Fall	B4N3	FD_00786_EF-1a [Fusarium sp.]	651 / 651 (100%)	Fusarium oxysporum strain NRRL 46602	661/666 (99%)
Fall	B4N2	FD_00786_EF-1a [Fusarium sp.]	651 / 651 (100%)	Fusarium oxysporum strain NRRL 46602	655/658 (99%)
Fall	B4N1	FD_01119_EF-1a [Fusarium graminearum]	642 / 644 (99.68%)	Gibberella zeae isolate CS3005	669/674 (99%)
Fall	B4N4	FD_01378_EF-1a [Fusarium proliferatum]	627 / 635 (98.74%)	Fusarium proliferatum isolate 2-91	652/655 (99%)
Fall	B5N2	FD_00986_EF-1a [Fusarium graminearum]	640 / 641 (99.84%)	Gibberella zeae isolate CS3005	669/675 (99%)
Fall	B5N1	FD_01119_EF-1a [Fusarium graminearum]	641 / 644 (99.53%)	Gibberella zeae isolate CS3005	675/681 (99%)
Fall	B6N1	FD_00805_EF-1a [Fusarium sp.]	655 / 655 (100%)	Fusarium oxysporum strain LYF025	663/668 (99%)
Fall	B7N1	FD_01119_EF-1a [Fusarium graminearum]	627 / 629 (99.68%)	Gibberella zeae isolate CS3005	657/662 (99%)
Fall	B9N1	FD_00986_EF-1a [Fusarium graminearum]	641 / 643 (99.68%)	Gibberella zeae isolate CS3005	670/676 (99%)
Fall	B9N2	FD_00986_EF-1a [Fusarium graminearum]	628 / 628 (100%)	Gibberella zeae isolate CS3005	657/661 (99%)
Fall	B9N3	FD_00986_EF-1a [Fusarium graminearum]	637 / 639 (99.68%)	Gibberella zeae isolate CS3005	656/658 (99%)
Fall	B9N5	FD_01119_EF-1a [Fusarium graminearum]	629 / 630 (99.84%)	Gibberella zeae isolate CS3005	658/662 (99%)
Fall	B21N1	FD_01119_EF-1a [*Fusarium graminearum*]	609 / 611 (99.67%)	Gibberella zeae isolate G5S	609/610 (99%)
Fall	B21N2	GFSC isolate NRRL 46612, MLST-Gibberella fujikuroi species complex	538 / 544 (98.89%)	Gibberella fujikuroi var.	543/545 (99%)
Fall	B21N3	FD_01119_EF-1a [*Fusarium graminearum*]	618 / 619 (99.83%)	Gibberella zeae isolate G5S	621/622 (99%)
Fall	B21N4	F. chlamydosporum species complex isolate NRRL 28578, MLST1-a	634 / 635 (99.84%)	Fusarium sp. NRRL 28578	648/652 (99%)
Fall	B21N5	FD_00986_EF-1a [Fusarium graminearum]	613 / 614 (99.83%)	Gibberella zeae isolate G5S	619/621 (99%)

Fall	B21N8	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	627 / 628 (99.84%)	Fusarium sp. NRRL 45996	627/628 (99%)
Fall	B21N9	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	621 / 625 (99.36%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	623/625 (99%)
Fall	B22N1	FD_01857_EF-1a [Fusarium sp.]	601 / 602 (99.83%)	Gibberella fujikuroi partial tef-1 gene	612/614 (99%)
Fall	B22N2	FD_01304_EF-1a [*Fusarium sp.*]	616 / 619 (99.51%)	Fusarium sporotrichioides strain NRRL 29977	624/628 (99%)
Fall	B22N3	FD_01304_EF-1a [Fusarium sp.]	622 / 625 (99.52%)	Fusarium sporotrichioides strain NRRL 29977	623/625 (99%)
Fall	B23N1	FD_01858_EF-1a [Fusarium sp.]	608 / 611 (99.5%)	Fusarium proliferatum isolate 001B	623/627 (99%)
Fall	B23N2	FD_01858_EF-1a [Fusarium sp.]	607 / 610 (99.5%)	Fusarium proliferatum partial tef-1 gene	619/621 (99%)
Fall	B23N3	FD_01857_EF-1a [Fusarium sp.]	602 / 604 (99.66%)	Gibberella fujikuroi isolate V22	608/610 (99%)
Fall	B23N4	FD_01853_EF-1a [Fusarium sp.]	520 / 522 (99.61%)	Fusarium sporotrichioides strain NRRL 53434	521/522 (99%)
Fall	B23N5	FD_01857_EF-1a [Fusarium sp.]	603 / 604 (99.83%)	Gibberella fujikuroi isolate V95	616/620 (99%)
Fall	B23N6	FD_01857_EF-1a [Fusarium sp.]	604 / 606 (99.66%)	Gibberella fujikuroi isolate V22	615/618 (99%)
Fall	B23N7	FD_01857_EF-1a [Fusarium sp.]	605 / 607 (99.67%)	Gibberella fujikuroi isolate V22	615/618 (99%)
Fall	B23N8	FD_01857_EF-1a [Fusarium sp.]	603 / 604 (99.83%)	Gibberella fujikuroi isolate V95	617/621 (99%)
Fall	B23N9	FD_01378_EF-1a [Fusarium proliferatum]	607 / 615 (98.69%)	Gibberella fujikuroi var. intermedia partial tef-1 gene	629/634 (99%)
Fall	B24N2	FD_01119_EF-1a [Fusarium graminearum]	614 / 616 (99.67%)	Gibberella zeae isolate G5S	618/620 (99%)
Fall	B24N3	FD_01119_EF-1a [Fusarium graminearum]	626 / 630 (99.36%)	Gibberella zeae isolate G5S	627/630 (99%)
Fall	B24N4	FD_01119_EF-1a [Fusarium graminearum]	614 / 616 (99.67%)	Gibberella zeae isolate G5S	619/621 (99%)
Fall	B24N5	FD_01858_EF-1a [Fusarium sp.]	608 / 610 (99.67%)	Fusarium proliferatum isolate 001B	625/628 (99%)
Fall	B24N6	FD_01858_EF-1a [Fusarium sp.]	608 / 610 (99.67%)	Fusarium proliferatum isolate 001B	616/617 (99%)
Fall	B24N7	FD_00986_EF-1a [Fusarium graminearum]	574 / 581 (98.79%)	Gibberella zeae strain KB1171	574/581 (99%)
Fall	B24N8	FD_00986_EF-1a [Fusarium graminearum]	613 / 614 (99.83%)	Gibberella zeae isolate G5S	619/621 (99%)
Fall	B24N9	FD_01119_EF-1a [Fusarium graminearum]	613 / 615 (99.67%)	Gibberella zeae strain LMSA 1.09.107	619/621 (99%)
Fall	B24N10	FD_00986_EF-1a [*Fusarium graminearum*]	629 / 629 (100%)	Gibberella zeae strain NRRL 31084	629/629 (100%)
Fall	B24N11	FD_01119_EF-1a [Fusarium graminearum]	633 / 634 (99.84%)	Gibberella zeae strain LMSA 1.09.106	654/655 (99%)
Fall	B24N15	FD_00986_EF-1a [*Fusarium graminearum*]	637 / 643 (99.06%)	Gibberella zeae strain LMSA 1.09.105	678/686 (99%)
Fall	B24N16	FD_01119_EF-1a [*Fusarium graminearum*]	630 / 630 (100%)	Gibberella zeae strain LMSA 1.09.106	647/647 (100%)
Fall	B24N17	FD_00986_EF-1a [*Fusarium graminearum*]	579 / 584 (99.14%)	Gibberella zeae strain NRRL 31084	579/584 (99%)
Fall	B24N20	FD_01119_EF-1a [*Fusarium graminearum*]	622 / 628 (99.04%)	Gibberella zeae isolate CS3005	641/647 (99%)
Fall	B24N22	FD_01119_EF-1a [*Fusarium graminearum*]	614 / 615 (99.83%)	Gibberella zeae isolate G5S	620/621 (99%)
Fall	B24N25	FD_01119_EF-1a [*Fusarium graminearum*]	615 / 615 (100%)	Gibberella zeae strain LMSA 1.09.106	620/621 (99%)
Fall	B24N28	FD_01119_EF-1a [*Fusarium graminearum*]	615 / 615 (100%)	Gibberella zeae strain LMSA 1.09.106	619/620 (99%)

Fall	B24N30	FD_01114_EF-1a [*Fusarium graminearum*]	629 / 633 (99.36%)	Gibberella zeae isolate CS3005	651/656 (99%)
Fall	B24N31	FD_01119_EF-1a [*Fusarium graminearum*]	597 / 599 (99.66%)	Gibberella zeae isolate G5S	605/608 (99%)
Fall	B24N32	FD_01119_EF-1a [Fusarium graminearum]	620 / 623 (99.51%)	Gibberella zeae strain ATCC 60309	637/638 (99%)
Fall	B24N33	FD_00986_EF-1a [*Fusarium graminearum*]	627 / 629 (99.68%)	Gibberella zeae isolate M02-7035S-2 DCPA	641/643 (99%)
Fall	B24N34	FD_01119_EF-1a [*Fusarium graminearum*]	629 / 630 (99.84%)	Gibberella zeae isolate G5S	647/647 (100%)
Fall	B24N35	FD_01304_EF-1a [*Fusarium sp.*]	629 / 632 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	656/661 (99%)
Fall	B25N1	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (97.58%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	634/638 (99%)
Fall	B25N2	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	605 / 644 (93.94%)	Fusarium cf. incarnatum isolate M02-7079S-5	635/655 (97%)
Fall	B25N3	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	633 / 634 (99.84%)	Fusarium sp. NRRL 5537	637/639 (99%)
Fall	B25N4	F. solani species complex isolate NRRL 32821, MLST12-e	116 / 119 (97.47%)	Beauveria bassiana isolate 2641	545/674 (81%)
Fall	B26N1	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	620 / 634 (97.79%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	637/638 (99%)
Fall	B26N3	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	613 / 628 (97.61%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	626/627 (99%)
Fall	B26N4	FD_01119_EF-1a [*Fusarium graminearum*]	627 / 630 (99.52%)	Gibberella zeae strain ATCC 60309	647/649 (99%)
Fall	B26N5	FD_00986_EF-1a [*Fusarium graminearum*]	612 / 612 (100%)	Gibberella zeae strain NRRL 31084	617/618 (99%)
Fall	B26N6	F. incarnatum-equiseti species complex isolate NRRL 34039, MLST1-b	670 / 672 (99.7%)	Fusarium sp. NRRL 34039	670/672 (99%)
Fall	B27N1	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	630 / 635 (99.21%)	Fusarium lacertarum strain NRRL 20423	630/635 (99%)
Fall	B27N2	FD_01857_EF-1a [*Fusarium sp.*]	603 / 604 (99.83%)	Gibberella fujikuroi isolate V95	616/620 (99%)
Fall	B27N3	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	610 / 613 (99.51%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	618/620 (99%)
Fall	B27N4	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	632 / 634 (99.68%)	Fusarium sp. NRRL 32522	632/634 (99%)
Fall	B27N5	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	606 / 608 (99.67%)	Fusarium sp. NRRL 28029	619/623 (99%)
Fall	B27N6	F. incarnatum-equiseti species complex isolate NRRL 34034, MLST1-c	639 / 639 (100%)	Fusarium equiseti isolate 44	642/642 (100%)
Fall	B27N7	GFSC isolate NRRL 31418, MLST-Gibberella fujikuroi species complex	428 / 429 (99.76%)	Gibberella fujikuroi strain EF01	427/429 (99%)
Fall	B28N2	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (97.58%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	634/638 (99%)
Fall	B28N4	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	625 / 627 (99.68%)	Fusarium sp. NRRL 32522	625/627 (99%)
Fall	B28N5	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	619 / 634 (97.63%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	639/642 (99%)
Fall	B28N6	F. incarnatum-equiseti species complex isolate NRRL 34005, MLST24-a	640 / 642 (99.68%)	Fusarium cf. incarnatum M03-11345S-1 DCPA	653/655 (99%)
Fall	B28N7	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	641 / 643 (99.68%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	650/651 (99%)
Fall	B28N8	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	612 / 616 (99.35%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	625/629 (99%)
Fall	B28N9	FD_01857_EF-1a [*Fusarium sp.*]	602 / 604 (99.66%)	Gibberella fujikuroi isolate V95	617/622 (99%)
Fall	B28N10	FD_01858_EF-1a [*Fusarium sp.*]	603 / 605 (99.66%)	Fusarium proliferatum isolate 001B	616/618 (99%)
Fall	B68N1	FD_01319_EF-1a [*Fusarium sp.*]	563 / 619 (90.95%)	Fusarium cf. incarnatum	598/639 (94%)

Fall	B69N1	FD_00801_EF-1a | F. oxysporum species complex 231	586 / 620 (94.51%)	Fusarium oxysporum strain NRRL 52698	598/634 (94%)
Fall	B70N2	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	593 / 594 (99.83%)	Fusarium proliferatum partial tef-1 gene	597/597 (100%)
Fall	B70N4	FD_01321_EF-1a [*Fusarium sp.*]	599 / 623 (96.14%)	Fusarium equiseti strain AGrocketbis	616/619 (99%)
Fall	B71N2	FD_01320_EF-1a [*Fusarium pallidoroseum*]	449 / 456 (98.46%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	462/463 (99%)
Fall	B86N1	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	522 / 535 (97.57%)	Gibberella fujikuroi partial tef-1 gene	536/538 (99%)
Fall	B87N5	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	525 / 537 (97.76%)	Gibberella fujikuroi partial tef-1 gene	538/539 (99%)
Fall	B87N8	FD_01319_EF-1a [*Fusarium sp.*]	565 / 607 (93.08%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b and 25-c clone spt046	613/614 (99%)
Fall	B87N2	FD_01321_EF-1a [*Fusarium sp.*]	353 / 369 (95.66%)	Fusarium sp. NRRL 43637	374/378 (99%)
Fall	B87N3	FD_01321_EF-1a [*Fusarium sp.*]	368 / 382 (96.33%)	Fusarium sp. NRRL 43637	391/391 (100%)
Fall	B87N4	FD_01321_EF-1a [*Fusarium sp.*]	579 / 601 (96.33%)	Fusarium sp. NRRL 43637	602/603 (99%)
Fall	B87N6	FD_01321_EF-1a [*Fusarium sp.*]	623 / 649 (95.99%)	Fusarium sp. NRRL 43637	642/644 (99%)
Fall	B87N7	FD_01321_EF-1a [*Fusarium sp.*]	578 / 601 (96.17%)	Fusarium sp. NRRL 43637	602/604 (99%)
Fall	B91N1	FD_01119_EF-1a [*Fusarium graminearum*]	550 / 607 (90.6%)	Gibberella zeae isolate G5S	560/619 (90%)
Fall	B92N2	FD_01378_EF-1a [*Fusarium proliferatum*]	605 / 620 (97.58%)	Gibberella intermedia isolate 3075	613/627 (98%)
Fall	B92N1	FD_01388_EF-1a [*Fusarium verticillioides*]	513 / 513 (100%)	Gibberella moniliformis isolate B4	513/513 (100%)
Winter	B12N1	FD_01373_EF-1a [Fusarium solani]	687 / 689 (99.7%)	Fusarium sp. NRRL 46598	690/690 (100%)

Table 4. Comparisons of Fusarium-ID and GenBank for the isolates of *Fusarium* collected with an unmanned aerial vehicle (UAV) 100 m above ground level across all seasons over four calendar years (2009, 2010, 2011, & 2012).

Season	Isolate	Identification based on Fusarium-ID Query	Fusarium-ID (%)	Identification based on GenBank Query	Genbank (%)
Spring	F134N9	F. oxysporum species complex isolate NRRL 26989619 / 620 (99.83%)	619 / 620 (99.83%)	Fusarium oxysporum f. sp. lycopersici strain OSU451	624/626 (99%)
Spring	F134N1	FD_00785_EF-1a [*Fusarium sp.*]	653 / 653 (100%)	Fusarium oxysporum strain NRRL 46605	653/653 (100%)
Spring	F134N10	FD_01304_EF-1a [Fusarium sp.]	628 / 631 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	645/648 (99%)
Spring	F134N3	FD_01320_EF-1a [Fusarium pallidoroseum]	661 / 662 (99.84%)	Fusarium sp. NRRL 43622	667/670 (99%)
Spring	F134N7	FD_01321_EF-1a [Fusarium sp.]	631 / 659 (95.75%)	Fusarium sp. NRRL 34034	665/669 (99%)
Spring	F135N1	FD_01321_EF-1a [Fusarium sp.]	634 / 660 (96.06%)	Fusarium sp. NRRL 36323	665/666 (99%)
Spring	F135N6	FD_01321_EF-1a [Fusarium sp.]	565 / 603 (93.69%)	Fusarium sp. NRRL 32997	650/662 (98%)
Spring	F136N9	FD_01320_EF-1a [Fusarium pallidoroseum]	663 / 663 (100%)	Fusarium sp. NRRL 43622	663/663 (100%)
Spring	F137N3	FD_01320_EF-1a [Fusarium pallidoroseum]	615 / 633 (97.15%)	Fusarium cf. incarnatum H04-777S-1 PCNB	652/673 (97%)
Spring	F137N4	FD_01320_EF-1a [Fusarium pallidoroseum]	663 / 663 (100%)	Fusarium sp. NRRL 43622	669/671 (99%)
Spring	F138N9	F. incarnatum-equiseti species complex isolate NRRL 28029	608 / 610 (99.67%)	Fusarium sp. NRRL 28029	611/614 (99%)
Spring	F138N8	F. incarnatum-equiseti species complex isolate NRRL 5537	642 / 643 (99.84%)	Fusarium sp. NRRL 5537	642/643 (99%)
Spring	F138N4	FD_00785_EF-1a [Fusarium sp.]	675 / 681 (99.11%)	Fusarium oxysporum f. sp. melonis isolate TX388	673/676 (99%)
Spring	F138N5	FD_00805_EF-1a [Fusarium sp.]	655 / 656 (99.84%)	Fusarium oxysporum strain LYF025	658/662 (99%)
Spring	F138N1	FD_01320_EF-1a [*Fusarium pallidoroseum*]	594 / 649 (91.52%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7097S-1 DCPA	615/664 (93%)
Spring	F139N6	F. incarnatum-equiseti species complex isolate NRRL 5537	642 / 643 (99.84%)	Fusarium sp. NRRL 5537	642/643 (99%)
Spring	F139N7	FD_00809_EF-1a [*Fusarium sp.*]	653 / 653 (100%)	Fusarium sp. F67	661/662 (99%)
Spring	F139N9	FD_01320_EF-1a [Fusarium pallidoroseum]	656 / 664 (98.79%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7097S-1 DCPA	677/683 (99%)
Spring	F139N5	FD_01321_EF-1a [Fusarium sp.]	629 / 665 (94.58%)	Fusarium sp. NRRL 5537	669/671 (99%)
Spring	F139N8	FD_01321_EF-1a [*Fusarium sp.*]	627 / 663 (94.57%)	Fusarium sp. NRRL 5537	668/670 (99%)
Spring	F140N7	FD_00802_EF-1a [Fusarium sp.]	675 / 682 (98.97%)	Fusarium oxysporum f. sp. lycopersici strain OSU451	676/683 (99%)
Spring	F140N3	FD_01376_EF-1a [Fusarium oxysporum]	673 / 679 (99.11%)	Fusarium oxysporum isolate Lb4	669/672 (99%)
Spring	F141N2	FD_00785_EF-1a [Fusarium sp.]	680 / 685 (99.27%)	Fusarium oxysporum strain NRRL 46605	680/685 (99%)
Spring	F141N8	FD_00986_EF-1a [*Fusarium graminearum*]	628 / 629 (99.84%)	Gibberella zeae isolate CS3005	645/649 (99%)

Spring	F141N4	FD_01321_EF-1a [Fusarium sp.]	615 / 667 (92.2%)	Fusarium sp. NRRL 32997	664/677 (98%)
Spring	F141N5	FD_01321_EF-1a [*Fusarium sp.*]	625 / 662 (94.41%)	Fusarium sp. NRRL 5537	659/662 (99%)
Spring	F141N7	FD_01321_EF-1a [Fusarium sp.]	636 / 660 (96.36%)	Fusarium sp. NRRL 45996	664/665 (99%)
Spring	F142N5	FD_01320_EF-1a [*Fusarium pallidoroseum*]	655 / 663 (98.79%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7097S-1 DCPA	676/682 (99%)
Spring	ISF159N17	FD_01321_EF-1a [*Fusarium sp.*]	628 / 655 (95.87%)	Fusarium sp. NRRL 28029	647/649 (99%)
Spring	OHF159N5	FD_01317_EF-1a [*Fusarium sp.*]	607 / 624 (97.27%)	Gibberella avenacea voucher FRC R-9369	613/617 (99%)
Spring	ISF160N18	FD_01304_EF-1a [Fusarium sp.]	630 / 632 (99.68%)	Fusarium langsethiae strain NRRL 53422/2321/2	649/652 (99%)
Spring	ISF160N7	FD_01321_EF-1a [*Fusarium sp.*]	615 / 652 (94.32%)	Fusarium sp. NRRL 5537	646/648 (99%)
Spring	OSF160N7	FD_00386_EF-1a [*Fusarium sp.*]	646 / 648 (99.69%)	Fusarium oxysporum isolate SAT77	646/647 (99%)
Spring	OSF160N6	FD_00793_EF-1a [*Fusarium sp.*]	650 / 651 (99.84%)	Fusarium oxysporum isolate Lb4	655/657 (99%)
Spring	OSF160N9	FD_01327_EF-1a [*Fusarium sp.*]	662 / 664 (99.69%)	Fusarium polyphialidicum isolate F0016	657/661 (99%)
Spring	IHF161N14	FD_00802_EF-1a [*Fusarium sp.*]	652 / 654 (99.69%)	Fusarium oxysporum f. sp. lycopersici strain OSU451	652/654 (99%)
Spring	ISF161N13	FD_01261_EF-1a [*Fusarium oxysporum*]	577 / 579 (99.65%)	Fusarium oxysporum isolate NBAII-Fu1	577/579 (99%)
Spring	ISF161N15	FD_01261_EF-1a [*Fusarium oxysporum*]	619 / 620 (99.83%)	Fusarium oxysporum f. sp. lycopersici strain OSU451	628/631 (99%)
Spring	ISF161N16	FD_01317_EF-1a [*Fusarium sp.*]	674 / 685 (98.39%)	Fusarium avenaceum strain CC39	673/684 (98%)
Spring	ISF161N18	FD_01321_EF-1a [*Fusarium sp.*]	614 / 652 (94.17%)	Fusarium sp. NRRL 5537	645/648 (99%)
Spring	OSF161N23	FD_01288_EF-1a [*Fusarium sp.*]	636 / 647 (98.29%)	Fusarium solani strain NRRL 32798	646/647 (99%)
Spring	OSF161N24	FD_01288_EF-1a [*Fusarium sp.*]	636 / 648 (98.14%)	Fusarium solani strain NRRL 32798	646/648 (99%)
Spring	OSF161N1	FD_01321_EF-1a [*Fusarium sp.*]	644 / 670 (96.11%)	Fusarium sp. NRRL 45996	663/665 (99%)
Spring	OSF161N19	FD_01321_EF-1a [*Fusarium sp.*]	658 / 666 (98.79%)	Fusarium equiseti strain 163b	666/666 (100%)
Spring	ISF162N7	FD_01321_EF-1a [*Fusarium sp.*]	614 / 652 (94.17%)	Fusarium sp. NRRL 5537	645/648 (99%)
Spring	OSF162N12	FD_00785_EF-1a [*Fusarium sp.*]	646 / 647 (99.84%)	Fusarium sp. 45BMC	650/650 (100%)
Spring	OSF162N1	FD_01321_EF-1a [*Fusarium sp.*]	613 / 631 (97.14%)	Fusarium equiseti strain 84b	625/643 (97%)
Spring	OSF162N13	FD_01371_EF-1a [*Fusarium solani*]	681 / 681 (100%)	Fusarium solani partial tef-1a gene	686/688 (99%)
Spring	ISF163N24	FD_01321_EF-1a [Fusarium sp.]	633 / 651 (97.23%)	Fusarium sp. NRRL 43680 haplotype FIESC 4-a	643/659 (98%)
Spring	ISF163N23	FD_01321_EF-1a [Fusarium sp.]	615 / 652 (94.32%)	Fusarium sp. NRRL 5537	646/648 (99%)
Spring	ISF164N10	FD_01321_EF-1a [*Fusarium sp.*]	615 / 652 (94.32%)	Fusarium sp. NRRL 5537	646/648 (99%)
Spring	ISF164N18	FD_01321_EF-1a [*Fusarium sp.*]	645 / 669 (96.41%)	Fusarium sp. NRRL 45996	664/664 (100%)
Spring	ISF164N20	FD_01373_EF-1a [*Fusarium solani*]	651 / 654 (99.54%)	Fusarium solani f. radicicola gene	653/654 (99%)
Spring	ISF164N22	FD_01373_EF-1a [*Fusarium solani*]	651 / 654 (99.54%)	Fusarium solani f. radicicola gene	653/654 (99%)

Spring	OSF164N16	FD_00805_EF-1a [*Fusarium sp.*]	646 / 647 (99.84%)	Fusarium oxysporum isolate 57	648/651 (99%)
Spring	OSF164N1	FD_01321_EF-1a [*Fusarium sp.*]	625 / 661 (94.55%)	Fusarium sp. NRRL 5537	652/652 (100%)
Spring	OSF164N4	FD_01321_EF-1a [*Fusarium sp.*]	657 / 666 (98.64%)	Fusarium equiseti strain 163b	665/666 (99%)
Spring	ISF166N5	FD_01041_EF-1a	635 / 652 (97.39%)	Fusarium solani strain NRRL 22656	653/657 (99%)
Spring	ISF166N10	FD_01313_EF-1a [*Fusarium nelsonii*]	620 / 641 (96.72%)	Fusarium sp. NRRL 43630	652/653 (99%)
Spring	ISF166N2	FD_01325_EF-1a [*Fusarium aywerti*]	507 / 557 (91.02%)	Fusarium brachygibbosum strain NRRL 34033	625/628 (99%)
Spring	IF170N1	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	636 / 652 (97.54%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	660/664 (99%)
Spring	IF170N2	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	637 / 653 (97.54%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	661/665 (99%)
Spring	IF171N1	F. oxysporum species complex isolate NRRL 40182, MLST99	648 / 649 (99.84%)	Fusarium oxysporum strain LYF025	651/655 (99%)
Spring	IF171N2	F. oxysporum species complex isolate NRRL 40182, MLST99	646 / 648 (99.69%)	Fusarium oxysporum isolate 57	649/653 (99%)
Spring	IF171N3	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	618 / 618 (100%)	Gibberella fujikuroi isolate PRC	646/649 (99%)
Spring	IF171N4	FD_01317_EF-1a [*Fusarium sp.*]	642 / 651 (98.61%)	Fusarium avenaceum strain CC32	652/660 (99%)
Spring	IF171N5	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	643 / 643 (100%)	Fusarium sp. NRRL 5537	655/657 (99%)
Spring	IF171N6	FD_01119_EF-1a [*Fusarium graminearum*]	640 / 644 (99.37%)	Gibberella zeae isolate CS3005	677/681 (99%)
Spring	IF171N7	F. oxysporum species complex isolate NRRL 39464, MLST232	680 / 683 (99.56%)	Fusarium oxysporum f. sp. vasinfectum isolate NRRL25231	681/684 (99%)
Spring	OF171N1	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	313 / 336 (93.15%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	591/700 (84%)
Spring	OF171N2	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	640 / 678 (94.39%)	Fusarium cf. incarnatum DFH-2010	669/688 (97%)
Spring	OF171N3	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	625 / 643 (97.2%)	Gibberella fujikuroi isolate PRC 2a	652/672 (97%)
Spring	OF171N4	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	640 / 641 (99.84%)	Gibberella fujikuroi isolate PRC 2a	672/674 (99%)
Spring	OF171N5	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	673 / 674 (99.85%)	Fusarium sp. NRRL 5537	673/674 (99%)
Spring	OF171N6	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	645 / 646 (99.84%)	Fusarium sp. NRRL 5537	652/654 (99%)
Spring	IF173N1	FD_00986_EF-1a [*Fusarium graminearum*]	626 / 628 (99.68%)	Gibberella zeae strain NRRL 31084	637/639 (99%)
Spring	IF173N2	FD_00986_EF-1a [*Fusarium graminearum*]	642 / 643 (99.84%)	Gibberella zeae isolate CS3005	679/681 (99%)
Spring	OF173N2	F. oxysporum species complex isolate NRRL 39464, MLST232	677 / 684 (98.97%)	Fusarium oxysporum f. sp. lycopersici strain OSU451	678/684 (99%)
Spring	IF174N1	FD_01345_EF-1a [*Fusarium lateritium*]	638 / 665 (95.93%)	Fusarium lateritium isolate F0104	649/664 (98%)
Spring	IF174N3	FD_01119_EF-1a [*Fusarium graminearum*]	612 / 615 (99.51%)	Gibberella zeae strain ATCC 60309	624/627 (99%)
Spring	IF174N4	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	634 / 650 (97.53%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	651/654 (99%)
Spring	IF174N5	FD_01304_EF-1a [*Fusarium sp.*]	639 / 643 (99.37%)	Fusarium sporotrichioides strain NRRL 29977	651/654 (99%)
Spring	OF174N1	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	616 / 618 (99.67%)	Gibberella fujikuroi isolate PRC	641/646 (99%)
Spring	OF174N2	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	633 / 673 (94.05%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	663/684 (97%)

Spring	IF175N1	FD_00986_EF-1a [*Fusarium graminearum*]	642 / 646 (99.38%)	Gibberella zeae isolate CS3005	673/678 (99%)
Spring	IF175N2	FD_01317_EF-1a [*Fusarium sp.*]	682 / 688 (99.12%)	Fusarium avenaceum strain CC32	683/687 (99%)
Spring	IF175N3	FD_00986_EF-1a [*Fusarium graminearum*]	641 / 643 (99.68%)	Gibberella zeae isolate CS3005	674/677 (99%)
Spring	IF175N4	FD_00986_EF-1a [*Fusarium graminearum*]	626 / 628 (99.68%)	Gibberella zeae strain NRRL 31084	638/641 (99%)
Spring	OF175N1	FD_00986_EF-1a [*Fusarium graminearum*]	628 / 628 (100%)	Gibberella zeae isolate CS3005	645/646 (99%)
Spring	OF175N2	FD_01857_EF-1a [*Fusarium sp.*]	618 / 618 (100%)	Gibberella fujikuroi isolate PRC	652/657 (99%)
Spring	OF175N3	FD_00986_EF-1a [*Fusarium graminearum*]	628 / 628 (100%)	Gibberella zeae isolate CS3005	658/662 (99%)
Spring	OF175N4	FD_01119_EF-1a [*Fusarium graminearum*]	641 / 647 (99.07%)	Gibberella zeae isolate CS3005	672/679 (99%)
Spring	OF175N5	FD_01857_EF-1a [*Fusarium sp.*]	639 / 640 (99.84%)	Gibberella fujikuroi isolate PRC	665/667 (99%)
Spring	IF176N1	F. oxysporum species complex isolate NRRL 40182, MLST99	621 / 622 (99.83%)	Fusarium oxysporum strain NRRL28359	634/640 (99%)
Spring	IF176N2	FD_01119_EF-1a [*Fusarium graminearum*]	614 / 615 (99.83%)	Gibberella zeae isolate G5S	641/643 (99%)
Spring	OF176N1	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	645 / 660 (97.72%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	662/663 (99%)
Spring	OF176N2	FD_01119_EF-1a [*Fusarium graminearum*]	629 / 630 (99.84%)	Gibberella zeae isolate G5S	644/644 (100%)
Spring	OF176N3	FD_01857_EF-1a [*Fusarium sp.*]	633 / 636 (99.52%)	Gibberella fujikuroi isolate PRC	646/650 (99%)
Spring	OF177N1	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	642 / 643 (99.84%)	Fusarium sp. NRRL 28029	659/664 (99%)
Spring	OF177N2	FD_01304_EF-1a [*Fusarium sp.*]	630 / 631 (99.84%)	Fusarium langsethiae strain NRRL 53422/2321/2	652/654 (99%)
Spring	IF178N1	FD_01304_EF-1a [*Fusarium sp.*]	628 / 631 (99.52%)	Fusarium sporotrichioides strain NRRL 29977	645/648 (99%)
Spring	IF178N2	FD_01858_EF-1a [*Fusarium sp.*]	607 / 611 (99.34%)	Gibberella intermedia strain PUF021	623/629 (99%)
Spring	IF178N3	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	662 / 665 (99.54%)	Fusarium proliferatum MUCL 31970	673/678 (99%)
Spring	OF178N1	FD_00986_EF-1a [*Fusarium graminearum*]	627 / 628 (99.84%)	Gibberella zeae isolate CS3005	654/660 (99%)
Spring	OF178N2	FD_01304_EF-1a [*Fusarium sp.*]	630 / 631 (99.84%)	Fusarium langsethiae strain NRRL 53422/2321/2	658/662 (99%)
Spring	IF179N1	F. oxysporum species complex isolate NRRL 38592, MLST222	677 / 679 (99.7%)	Fusarium oxysporum strain NRRL 46602	676/680 (99%)
Spring	IF179N3	F. incarnatum-equiseti species complex isolate NRRL 45997, MLST5-f	670 / 672 (99.7%)	Fusarium sp. NRRL 43680 haplotype FIESC 4-a	675/679 (99%)
Spring	IF179N4	FD_01119_EF-1a [*Fusarium graminearum*]	626 / 630 (99.36%)	Gibberella zeae strain ATCC 60309	645/648 (99%)
Spring	IF179N5	FD_01304_EF-1a [*Fusarium sp.*]	627 / 631 (99.36%)	Fusarium langsethiae strain NRRL 53422/2321/2	648/653 (99%)
Spring	IF179N6	FD_01857_EF-1a [*Fusarium sp.*]	615 / 618 (99.51%)	Gibberella fujikuroi isolate V22	637/641 (99%)
Spring	IF179N7	FD_01317_EF-1a [*Fusarium sp.*]	672 / 678 (99.11%)	Fusarium avenaceum strain CC32	674/677 (99%)
Spring	OF179N1	FD_01304_EF-1a [*Fusarium sp.*]	630 / 631 (99.84%)	Fusarium langsethiae strain NRRL 53422/2321/2	650/652 (99%)
Spring	OF179N3	FD_00986_EF-1a [*Fusarium graminearum*]	628 / 646 (97.21%)	Gibberella zeae isolate CS3005	657/676 (97%)
Spring	OF228N1	F. incarnatum-equiseti species complex 4-b	601 / 641 (93.75%)	Fusarium cf. incarnatum	640/644(99%)
Spring	OF228N2	FD_01857_EF-1a [Fusarium sp.]	600 / 602 (99.66%)	Gibberella intermedia	612/615(99%)
Spring	OF228N3	FD_01304_EF-1a [Fusarium sp.]	599 / 601 (99.66%)	Fusarium sporotrichioides	606/608(99%)
Spring	OF228N4	FD_01304_EF-1a [Fusarium sp.]	579 / 581 (99.65%)	Fusarium sporotrichioides	600/601(99%)

Spring	OF228N6	FD_01524_EF-1a | F. solani species complex 5-g NRRL25388	622 / 622 (100%)	Fusarium solani	622/622(100%)
Spring	OF228N8	FD_01304_EF-1a [Fusarium sp.]	625 / 627 (99.68%)	Fusarium sporotrichioides	636/637(99%)
Spring	OF230N5	FD_01857_EF-1a [Fusarium sp.]	603 / 603 (100%)	Gibberella fujikuroi	614/616(99%)
Spring	OF230N6	FD_01375_EF-1a [Fusarium oxysporum]	618 / 618 (100%)	Fusarium oxysporum	618/618(100%)
Spring	OF230N7	FD_01614_EF-1a | F. incarnatum-equiseti species complex 8-a NRRL5537	674 / 676 (99.7%)	Fusarium equiseti	674/676(99%)
Spring	IF228N1	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a NRRL45996	657 / 663 (99.09%)	Fusarium equiseti	645/655(98%)
Spring	IF228N2	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a NRRL45996	594 / 665 (89.32%)	Fusarium equiseti	591/665(89%)
Spring	IF228N3	FD_01674_EF-1a | F. incarnatum-equiseti species complex 2-a NRRL36401	607 / 673 (90.19%)	Fusarium equiseti	610/672(91%)
Spring	IF230N1	FD_01389_EF-1a [Fusarium proliferatum]	612 / 615 (99.51%)	Gibberella intermedia	613/615(99%)
Spring	IF230N2	FD_01389_EF-1a [Fusarium proliferatum]	593 / 595 (99.66%)	Gibberella intermedia	594/595(99%)
Spring	IF230N4	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a NRRL45996	652 / 652 (100%)	Fusarium equiseti	654/658(99%)
Summer	F143N5	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	636 / 640 (99.37%)	Fusarium sp. NRRL 28029	640/645 (99%)
Summer	F143N11	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	639 / 641 (99.68%)	Fusarium sp. NRRL 28029	643/646 (99%)
Summer	F143N2	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	597 / 600 (99.5%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	608/612 (99%)
Summer	F143N4	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	636 / 641 (99.21%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	650/654 (99%)
Summer	F143N8	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	649 / 653 (99.38%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	666/670 (99%)
Summer	F143N10	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	640 / 645 (99.22%)	Fusarium cf. incarnatum H04-777S-1 PCNB	658/662 (99%)
Summer	F143N16	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	646 / 648 (99.69%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	657/660 (99%)
Summer	F143N17	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	673 / 676 (99.55%)	Fusarium cf. incarnatum H04-777S-1 PCNB	687/688 (99%)
Summer	F143N20	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	648 / 654 (99.08%)	Fusarium cf. incarnatum H04-777S-1 PCNB	666/671 (99%)
Summer	F143N21	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	640 / 645 (99.22%)	Fusarium cf. incarnatum H04-777S-1 PCNB	658/662 (99%)
Summer	F143N26	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	640 / 645 (99.22%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	658/666 (99%)
Summer	F143N27	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	651 / 654 (99.54%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	662/666 (99%)
Summer	F143N32	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	642 / 645 (99.53%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	662/669 (99%)
Summer	F143N33	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	645 / 650 (99.23%)	Fusarium cf. incarnatum H04-777S-1 PCNB	663/667 (99%)
Summer	F143N35	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	644 / 647 (99.53%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	655/659 (99%)
Summer	F143N15	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	632 / 651 (97.08%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	653/659 (99%)
Summer	F143N3	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	635 / 651 (97.54%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	656/659 (99%)
Summer	F143N9	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	640 / 657 (97.41%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	657/660 (99%)
Summer	F143N13	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	640 / 662 (96.67%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	657/665 (99%)
Summer	F143N18	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	633 / 650 (97.38%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	650/653 (99%)

Summer	F143N25	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	667 / 683 (97.65%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	684/686 (99%)
Summer	F143N28	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	661 / 677 (97.63%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	678/680 (99%)
Summer	F143N30	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	635 / 651 (97.54%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	656/659 (99%)
Summer	F143N31	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	639 / 656 (97.4%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	656/659 (99%)
Summer	F143N36	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	636 / 651 (97.69%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	657/659 (99%)
Summer	F143N39	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	619 / 635 (97.48%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	636/638 (99%)
Summer	F143N24	F. incarnatum-equiseti species complex isolate NRRL 34005, MLST24-a	638 / 642 (99.37%)	Fusarium cf. incarnatum M03-11345S-1 DCPA	650/654 (99%)
Summer	F143N12	F. incarnatum-equiseti species complex isolate NRRL 36323, MLST3-a	639 / 640 (99.84%)	Fusarium sp. NRRL 36323	645/647 (99%)
Summer	F143N7	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	646 / 650 (99.38%)	Fusarium sp. NRRL 45996	646/650 (99%)
Summer	F143N34	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	650 / 652 (99.69%)	Fusarium sp. NRRL 5537	650/652 (99%)
Summer	F143N37	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	640 / 641 (99.84%)	Fusarium sp. NRRL 5537	651/654 (99%)
Summer	F143N38	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	652 / 652 (100%)	Fusarium sp. NRRL 5537	652/652 (100%)
Summer	F143N1	F. oxysporum species complex isolate NRRL 38599, MLST67	660 / 662 (99.69%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	662/664 (99%)
Summer	F143N14	F. oxysporum species complex isolate NRRL 38599, MLST67	650 / 653 (99.54%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	659/664 (99%)
Summer	F143N23	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	667 / 669 (99.7%)	Fusarium proliferatum MUCL 31970	667/674 (99%)
Summer	F143N22	FD_01857_EF-1a [*Fusarium sp.*]	623 / 626 (99.52%)	Gibberella fujikuroi partial tef-1 gene	645/651 (99%)
Summer	F144N40	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	675 / 676 (99.85%)	Fusarium sp. NRRL 28029	675/676 (99%)
Summer	F144N16	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	641 / 646 (99.22%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	656/663 (99%)
Summer	F144N18	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	652 / 654 (99.69%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	668/673 (99%)
Summer	F144N34	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	645 / 648 (99.53%)	Fusarium cf. incarnatum H04-777S-1 PCNB	663/665 (99%)
Summer	F144N36	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	649 / 654 (99.23%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	662/666 (99%)
Summer	F144N42	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	622 / 624 (99.67%)	Fusarium sp. NRRL 32522	628/631 (99%)
Summer	F144N49	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	641 / 645 (99.37%)	Fusarium cf. incarnatum H04-777S-1 PCNB	653/655 (99%)
Summer	F144N52	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	648 / 653 (99.23%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	673/679 (99%)
Summer	F144N53	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	645 / 649 (99.38%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	658/661 (99%)
Summer	F144N54	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	641 / 643 (99.68%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	652/655 (99%)
Summer	F144N57	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	653 / 654 (99.84%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	662/664 (99%)
Summer	F144N64	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	640 / 643 (99.53%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	659/662 (99%)
Summer	F144N65	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	671 / 672 (99.85%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	682/684 (99%)
Summer	F144N72	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	647 / 654 (98.92%)	Fusarium cf. incarnatum H04-777S-1 PCNB	661/666 (99%)
Summer	F144N15	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	559 / 576 (97.04%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	566/571 (99%)

Summer	F144N19	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	650 / 652 (99.69%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	661/664 (99%)
Summer	F144N13	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	643 / 657 (97.86%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	664/665 (99%)
Summer	F144N17	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	638 / 653 (97.7%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	655/656 (99%)
Summer	F144N28	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	644 / 660 (97.57%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	661/663 (99%)
Summer	F144N38	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	662 / 677 (97.78%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	679/680 (99%)
Summer	F144N39	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	633 / 649 (97.53%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	656/659 (99%)
Summer	F144N51	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	634 / 651 (97.38%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	651/654 (99%)
Summer	F144N58	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	634 / 651 (97.38%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	655/659 (99%)
Summer	F144N59	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	638 / 656 (97.25%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	655/659 (99%)
Summer	F144N60	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	639 / 656 (97.4%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	656/659 (99%)
Summer	F144N71	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	645 / 660 (97.72%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	662/663 (99%)
Summer	F144N47	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	664 / 680 (97.64%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	681/683 (99%)
Summer	F144N37	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	639 / 648 (98.61%)	Fusarium sp. NRRL 32997	639/648 (99%)
Summer	F144N32	F. incarnatum-equiseti species complex isolate NRRL 34005, MLST24-a	672 / 677 (99.26%)	Fusarium cf. incarnatum M03-11345S-1 DCPA	689/694 (99%)
Summer	F144N69	F. incarnatum-equiseti species complex isolate NRRL 34005, MLST24-a	667 / 669 (99.7%)	Fusarium cf. incarnatum M03-11345S-1 DCPA	679/681 (99%)
Summer	F144N1	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	637 / 638 (99.84%)	Fusarium sp. NRRL 5537	637/638 (99%)
Summer	F144N27	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	671 / 674 (99.55%)	Fusarium sp. NRRL 5537	671/674 (99%)
Summer	F144N48	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	652 / 652 (100%)	Fusarium sp. NRRL 5537	652/652 (100%)
Summer	F144N62	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	636 / 638 (99.68%)	Fusarium sp. NRRL 5537	636/638 (99%)
Summer	F144N63	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	672 / 675 (99.55%)	Fusarium sp. NRRL 5537	672/675 (99%)
Summer	F144N67	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	639 / 643 (99.37%)	Fusarium sp. NRRL 5537	648/654 (99%)
Summer	F144N68	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	650 / 653 (99.54%)	Fusarium sp. NRRL 5537	650/653 (99%)
Summer	F144N24	F. oxysporum species complex isolate NRRL 38599, MLST67	659 / 660 (99.84%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	661/662 (99%)
Summer	F144N31	F. oxysporum species complex isolate NRRL 38599, MLST67	662 / 664 (99.69%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	665/667 (99%)
Summer	F144N4	FD_01304_EF-1a [*Fusarium sp.*]	638 / 641 (99.53%)	Fusarium sporotrichioides strain F95	662/667 (99%)
Summer	F144N41	FD_01304_EF-1a [*Fusarium sp.*]	645 / 646 (99.84%)	Fusarium sporotrichioides strain F95	685/688 (99%)
Summer	F144N21	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	665 / 668 (99.55%)	Fusarium proliferatum MUCL 31970	665/672 (99%)
Summer	F144N55	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	609 / 610 (99.83%)	Fusarium proliferatum isolate 2-91	619/622 (99%)
Summer	F144N56	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	665 / 668 (99.55%)	Fusarium proliferatum MUCL 31970	676/683 (99%)
Summer	F144N20	FD_01853_EF-1a [*Fusarium sp.*]	627 / 631 (99.36%)	Fusarium sporotrichioides strain NRRL 53434/2616/11	662/668 (99%)
Summer	F144N29	FD_01853_EF-1a [*Fusarium sp.*]	643 / 646 (99.53%)	Fusarium sporotrichioides strain F95	685/688 (99%)

Summer	F144N2	FD_01857_EF-1a [*Fusarium sp.*]	637 / 640 (99.53%)	Gibberella fujikuroi isolate 11-93	670/677 (99%)
Summer	F144N3	FD_01857_EF-1a [*Fusarium sp.*]	627 / 633 (99.05%)	Gibberella fujikuroi strain NRRL 43470	627/632 (99%)
Summer	F144N5	FD_01857_EF-1a [*Fusarium sp.*]	637 / 640 (99.53%)	Gibberella fujikuroi isolate 11-93	671/678 (99%)
Summer	F144N12	FD_01857_EF-1a [*Fusarium sp.*]	631 / 635 (99.37%)	Gibberella fujikuroi partial tef-1 gene	643/649 (99%)
Summer	F144N22	FD_01857_EF-1a [*Fusarium sp.*]	607 / 609 (99.67%)	Gibberella fujikuroi partial tef-1 gene	649/657 (99%)
Summer	F144N23	FD_01857_EF-1a [*Fusarium sp.*]	612 / 613 (99.83%)	Gibberella fujikuroi partial tef-1 gene	646/651 (99%)
Summer	F144N26	FD_01857_EF-1a [*Fusarium sp.*]	637 / 640 (99.53%)	Gibberella fujikuroi isolate 11-93	656/663 (99%)
Summer	F144N45	FD_01857_EF-1a [*Fusarium sp.*]	616 / 618 (99.67%)	Gibberella fujikuroi strain NRRL 43470	624/626 (99%)
Summer	F144N46	FD_01857_EF-1a [*Fusarium sp.*]	624 / 627 (99.52%)	Gibberella fujikuroi partial tef-1 gene	640/643 (99%)
Summer	F144N66	FD_01857_EF-1a [*Fusarium sp.*]	639 / 640 (99.84%)	Gibberella fujikuroi isolate 11-93	672/677 (99%)
Summer	F144N70	FD_01857_EF-1a [*Fusarium sp.*]	639 / 640 (99.84%)	Gibberella fujikuroi isolate 14-22	672/677 (99%)
Summer	F144N25	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	628 / 630 (99.68%)	Gibberella fujikuroi partial tef-1 gene	648/652 (99%)
Summer	F145N22	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	668 / 675 (98.96%)	Fusarium lacertarum strain NRRL 20423	668/675 (99%)
Summer	F145N7	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	657 / 659 (99.69%)	Fusarium sp. NRRL 28029	657/659 (99%)
Summer	F145N10	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	635 / 640 (99.21%)	Fusarium sp. NRRL 28029	639/645 (99%)
Summer	F145N14	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	671 / 674 (99.55%)	Fusarium sp. NRRL 28029	671/674 (99%)
Summer	F145N18	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	670 / 674 (99.4%)	Fusarium sp. NRRL 28029	670/674 (99%)
Summer	F145N27	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	645 / 649 (99.38%)	Fusarium sp. NRRL 28029	645/649 (99%)
Summer	F145N29	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	672 / 674 (99.7%)	Fusarium sp. NRRL 28029	672/674 (99%)
Summer	F145N31	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	646 / 649 (99.53%)	Fusarium sp. NRRL 28029	646/649 (99%)
Summer	F145N36	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	670 / 673 (99.55%)	Fusarium sp. NRRL 28029	670/673 (99%)
Summer	F145N42	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	655 / 657 (99.69%)	Fusarium sp. NRRL 28029	658/661 (99%)
Summer	F145N8	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	625 / 629 (99.36%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	631/634 (99%)
Summer	F145N13	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	652 / 655 (99.54%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	659/662 (99%)
Summer	F145N25	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	648 / 654 (99.08%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	660/667 (99%)
Summer	F145N30	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	675 / 678 (99.55%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7097S-1 DCPA	687/691 (99%)
Summer	F145N32	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	671 / 672 (99.85%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	682/684 (99%)
Summer	F145N34	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	648 / 654 (99.08%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	655/660 (99%)
Summer	F145N37	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	642 / 645 (99.53%)	Fusarium sp. NRRL 32522	642/645 (99%)
Summer	F145N38	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	672 / 678 (99.11%)	Fusarium cf. incarnatum H04-777S-1 PCNB	682/686 (99%)
Summer	F145N39	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	625 / 628 (99.52%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	638/643 (99%)

Summer	F145N40	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	649 / 660 (98.33%)	Fusarium sp. NRRL 32522	654/667 (99%)
Summer	F145N41	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	659 / 662 (99.54%)	Fusarium sp. NRRL 32522	663/667 (99%)
Summer	F145N19	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	611 / 626 (97.6%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	637/641 (99%)
Summer	F145N20	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	633 / 651 (97.23%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	654/659 (99%)
Summer	F145N26	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	651 / 667 (97.6%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	664/666 (99%)
Summer	F145N43	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	663 / 680 (97.5%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	680/683 (99%)
Summer	F145N44	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	641 / 656 (97.71%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	658/659 (99%)
Summer	F145N33	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	662 / 680 (97.35%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	679/683 (99%)
Summer	F145N2	F. incarnatum-equiseti species complex isolate NRRL 43730, MLST16-c	624 / 629 (99.2%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	631/635 (99%)
Summer	F145N3	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	673 / 675 (99.7%)	Fusarium sp. NRRL 45996	673/675 (99%)
Summer	F145N4	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	670 / 674 (99.4%)	Fusarium sp. NRRL 45996	670/674 (99%)
Summer	F145N16	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	652 / 654 (99.69%)	Fusarium sp. NRRL 5537	655/658 (99%)
Summer	F145N23	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	674 / 677 (99.55%)	Fusarium sp. NRRL 5537	674/677 (99%)
Summer	F145N24	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	671 / 675 (99.4%)	Fusarium sp. NRRL 5537	671/675 (99%)
Summer	F145N45	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	673 / 674 (99.85%)	Fusarium sp. NRRL 5537	673/674 (99%)
Summer	F145N35	F. oxysporum species complex isolate NRRL 38592, MLST222	683 / 686 (99.56%)	Fusarium oxysporum strain NRRL 46602	681/686 (99%)
Summer	F145N46	F. oxysporum species complex isolate NRRL 38599, MLST67	660 / 661 (99.84%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	667/670 (99%)
Summer	F145N12	FD_01304_EF-1a [*Fusarium sp.*]	643 / 646 (99.53%)	Fusarium langsethiae strain NRRL 53422/2321/2	677/680 (99%)
Summer	F145N17	FD_01304_EF-1a [*Fusarium sp.*]	642 / 646 (99.38%)	Fusarium sporotrichioides strain F95	682/688 (99%)
Summer	F145N15	FD_01857_EF-1a [*Fusarium sp.*]	638 / 640 (99.68%)	Gibberella fujikuroi isolate 11-93	672/678 (99%)
Summer	F145N28	FD_01857_EF-1a [*Fusarium sp.*]	623 / 626 (99.52%)	Gibberella fujikuroi isolate 11-93	669/678 (99%)
Summer	F145N21	FD_01857_EF-1a [Fusarium sp.]	623 / 626 (99.52%)	Gibberella fujikuroi partial tef-1 gene	647/651 (99%)
Summer	F146N16	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	640 / 644 (99.37%)	Fusarium lacertarum strain NRRL 20423	651/658 (99%)
Summer	F146N18	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	668 / 675 (98.96%)	Fusarium lacertarum strain NRRL 20423	668/675 (99%)
Summer	F146N19	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	651 / 658 (98.93%)	Fusarium lacertarum strain NRRL 20423	651/658 (99%)
Summer	F146N24	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	667 / 676 (98.66%)	Fusarium lacertarum strain NRRL 20423	667/676 (99%)
Summer	F146N25	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	624 / 676 (92.3%)	Fusarium lacertarum strain NRRL 20423	624/676 (93%)
Summer	F146N36	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	668 / 675 (98.96%)	Fusarium lacertarum strain NRRL 20423	668/675 (99%)
Summer	F146N3	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	524 / 524 (100%)	Fusarium sp. NRRL 28029	539/542 (99%)
Summer	F146N6	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	644 / 645 (99.84%)	Fusarium sp. NRRL 28029	644/645 (99%)
Summer	F146N7	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	629 / 631 (99.68%)	Fusarium sp. NRRL 28029	632/635 (99%)

Summer	F146N28	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	645 / 649 (99.38%)	Fusarium sp. NRRL 28029	645/649 (99%)
Summer	F146N29	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	670 / 674 (99.4%)	Fusarium sp. NRRL 28029	670/674 (99%)
Summer	F146N42	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	653 / 656 (99.54%)	Fusarium sp. NRRL 28029	667/673 (99%)
Summer	F146N46	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	671 / 675 (99.4%)	Fusarium sp. NRRL 28029	671/675 (99%)
Summer	F146N17	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	670 / 677 (98.96%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	692/698 (99%)
Summer	F146N21	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	645 / 650 (99.23%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7097S-1 DCPA	656/662 (99%)
Summer	F146N23	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	612 / 616 (99.35%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	632/638 (99%)
Summer	F146N26	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	620 / 622 (99.67%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	627/629 (99%)
Summer	F146N35	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	677 / 679 (99.7%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7097S-1 DCPA	681/684 (99%)
Summer	F146N20	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	611 / 626 (97.6%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	633/636 (99%)
Summer	F146N27	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	670 / 687 (97.52%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	687/690 (99%)
Summer	F146N39	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	665 / 684 (97.22%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	682/687 (99%)
Summer	F146N43	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (97.58%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	628/631 (99%)
Summer	F146N49	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	667 / 684 (97.51%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	684/687 (99%)
Summer	F146N50	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	641 / 655 (97.86%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	660/661 (99%)
Summer	F146N15	F. incarnatum-equiseti species complex isolate NRRL 34039, MLST1-b	669 / 674 (99.25%)	Fusarium sp. NRRL 34039	669/674 (99%)
Summer	F146N2	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	596 / 602 (99%)	Fusarium sp. NRRL 45996	599/606 (99%)
Summer	F146N5	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	602 / 616 (97.72%)	Fusarium sp. NRRL 45996	617/634 (98%)
Summer	F146N22	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	648 / 650 (99.69%)	Fusarium sp. NRRL 45996	648/650 (99%)
Summer	F146N30	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	668 / 672 (99.4%)	Fusarium sp. NRRL 45996	668/672 (99%)
Summer	F146N32	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	671 / 674 (99.55%)	Fusarium sp. NRRL 45996	671/674 (99%)
Summer	F146N33	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	671 / 675 (99.4%)	Fusarium sp. NRRL 45996	671/675 (99%)
Summer	F146N1	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	668 / 677 (98.67%)	Fusarium sp. NRRL 45996	668/677 (99%)
Summer	F146N4	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	590 / 623 (94.7%)	Fusarium sp. NRRL 45996	593/627 (95%)
Summer	F146N34	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	674 / 675 (99.85%)	Fusarium sp. NRRL 45996	674/675 (99%)
Summer	F146N8	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	609 / 610 (99.83%)	Fusarium sp. NRRL 5537	616/618 (99%)
Summer	F146N9	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	647 / 650 (99.53%)	Fusarium sp. NRRL 5537	647/650 (99%)
Summer	F146N40	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	671 / 674 (99.55%)	Fusarium sp. NRRL 5537	671/674 (99%)
Summer	F146N45	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	673 / 677 (99.4%)	Fusarium sp. NRRL 5537	673/677 (99%)
Summer	F146N13	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	674 / 677 (99.55%)	Fusarium sp. NRRL 5537	674/677 (99%)
Summer	F146N11	F. oxysporum species complex isolate NRRL 38591, MLST191	684 / 686 (99.7%)	Fusarium oxysporum f. sp. pisi isolate Fopi002	687/689 (99%)

Summer	F146N12	F. oxysporum species complex isolate NRRL 38591, MLST191	682 / 685 (99.56%)	Fusarium oxysporum strain NRRL 46605	682/685 (99%)
Summer	F146N14	F. oxysporum species complex isolate NRRL 38599, MLST67	682 / 684 (99.7%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	682/684 (99%)
Summer	F146N44	FD_01304_EF-1a [*Fusarium sp.*]	643 / 646 (99.53%)	Fusarium sporotrichioides strain F95	680/684 (99%)
Summer	F146N10	FD_01857_EF-1a [*Fusarium sp.*]	638 / 640 (99.68%)	Gibberella fujikuroi isolate V95	660/662 (99%)
Summer	F146N37	FD_01857_EF-1a [*Fusarium sp.*]	615 / 617 (99.67%)	Gibberella fujikuroi isolate V95	626/628 (99%)
Summer	F146N38	FD_01857_EF-1a [*Fusarium sp.*]	610 / 613 (99.51%)	Gibberella fujikuroi isolate V95	624/630 (99%)
Summer	F146N41	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	637 / 640 (99.53%)	Gibberella fujikuroi isolate 14-22	669/676 (99%)
Summer	F146N47	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	637 / 640 (99.53%)	Gibberella fujikuroi isolate 14-22	669/676 (99%)
Summer	IF180N2	FD_01379_EF-1a [*Fusarium proliferatum*]	618 / 641 (96.41%)	Gibberella intermedia isolate 5R3	624/645 (97%)
Summer	OF180N4	FD_00801_EF-1a | F. oxysporum species complex 231 NRRL38885	516 / 587 (87.9%)	Fusarium sp. 45BMC	565/649 (87%)
Summer	OF180N2	FD_01299_EF-1a [*Fusarium globosum*]	576 / 591 (97.46%)	Gibberella fujikuroi isolate V22	590/591 (99%)
Summer	OF180N3	FD_01321_EF-1a [*Fusarium sp.*]	485 / 505 (96.03%)	Fusarium sp. NRRL 43637	501/502 (99%)
Summer	IF181N2	FD_01388_EF-1a [*Fusarium verticillioides*]	502 / 503 (99.8%)	Fusarium oxysporum isolate FSY0951	506/508 (99%)
Summer	OF181N7	FD_01320_EF-1a [*Fusarium pallidoroseum*]	595 / 616 (96.59%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt116	614/629 (98%)
Summer	OF181N3	FD_01321_EF-1a [*Fusarium sp.*]	586 / 608 (96.38%)	Fusarium sp. NRRL 43637	635/642 (99%)
Summer	OF183N1	FD_01321_EF-1a [*Fusarium sp.*]	600 / 653 (91.88%)	Fusarium sp. NRRL 43637	610/651 (94%)
Summer	OF184N1	FD_01321_EF-1a [*Fusarium sp.*]	572 / 596 (95.97%)	Fusarium sp. NRRL 36318	592/592 (100%)
Summer	OF184N2	FD_01321_EF-1a [*Fusarium sp.*]	411 / 448 (91.74%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	463/465 (99%)
Summer	OF184N3	FD_01321_EF-1a [*Fusarium sp.*]	428 / 509 (84.08%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	562/653 (86%)
Summer	IF185N2	FD_01169_EF-1a GFSC Gibberella fujikuroi species complex NRRL13566	463 / 474 (97.67%)	Gibberella fujikuroi isolate 3101	481/487 (99%)
Summer	IF185N3	FD_01169_EF-1a GFSC Gibberella fujikuroi species complex NRRL13566	532 / 544 (97.79%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	548/550 (99%)
Summer	IF185N4	FD_01319_EF-1a [*Fusarium sp.*]	536 / 580 (92.41%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	579/580 (99%)
Summer	OF185N4	FD_01320_EF-1a [*Fusarium pallidoroseum*]	561 / 569 (98.59%)	Fusarium sp. NRRL 31167	580/582 (99%)
Summer	OF185N1	FD_01321_EF-1a [*Fusarium sp.*]	604 / 628 (96.17%)	Fusarium sp. NRRL 43637	627/629 (99%)
Summer	OF185N2	FD_01321_EF-1a [*Fusarium sp.*]	622 / 646 (96.28%)	Fusarium sp. NRRL 43637	645/646 (99%)
Summer	OF185N3	FD_01378_EF-1a [*Fusarium proliferatum*]	552 / 558 (98.92%)	Gibberella intermedia clone spt146	557/559 (99%)
Summer	IF186N5	FD_01268_EF-1a | F. oxysporum species complex 88 NRRL26961	538 / 538 (100%)	Fusarium oxysporum f. sp. melonis partial tef1a gene	538/538 (100%)
Summer	IF186N3	FD_01320_EF-1a [*Fusarium pallidoroseum*]	575 / 619 (92.89%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	597/635 (94%)
Summer	OF186N4	FD_01321_EF-1a [*Fusarium sp.*]	591 / 652 (90.64%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	618/661 (93%)
Summer	OF186N7	FD_01321_EF-1a [*Fusarium sp.*]	595 / 652 (91.25%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	620/661 (94%)
Summer	IF187N1	FD_01321_EF-1a [*Fusarium sp.*]	505 / 528 (95.64%)	Fusarium cf. incarnatum MLST 3-b clone spt072	539/541 (99%)

Summer	IF187N2	FD_01321_EF-1a [*Fusarium sp.*]	478 / 497 (96.17%)	Fusarium cf. incarnatum MLST 3-b clone spt072	504/505 (99%)
Summer	OF187N6	FD_01321_EF-1a [*Fusarium sp.*]	528 / 550 (96%)	Fusarium sp. NRRL 43637	549/552 (99%)
Summer	OF187N2	FD_01321_EF-1a [*Fusarium sp.*]	581 / 606 (95.87%)	Fusarium cf. incarnatum MLST 1-c clone spt113	606/608 (99%)
Summer	IF188N3	FD_01321_EF-1a [*Fusarium sp.*]	614 / 636 (96.54%)	Fusarium sp. NRRL 43637	659/663 (99%)
Summer	IF188N11	FD_01321_EF-1a [*Fusarium sp.*]	472 / 506 (93.28%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	527/539 (98%)
Summer	OF188N8	FD_01168_EF-1a GFSC Gibberella fujikuroi species complex NRRL22944	603 / 610 (98.85%)	Gibberella intermedia clone spt146	621/627 (99%)
Summer	OF188N1	FD_01169_EF-1a GFSC Gibberella fujikuroi species complex NRRL13566	581 / 595 (97.64%)	Gibberella fujikuroi isolate 3208	577/578 (99%)
Summer	IF189N2	FD_01162_EF-1a | GFSC Gibberella fujikuroi species complex NRRL26794	531 / 637 (83.35%)	Fusarium cf. incarnatum MLST 1-c clone spt113	518/598 (87%)
Summer	IF189N10	FD_01321_EF-1a [*Fusarium sp.*]	605 / 628 (96.33%)	Fusarium sp. NRRL 43637	628/629 (99%)
Summer	IF189N13	FD_01321_EF-1a [*Fusarium sp.*]	330 / 355 (92.95%)	Fusarium sp. NRRL 52776	385/397 (97%)
Summer	OF189N7	FD_01119_EF-1a [*Fusarium graminearum*]	507 / 572 (88.63%)	Fusarium cf. incarnatum MLST 1-c clone spt113	572/651 (88%)
Summer	OF189N2	FD_01320_EF-1a [*Fusarium pallidoroseum*]	439 / 447 (98.21%)	Fusarium sp. NRRL 31167	450/452 (99%)
Summer	OF189N3	FD_01321_EF-1a [*Fusarium sp.*]	586 / 610 (96.06%)	Fusarium cf. incarnatum MLST 1-c clone spt113	627/630 (99%)
Summer	OF189N12	FD_01321_EF-1a [Fusarium sp.]	621 / 646 (96.13%)	Fusarium sp. NRRL 43637	644/646 (99%)
Summer	IF190N5	FD_01321_EF-1a [*Fusarium sp.*]	475 / 507 (93.68%)	Fusarium cf. incarnatum MLSTs 1-a, 1-c and 4-b clone spt105	526/544 (97%)
Summer	OF190N6	FD_01205_EF-1a | F. oxysporum species complex 38 NRRL26022	309 / 354 (87.28%)	Fusarium oxysporum strain FCC3171	567/652 (87%)
Summer	OF190N3	FD_01320_EF-1a [*Fusarium pallidoroseum*]	344 / 378 (91%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	371/382 (97%)
Summer	OF190N1	FD_01321_EF-1a [*Fusarium sp.*]	642 / 672 (95.53%)	Fusarium cf. incarnatum MLST 1-c clone spt113	672/680 (99%)
Summer	OF190N4	FD_01321_EF-1a [*Fusarium sp.*]	583 / 606 (96.2%)	Fusarium equiseti strain AGrocketbis	605/607 (99%)
Summer	OF190N7	FD_01321_EF-1a [*Fusarium sp.*]	609 / 634 (96.05%)	Fusarium cf. incarnatum MLST 1-c clone spt113	636/637 (99%)
Summer	OF190N8	FD_01321_EF-1a [*Fusarium sp.*]	576 / 601 (95.84%)	Fusarium cf. incarnatum MLST 3-b clone spt072	599/602 (99%)
Summer	OF191N6	FD_01320_EF-1a [*Fusarium pallidoroseum*]	538 / 545 (98.71%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt116	545/545 (100%)
Summer	OF191N8	FD_01320_EF-1a [*Fusarium pallidoroseum*]	545 / 553 (98.55%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt116	552/553 (99%)
Summer	OF191N3	FD_01321_EF-1a [*Fusarium sp.*]	618 / 646 (95.66%)	Fusarium cf. incarnatum MLST 1-c clone spt113	651/654 (99%)
Summer	OF191N7	FD_01321_EF-1a [*Fusarium sp.*]	621 / 646 (96.13%)	Fusarium sp. NRRL 43637	644/646 (99%)
Summer	IF192N1	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	603 / 618 (97.57%)	Gibberella fujikuroi isolate V22	633/635 (99%)
Summer	IF192N7	FD_01267_EF-1a | F. oxysporum species complex 89 NRRL26962	580 / 580 (100%)	Fusarium oxysporum f. sp. melonis partial tef1a gene	585/586 (99%)
Summer	IF192N5	FD_01321_EF-1a [*Fusarium sp.*]	583 / 605 (96.36%)	Fusarium sp. NRRL 43637	617/619 (99%)
Summer	IF192N8	FD_01321_EF-1a [*Fusarium sp.*]	625 / 650 (96.15%)	Fusarium sp. NRRL 43637	644/645 (99%)
Summer	OF192N3	FD_01169_EF-1a GFSC NRRL13566 Gibberella fujikuroi species complex	511 / 522 (97.89%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	532/535 (99%)
Summer	OF192N2	FD_01248_EF-1a | F. oxysporum species complex 91 NRRL28406	261 / 309 (84.46%)	Fusarium oxysporum isolate FXM0831	552/655 (84%)

Summer	OF192N1	FD_01321_EF-1a [*Fusarium sp.*]	581 / 643 (90.35%)	Fusarium sp. NRRL 43623	598/653 (92%)
Summer	OF192N4	FD_01321_EF-1a [*Fusarium sp.*]	526 / 547 (96.16%)	Fusarium sp. NRRL 43637	547/549 (99%)
Summer	OF192N7	FD_01321_EF-1a [*Fusarium sp.*]	625 / 651 (96%)	Fusarium sp. NRRL 43637	644/646 (99%)
Summer	IF193N1	FD_01320_EF-1a [*Fusarium pallidoroseum*]	585 / 614 (95.27%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt142	607/637 (95%)
Summer	IF194N3	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	430 / 447 (96.19%)	Gibberella intermedia clone spt067	469/494 (95%)
Summer	IF194N7	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	498 / 592 (84.12%)	Gibberella intermedia strain PUF018	545/654 (83%)
Summer	IF194N15	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	602 / 610 (98.68%)	Fusarium proliferatum partial tef-1 gene	612/616 (99%)
Summer	IF194N14	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	604 / 618 (97.73%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	637/641 (99%)
Summer	IF194N24	FD_01205_EF-1a | F. oxysporum species complex 38 NRRL26022	337 / 364 (92.58%)	Fusarium oxysporum strain NRRL 46602	583/674 (86%)
Summer	IF194N32	FD_01269_EF-1a | F. oxysporum species complex 87 NRRL26960	499 / 500 (99.8%)	Fusarium oxysporum strain NRRL 53084	505/506 (99%)
Summer	IF194N1	FD_01320_EF-1a [*Fusarium pallidoroseum*]	582 / 631 (92.23%)	Fusarium sp. NRRL 43637	599/642 (93%)
Summer	IF194N8	FD_01320_EF-1a [*Fusarium pallidoroseum*]	538 / 547 (98.35%)	Fusarium sp. NRRL 31167	545/547 (99%)
Summer	IF194N16	FD_01320_EF-1a [*Fusarium pallidoroseum*]	489 / 496 (98.58%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	502/503 (99%)
Summer	IF194N28	FD_01320_EF-1a [*Fusarium pallidoroseum*]	615 / 623 (98.71%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt116	639/643 (99%)
Summer	IF194N30	FD_01320_EF-1a [*Fusarium pallidoroseum*]	555 / 563 (98.57%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt116	574/576 (99%)
Summer	IF194N2	FD_01321_EF-1a [*Fusarium sp.*]	604 / 628 (96.17%)	Fusarium sp. NRRL 36318	639/641 (99%)
Summer	IF194N5	FD_01321_EF-1a [*Fusarium sp.*]	626 / 650 (96.3%)	Fusarium sp. NRRL 43637	651/654 (99%)
Summer	IF194N6	FD_01321_EF-1a [*Fusarium sp.*]	605 / 627 (96.49%)	Fusarium sp. NRRL 43637	639/641 (99%)
Summer	IF194N10	FD_01321_EF-1a [*Fusarium sp.*]	612 / 678 (90.26%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	640/685 (93%)
Summer	IF194N11	FD_01321_EF-1a [*Fusarium sp.*]	589 / 639 (92.17%)	Fusarium sp. NRRL 43637	622/663 (94%)
Summer	IF194N12	FD_01321_EF-1a [*Fusarium sp.*]	555 / 578 (96.02%)	Fusarium sp. NRRL 43637	575/576 (99%)
Summer	IF194N17	FD_01321_EF-1a [*Fusarium sp.*]	592 / 625 (94.72%)	Fusarium cf. incarnatum MLST 1-c clone spt113	617/627 (98%)
Summer	IF194N18	FD_01321_EF-1a [*Fusarium sp.*]	556 / 638 (87.14%)	Fusarium cf. incarnatum MLST 1-c clone spt113	587/652 (90%)
Summer	IF194N19	FD_01321_EF-1a [*Fusarium sp.*]	614 / 636 (96.54%)	Fusarium sp. NRRL 43637	651/653 (99%)
Summer	IF194N20	FD_01321_EF-1a [*Fusarium sp.*]	604 / 630 (95.87%)	Fusarium cf. incarnatum MLST 1-c clone spt113	627/633 (99%)
Summer	IF194N21	FD_01321_EF-1a [*Fusarium sp.*]	416 / 449 (92.65%)	Fusarium sp. NRRL 52776	463/477 (97%)
Summer	IF194N23	FD_01321_EF-1a [*Fusarium sp.*]	556 / 579 (96.02%)	Fusarium equiseti strain AGrocketbis	590/592 (99%)
Summer	IF194N25	FD_01321_EF-1a [*Fusarium sp.*]	612 / 636 (96.22%)	Fusarium cf. incarnatum MLST 1-c clone spt113	654/658 (99%)
Summer	IF194N26	FD_01321_EF-1a [*Fusarium sp.*]	540 / 564 (95.74%)	Fusarium cf. incarnatum MLST 3-b clone spt072	574/577 (99%)
Summer	IF194N27	FD_01321_EF-1a [*Fusarium sp.*]	627 / 653 (96.01%)	Fusarium cf. incarnatum MLST 1-c clone spt113	653/654 (99%)
Summer	IF194N29	FD_01321_EF-1a [*Fusarium sp.*]	595 / 617 (96.43%)	Fusarium sp. NRRL 43637	624/625 (99%)

Summer	IF194N31	FD_01321_EF-1a [*Fusarium sp.*]	577 / 640 (90.15%)	Fusarium sp. NRRL 43623	605/663 (91%)
Summer	IF194N4	FD_01378_EF-1a [*Fusarium proliferatum*]	320 / 366 (87.43%)	Gibberella intermedia clone spt067	572/674 (85%)
Summer	OF194N7	FD_01168_EF-1a GFSC Gibberella fujikuroi species complex NRRL22944	513 / 517 (99.22%)	Fusarium proliferatum isolate 001B	523/524 (99%)
Summer	OF194N5	FD_01248_EF-1a F. oxysporum species complex 91 NRRL28406	595 / 628 (94.74%)	Fusarium oxysporum f. sp. gladioli strain NRRL28406	595/628 (95%)
Summer	OF194N1	FD_01321_EF-1a [*Fusarium sp.*]	489 / 507 (96.44%)	Fusarium sp. NRRL 43637	531/534 (99%)
Summer	OF194N2	FD_01321_EF-1a [*Fusarium sp.*]	550 / 597 (92.12%)	Fusarium cf. incarnatum MLSTs 1-a, 1-c and 4-b clone spt105	576/595 (97%)
Summer	OF194N3	FD_01321_EF-1a [*Fusarium sp.*]	495 / 518 (95.55%)	Fusarium cf. incarnatum MLST 1-c clone spt113	535/539 (99%)
Summer	OF194N4	FD_01321_EF-1a [*Fusarium sp.*]	565 / 620 (91.12%)	Fusarium sp. NRRL 52765	598/637 (94%)
Summer	OF194N9	FD_01321_EF-1a [*Fusarium sp.*]	553 / 577 (95.84%)	Fusarium equiseti strain AGrocketbis	571/573 (99%)
Summer	IF195N2	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	533 / 545 (97.79%)	Gibberella fujikuroi isolate 3208	545/545 (100%)
Summer	OF195N2	FD_01320_EF-1a [*Fusarium pallidoroseum*]	389 / 396 (98.23%)	Fusarium sp. NRRL 31167	400/402 (99%)
Summer	OF195N3	FD_01320_EF-1a [*Fusarium pallidoroseum*]	367 / 404 (90.84%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	407/409 (99%)
Summer	IF197N1	FD_01321_EF-1a [*Fusarium sp.*]	506 / 527 (96.01%)	Fusarium sp. NRRL 43637	544/548 (99%)
Summer	OF197N1	FD_01169_EF-1a NRRL13566 GFSC Gibberella fujikuroi species complex	442 / 450 (98.22%)	Gibberella cf. fujikuroi Trap_3_24_hr_Med_5 clone spt136	461/463 (99%)
Summer	OF197N2	FD_01375_EF-1a [*Fusarium oxysporum*]	312 / 361 (86.42%)	Fusarium sp. NRRL 52765	520/592 (88%)
Summer	IF198N2	FD_01321_EF-1a [*Fusarium sp.*]	612 / 634 (96.52%)	Fusarium sp. NRRL 43637	651/655 (99%)
Summer	OF198N3	FD_01321_EF-1a [*Fusarium sp.*]	437 / 455 (96.04%)	Fusarium sp. NRRL 43637	462/463 (99%)
Summer	OF198N4	FD_01321_EF-1a [*Fusarium sp.*]	508 / 529 (96.03%)	Fusarium sp. NRRL 43637	541/543 (99%)
Summer	IF199N4	FD_01321_EF-1a [*Fusarium sp.*]	535 / 556 (96.22%)	Fusarium sp. NRRL 43637	556/558 (99%)
Summer	IF199N9	FD_01321_EF-1a [*Fusarium sp.*]	473 / 504 (93.84%)	Fusarium cf. incarnatum MLSTs 1-a, 1-c and 4-b clone spt105	540/542 (99%)
Summer	OF199N10	FD_01119_EF-1a [*Fusarium graminearum*]	480 / 513 (93.56%)	Gibberella zeae strain F5051	525/572 (92%)
Summer	OF199N2	FD_01169_EF-1a NRRL13566 GFSC Gibberella fujikuroi species complex	611 / 631 (96.83%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	637/643 (99%)
Summer	OF199N9	FD_01319_EF-1a [*Fusarium sp.*]	490 / 526 (93.15%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b and 25-c clone spt046	539/541 (99%)
Summer	OF199N1	FD_01321_EF-1a [*Fusarium sp.*]	557 / 579 (96.2%)	Fusarium sp. NRRL 43637	591/593 (99%)
Summer	OF199N5	FD_01321_EF-1a [*Fusarium sp.*]	537 / 560 (95.89%)	Fusarium sp. NRRL 43637	571/574 (99%)
Summer	OF199N8	FD_01321_EF-1a [*Fusarium sp.*]	508 / 529 (96.03%)	Fusarium sp. NRRL 43637	542/544 (99%)
Summer	OF199N14	FD_01388_EF-1a [*Fusarium verticillioides*]	496 / 497 (99.79%)	Fusarium oxysporum isolate FSY0951	500/502 (99%)
Fall	F116N2	F. incarnatum-equiseti species complex isolate NRRL 20423, MLST4-a	629 / 634 (99.21%)	Fusarium equiseti isolate 1571B	638/644 (99%)
Fall	F116N3	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	641 / 641 (100%)	Fusarium sp. NRRL 45996	644/645 (99%)
Fall	F116N4	FD_01320_EF-1a [Fusarium pallidoroseum]	641 / 650 (98.61%)	Fusarium cf. incarnatum H04-777S-1 PCNB	671/680 (99%)
Fall	F117N1	FD_01119_EF-1a [Fusarium graminearum]	638 / 641 (99.53%)	Gibberella zeae isolate CS3005	655/657 (99%)

Fall	F119N2	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	643 / 643 (100%)	Fusarium sp. NRRL 5537	643/643 (100%)
Fall	F120N1	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	611 / 612 (99.83%)	Fusarium sp. NRRL 5537	627/631 (99%)
Fall	F120N2	FD_01321_EF-1a [Fusarium sp.]	613 / 661 (92.73%)	Fusarium cf. incarnatum H04-707S-4 PCNB	686/695 (99%)
Fall	F121N1	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	642 / 643 (99.84%)	Fusarium sp. NRRL 5537	645/647 (99%)
Fall	F121N3	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	609 / 612 (99.5%)	Fusarium sp. NRRL 5537	628/635 (99%)
Fall	F121N2	GFSC isolate NRRL 22016, MLSTGibberella fujikuroi species complex	610 / 612 (99.67%)	Fusarium subglutinans strain NRRL 22016	610/612 (99%)
Fall	F122N3	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	641 / 643 (99.68%)	Fusarium sp. NRRL 5537	646/649 (99%)
Fall	F122N5	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	632 / 632 (100%)	Fusarium sp. NRRL 5537	632/632 (100%)
Fall	F122N2	FD_00986_EF-1a [*Fusarium graminearum*]	613 / 613 (100%)	Gibberella zeae isolate M02-7035S-2 DCPA	639/640 (99%)
Fall	F122N4	FD_01857_EF-1a [*Fusarium sp.*]	603 / 604 (99.83%)	Gibberella fujikuroi isolate V95	612/615 (99%)
Fall	F125N2	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	596 / 597 (99.83%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	602/603 (99%)
Fall	F125N4	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	603 / 604 (99.83%)	Fusarium sp. NRRL 45996	608/610 (99%)
Fall	F125N5	FD_01321_EF-1a [Fusarium sp.]	635 / 659 (96.35%)	Fusarium sp. NRRL 45996	668/670 (99%)
Fall	F126N4	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	606 / 610 (99.34%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	612/615 (99%)
Fall	F126N8	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	623 / 626 (99.52%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	624/626 (99%)
Fall	F126N10	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	622 / 625 (99.52%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	624/625 (99%)
Fall	F126N3	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	603 / 618 (97.57%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	620/622 (99%)
Fall	F126N11	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	527 / 540 (97.59%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	538/539 (99%)
Fall	F126N15	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (97.58%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	634/638 (99%)
Fall	F126N20	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	638 / 639 (99.84%)	Fusarium sp. NRRL 5537	638/639 (99%)
Fall	F126N7	FD_00986_EF-1a [*Fusarium graminearum*]	618 / 619 (99.83%)	Gibberella zeae isolate M02-7035S-2 DCPA	633/634 (99%)
Fall	F126N6	FD_01114_EF-1a [*Fusarium graminearum*]	608 / 612 (99.34%)	Gibberella zeae isolate G5S	608/611 (99%)
Fall	F126N13	FD_01119_EF-1a [*Fusarium graminearum*]	613 / 615 (99.67%)	Gibberella zeae strain ATCC 60309	623/625 (99%)
Fall	F126N19	FD_01119_EF-1a [*Fusarium graminearum*]	614 / 615 (99.83%)	Gibberella zeae isolate G5S	619/620 (99%)
Fall	F126N21	FD_01169_EF-1a	624 / 640 (97.5%)	Gibberella fujikuroi isolate PRC 2a	658/661 (99%)
Fall	F126N30	FD_01304_EF-1a [*Fusarium sp.*]	627 / 630 (99.52%)	Fusarium sporotrichioides strain LMSA 1.09.114	644/647 (99%)
Fall	F126N18	FD_01319_EF-1a [Fusarium sp.]	594 / 643 (92.37%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	665/670 (99%)
Fall	F126N29	FD_01321_EF-1a [Fusarium sp.]	613 / 661 (92.73%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	686/695 (99%)
Fall	F126N1	FD_01857_EF-1a [*Fusarium sp.*]	600 / 602 (99.66%)	Gibberella fujikuroi partial tef-1 gene	605/608 (99%)
Fall	F126N12	FD_01857_EF-1a [*Fusarium sp.*]	602 / 604 (99.66%)	Gibberella fujikuroi isolate V22	608/610 (99%)
Fall	F126N14	FD_01857_EF-1a [*Fusarium sp.*]	603 / 604 (99.83%)	Gibberella fujikuroi isolate V95	617/621 (99%)

Fall	F126N23	FD_01862_EF-1a [*Fusarium sp.*]	624 / 626 (99.68%)	Fusarium subglutinans strain NRRL 22016	644/647 (99%)
Fall	F126N33	GFSC isolate NRRL 13618, MLSTGibberella fujikuroi species complex	606 / 617 (98.21%)	Fusarium bulbicola strain NRRL13618	609/621 (98%)
Fall	F126N31	GFSC isolate NRRL 22016, MLSTGibberella fujikuroi species complex	612 / 613 (99.83%)	Fusarium subglutinans strain NRRL 22016	615/617 (99%)
Fall	F126N22	GFSC isolate NRRL 22016, MLSTGibberella fujikuroi species complex	613 / 614 (99.83%)	Fusarium subglutinans strain NRRL 22016	613/614 (99%)
Fall	F127N3	FD_00986_EF-1a [Fusarium graminearum]	611 / 612 (99.83%)	Gibberella zeae strain NRRL 31084	615/617 (99%)
Fall	F127N2	FD_01321_EF-1a [Fusarium sp.]	626 / 649 (96.45%)	Fusarium sp. NRRL 45996	669/676 (99%)
Fall	F129N1	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	628 / 630 (99.68%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	639/643 (99%)
Fall	F147N5	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	609 / 610 (99.83%)	Fusarium sp. NRRL 45996	632/637 (99%)
Fall	F147N1	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	610 / 612 (99.67%)	Fusarium sp. NRRL 5537	627/632 (99%)
Fall	F148N8	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	596 / 604 (98.67%)	Fusarium sp. NRRL 32997	621/635 (98%)
Fall	F148N6	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	607 / 621 (97.74%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	636/640 (99%)
Fall	F148N7	FD_01304_EF-1a [Fusarium sp.]	615 / 617 (99.67%)	Fusarium sporotrichioides strain NRRL 29977	628/632 (99%)
Fall	F148N3	FD_01389_EF-1a_2 [*Fusarium proliferatum*]	609 / 610 (99.83%)	Fusarium proliferatum isolate 2-91	626/630 (99%)
Fall	F148N2	FD_01857_EF-1a [*Fusarium sp.*]	608 / 608 (100%)	Gibberella fujikuroi isolate V95	619/621 (99%)
Fall	F148N4	FD_01857_EF-1a [Fusarium sp.]	619 / 625 (99.04%)	Gibberella fujikuroi partial tef-1 gene	639/645 (99%)
Fall	F149N13	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	633 / 649 (97.53%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	652/655 (99%)
Fall	F149N25	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (97.58%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	637/642 (99%)
Fall	F149N11	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	635 / 651 (97.54%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	654/657 (99%)
Fall	F149N12	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	609 / 624 (97.59%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	628/630 (99%)
Fall	F149N21	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	576 / 612 (94.11%)	Fusarium cf. incarnatum H04-707S-4 PCNB	626/631 (99%)
Fall	F149N9	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	672 / 678 (99.11%)	Fusarium sp. NRRL 5537	672/678 (99%)
Fall	F149N23	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	614 / 614 (100%)	Fusarium sp. NRRL 5537	629/632 (99%)
Fall	F149N19	FD_01119_EF-1a [Fusarium graminearum]	625 / 629 (99.36%)	Gibberella zeae strain LMSA 1.09.107	614/615 (99%)
Fall	F149N20	FD_01304_EF-1a [Fusarium sp.]	628 / 631 (99.52%)	Fusarium langsethiae strain NRRL 53422/2321/2	653/658 (99%)
Fall	F149N24	FD_01304_EF-1a [Fusarium sp.]	618 / 621 (99.51%)	Fusarium sporotrichioides strain NRRL 29977	624/627 (99%)
Fall	F149N3	FD_01304_EF-1a [Fusarium sp.]	626 / 632 (99.05%)	Fusarium langsethiae strain NRRL 53422/2321/2	643/649 (99%)
Fall	F149N8	FD_01388_EF-1a [Fusarium verticillioides]	642 / 645 (99.53%)	Gibberella moniliformis strain PUMCH10XB00173	651/656 (99%)
Fall	F149N6	FD_01857_EF-1a [Fusarium sp.]	601 / 602 (99.83%)	Gibberella fujikuroi partial tef-1 gene	622/627 (99%)
Fall	F149N17	FD_01857_EF-1a [Fusarium sp.]	602 / 604 (99.66%)	Gibberella fujikuroi isolate V95	608/611 (99%)
Fall	F149N7	GFSC isolate NRRL 25331, MLSTGibberella fujikuroi species complex	615 / 624 (98.55%)	Gibberella circinata strain NRRL25331	620/630 (99%)
Fall	F150N3	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	607 / 609 (99.67%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	613/616 (99%)

Fall	F150N8	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	610 / 613 (99.51%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	626/630 (99%)
Fall	F150N2	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	608 / 611 (99.5%)	Fusarium cf. incarnatum M03-11241S-2 PCNB	617/619 (99%)
Fall	F150N13	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	591 / 605 (97.68%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	627/632 (99%)
Fall	F150N9	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	602 / 618 (97.41%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	626/630 (99%)
Fall	F150N10	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 621 (97.58%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	628/631 (99%)
Fall	F150N11	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	610 / 625 (97.6%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	627/629 (99%)
Fall	F150N14	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	606 / 620 (97.74%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	633/636 (99%)
Fall	F150N15	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	591 / 605 (97.68%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	610/611 (99%)
Fall	F150N5	FD_01304_EF-1a [Fusarium sp.]	614 / 617 (99.51%)	Fusarium sporotrichioides strain NRRL 29977	623/627 (99%)
Fall	F150N6	FD_01857_EF-1a [Fusarium sp.]	596 / 597 (99.83%)	Gibberella fujikuroi isolate V22	610/613 (99%)
Fall	F150N7	FD_01857_EF-1a [Fusarium sp.]	604 / 606 (99.66%)	Gibberella fujikuroi isolate V22	607/609 (99%)
Fall	F150N1	FD_01858_EF-1a [Fusarium sp.]	609 / 611 (99.67%)	Gibberella intermedia isolate C45	626/630 (99%)
Fall	F151N6	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	610/612 (99%)
Fall	F151N8	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	611 / 612 (99.83%)	Fusarium sp. NRRL 32522	618/621 (99%)
Fall	F151N1	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	604 / 619 (97.57%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	623/625 (99%)
Fall	F151N5	FD_00986_EF-1a [Fusarium graminearum]	511 / 535 (95.51%)	Gibberella zeae isolate CS3005	531/555 (96%)
Fall	F151N3	FD_00986_EF-1a [Fusarium graminearum]	618 / 619 (99.83%)	Gibberella zeae strain NRRL 31084	622/624 (99%)
Fall	F151N10	FD_01119_EF-1a [Fusarium graminearum]	625 / 628 (99.52%)	Gibberella zeae isolate G5S	611/612 (99%)
Fall	F151N9	FD_01119_EF-1a [Fusarium graminearum]	546 / 554 (98.55%)	Gibberella zeae isolate CS3005	622/668 (94%)
Fall	F151N4	FD_01857_EF-1a [Fusarium sp.]	587 / 588 (99.82%)	Gibberella fujikuroi isolate V22	607/611 (99%)
Fall	F152N2	F. oxysporum species complex isolate NRRL 28391, MLST103	618 / 619 (99.83%)	Fusarium oxysporum strain NRRL 43431	618/619 (99%)
Fall	F152N5	F. oxysporum species complex isolate NRRL 28391, MLST103	604 / 605 (99.83%)	Fusarium oxysporum strain NRRL 26404	615/618 (99%)
Fall	F152N4	GFSC isolate NRRL 25200, MLSTGibberella fujikuroi species complex	620 / 634 (97.79%)	Fusarium lactis strain NRRL25200	620/634 (98%)
Fall	F153N6	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	602 / 603 (99.83%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	609/610 (99%)
Fall	F153N8	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	553 / 564 (98.04%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	579/582 (99%)
Fall	F153N1	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	580 / 605 (95.86%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	604/617 (98%)
Fall	F153N2	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	601 / 616 (97.56%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	614/615 (99%)
Fall	F153N4	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	589 / 605 (97.35%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	608/611 (99%)
Fall	F153N13	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	634 / 651 (97.38%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	651/654 (99%)
Fall	F153N11	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	569 / 604 (94.2%)	Fusarium cf. incarnatum H04-707S-4 PCNB	622/625 (99%)
Fall	F153N12	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	609 / 610 (99.83%)	Fusarium sp. NRRL 5537	624/628 (99%)

Fall	F153N9	FD_01119_EF-1a [Fusarium graminearum]	647 / 650 (99.53%)	Gibberella zeae isolate G5S	613/613 (100%)
Fall	F153N10	FD_01307_EF-1a [Fusarium sp.]	531 / 554 (95.84%)	Gibberella pulicaris strain FRC R-07843	532/554 (97%)
Fall	F153N5	FD_01853_EF-1a [Fusarium sp.]	630 / 633 (99.52%)	Fusarium sporotrichioides strain F95	655/658 (99%)
Fall	F153N3	GFSC isolate NRRL 25200, MLSTGibberella fujikuroi species complex	605 / 618 (97.89%)	Fusarium lactis strain NRRL25200	613/628 (98%)
Fall	F154N4	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	616/619 (99%)
Fall	F154N3	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	598 / 598 (100%)	Fusarium sp. NRRL 32522	604/605 (99%)
Fall	F154N8	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	507 / 540 (93.88%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	533/554 (97%)
Fall	F154N6	F. oxysporum species complex isolate NRRL 40182, MLST99	629 / 629 (100%)	Fusarium oxysporum strain NRRL28359	628/629 (99%)
Fall	F154N2	FD_00986_EF-1a [Fusarium graminearum]	608 / 609 (99.83%)	Gibberella zeae strain NRRL 31084	617/621 (99%)
Fall	F154N1	FD_01114_EF-1a [Fusarium graminearum]	613 / 616 (99.51%)	Gibberella zeae strain LMSA 1.09.129	644/649 (99%)
Fall	F154N5	FD_01119_EF-1a [Fusarium graminearum]	604 / 618 (97.73%)	Gibberella zeae isolate CS3005	623/637 (98%)
Fall	F154N7	FD_01304_EF-1a [Fusarium sp.]	605 / 606 (99.83%)	Fusarium langsethiae strain NRRL 53422/2321/2	622/623 (99%)
Fall	F154N11	FD_01853_EF-1a [Fusarium sp.]	607 / 609 (99.67%)	Fusarium sporotrichioides strain NRRL 53434	613/615 (99%)
Fall	F155N7	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	610/612 (99%)
Fall	F155N10	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 599 (100%)	Fusarium sp. NRRL 32522	610/612 (99%)
Fall	F155N11	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	600 / 601 (99.83%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	612/614 (99%)
Fall	F155N8	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	598 / 599 (99.83%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	610/612 (99%)
Fall	F155N4	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	594 / 604 (98.34%)	Fusarium sp. NRRL 32997	599/610 (99%)
Fall	F155N5	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	597 / 606 (98.51%)	Fusarium sp. NRRL 32997	604/615 (99%)
Fall	F155N1	F. incarnatum-equiseti species complex isolate NRRL 34039, MLST1-b	603 / 605 (99.66%)	Fusarium sp. NRRL 34039	618/623 (99%)
Fall	F155N15	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	590 / 594 (99.32%)	Fusarium sp. NRRL 45996	609/617 (99%)
Fall	F155N13	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	654 / 655 (99.84%)	Fusarium sp. NRRL 5537	654/655 (99%)
Fall	F155N14	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	556 / 556 (100%)	Fusarium sp. NRRL 5537	574/577 (99%)
Fall	F155N6	F. oxysporum species complex isolate NRRL 26962, MLST89	623 / 625 (99.68%)	Fusarium sp. 45BMC	626/628 (99%)
Fall	F155N3	FD_01119_EF-1a [Fusarium graminearum]	628 / 629 (99.84%)	Gibberella zeae isolate CS3005	649/652 (99%)
Fall	F155N12	FD_01119_EF-1a [Fusarium graminearum]	573 / 580 (98.79%)	Gibberella zeae strain LMSA 1.09.107	579/587 (99%)
Fall	F155N2	FD_01857_EF-1a [Fusarium sp.]	584 / 587 (99.48%)	Gibberella fujikuroi isolate V95	598/604 (99%)
Fall	F156N10	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	597 / 600 (99.5%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	608/611 (99%)
Fall	F156N15	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	615 / 619 (99.35%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	628/632 (99%)
Fall	F156N19	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	614 / 615 (99.83%)	Fusarium sp. NRRL 32522	624/627 (99%)
Fall	F156N18	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	601 / 621 (96.77%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	628/637 (99%)

Fall	F156N5	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	595 / 603 (98.67%)	Fusarium sp. NRRL 32997	605/615 (99%)
Fall	F156N47	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	577 / 612 (94.28%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	615/640 (96%)
Fall	F156N13	F. incarnatum-equiseti species complex isolate NRRL 45996, MLST1-a	576 / 611 (94.27%)	Fusarium cf. incarnatum H04-707S-4 PCNB	629/633 (99%)
Fall	F156N36	F. incarnatum-equiseti species complex isolate NRRL 28029, MLST3-b	620 / 622 (99.67%)	Fusarium sp. NRRL 28029	627/630 (99%)
Fall	F156N28	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	614 / 615 (99.83%)	Fusarium sp. NRRL 32522	620/622 (99%)
Fall	F156N39	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	614 / 615 (99.83%)	Fusarium sp. NRRL 32522	620/622 (99%)
Fall	F156N45	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	599 / 615 (97.39%)	Fusarium sp. NRRL 32522	612/631 (97%)
Fall	F156N35	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	610 / 626 (97.44%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	636/641 (99%)
Fall	F156N21	F. incarnatum-equiseti species complex isolate NRRL 32997, MLST7-a	618 / 628 (98.4%)	Fusarium sp. NRRL 32997	624/635 (98%)
Fall	F156N43	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	574 / 609 (94.25%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	609/631 (97%)
Fall	F156N49	F. incarnatum-equiseti species complex isolate NRRL 36123, MLST4-b	569 / 606 (93.89%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7079S-5	597/621 (96%)
Fall	F156N24	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	612 / 612 (100%)	Fusarium sp. NRRL 5537	624/626 (99%)
Fall	F156N30	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	641 / 643 (99.68%)	Fusarium sp. NRRL 5537	641/643 (99%)
Fall	F156N42	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	625 / 626 (99.84%)	Fusarium sp. NRRL 5537	629/631 (99%)
Fall	F156N2	F. oxysporum species complex isolate NRRL 40182, MLST99	605 / 606 (99.83%)	Fusarium oxysporum strain NRRL 38361	619/623 (99%)
Fall	F156N44	F. oxysporum species complex isolate NRRL 26962, MLST89	619 / 620 (99.83%)	Fusarium sp. 45BMC	623/623 (100%)
Fall	F156N22	FD_00986_EF-1a [Fusarium graminearum]	619 / 620 (99.83%)	Gibberella zeae strain NRRL 31084	623/625 (99%)
Fall	F156N37	FD_01304_EF-1a [*Fusarium sp.*]	614 / 617 (99.51%)	Fusarium sporotrichioides strain NRRL 29977	618/621 (99%)
Fall	F156N41	FD_01304_EF-1a [*Fusarium sp.*]	628 / 631 (99.52%)	Fusarium sporotrichioides strain NRRL 29977	633/636 (99%)
Fall	F156N6	FD_01304_EF-1a [Fusarium sp.]	615 / 617 (99.67%)	Fusarium sporotrichioides strain NRRL 29977	625/628 (99%)
Fall	F156N33	FD_01317_EF-1a [*Fusarium sp.*]	607 / 623 (97.43%)	Gibberella avenacea voucher FRC R-9369	618/622 (99%)
Fall	F156N1	FD_01345_EF-1a [Fusarium lateritium]	610 / 635 (96.06%)	Fusarium lateritium isolate F0104	630/645 (98%)
Fall	F156N9	FD_01345_EF-1a [Fusarium lateritium]	626 / 652 (96.01%)	Fusarium lateritium isolate F0104	650/664 (98%)
Fall	F156N40	FD_01376_EF-1a [*Fusarium oxysporum*]	618 / 619 (99.83%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	623/625 (99%)
Fall	F156N11	FD_01843_EF-1a [Fusarium armeniacum]	594 / 597 (99.49%)	Fusarium armeniacum strain NRRL 6227	603/604 (99%)
Fall	F156N20	FD_01853_EF-1a [Fusarium sp.]	591 / 623 (94.86%)	Fusarium sporotrichioides strain NRRL 53434	596/628 (95%)
Fall	F156N27	FD_01857_EF-1a [*Fusarium sp.*]	603 / 604 (99.83%)	Gibberella fujikuroi isolate V95	613/616 (99%)
Fall	F156N32	FD_01857_EF-1a [*Fusarium sp.*]	614 / 616 (99.67%)	Gibberella fujikuroi isolate V22	618/620 (99%)
Fall	F156N3	FD_01857_EF-1a [Fusarium sp.]	596 / 600 (99.33%)	Gibberella fujikuroi isolate V95	599/604 (99%)
Fall	F156N4	FD_01857_EF-1a [Fusarium sp.]	545 / 546 (99.81%)	Gibberella fujikuroi isolate V22	561/564 (99%)
Fall	F156N14	FD_01857_EF-1a [Fusarium sp.]	602 / 604 (99.66%)	Gibberella fujikuroi isolate V95	617/622 (99%)

Fall	F156N29	FD_01857_EF-1a [Fusarium sp.]	608 / 611 (99.5%)	Gibberella fujikuroi isolate V22	614/617 (99%)
Fall	F156N16	GFSC isolate NRRL 44887, MLSTGibberella fujikuroi species complex	600 / 601 (99.83%)	Gibberella fujikuroi partial tef-1 gene	598/599 (99%)
Fall	F157N9	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	499 / 500 (99.8%)	Fusarium sp. NRRL 32522	503/505 (99%)
Fall	F157N10	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	475 / 480 (98.95%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7085S-4	477/480 (99%)
Fall	F157N12	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	612 / 613 (99.83%)	Fusarium cf. incarnatum DFH-2010 isolate M02-7033S-4	628/631 (99%)
Fall	F157N14	F. incarnatum-equiseti species complex isolate NRRL 32522, MLST18-b	336 / 336 (100%)	Fusarium sp. NRRL 32522	339/340 (99%)
Fall	F157N4	F. incarnatum-equiseti species complex isolate NRRL 32993, MLST25-b	610 / 624 (97.75%)	Fusarium cf. incarnatum M03-11209S-1 PCNB	629/630 (99%)
Fall	F157N1	F. incarnatum-equiseti species complex isolate NRRL 34005, MLST24-a	604 / 605 (99.83%)	Fusarium cf. incarnatum M03-11345S-1 DCPA	604/605 (99%)
Fall	F157N13	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	602 / 604 (99.66%)	Fusarium sp. NRRL 5537	606/609 (99%)
Fall	F157N15	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	534 / 536 (99.62%)	Fusarium sp. NRRL 5537	540/543 (99%)
Fall	F157N6	F. oxysporum species complex isolate NRRL 26962, MLST89	577 / 577 (100%)	Fusarium oxysporum	580/580 (100%)
Fall	F157N8	FD_00929_EF-1a [*Fusarium sp.*]	535 / 539 (99.25%)	Fusarium sporotrichioides strain NRRL 29977	541/544 (99%)
Fall	F157N7	FD_01304_EF-1a [*Fusarium sp.*]	620 / 623 (99.51%)	Fusarium sporotrichioides strain NRRL 29977	621/623 (99%)
Fall	F157N3	FD_01345_EF-1a [*Fusarium lateritium*]	624 / 651 (95.85%)	Fusarium lateritium isolate F0104	635/650 (98%)
Fall	F157N16	FD_01376_EF-1a [*Fusarium oxysporum*]	623 / 624 (99.83%)	Fusarium oxysporum f. sp. ciceris strain NRRL 32158	630/633 (99%)
Fall	F157N11	FD_01853_EF-1a [*Fusarium sp.*]	600 / 602 (99.66%)	Fusarium sporotrichioides strain NRRL 29977	600/602 (99%)
Fall	F157N2	FD_01857_EF-1a [*Fusarium sp.*]	584 / 594 (98.31%)	Gibberella fujikuroi isolate V95	595/607 (98%)
Fall	F157N5	FD_01857_EF-1a [*Fusarium sp.*]	611 / 614 (99.51%)	Gibberella fujikuroi isolate V22	614/617 (99%)
Fall	IF201N3	FD_01321_EF-1a [*Fusarium sp.*]	633 / 697 (90.81%)	Fusarium sp. NRRL 5537	663/690 (96%)
Fall	OF201N2	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	359 / 369 (97.28%)	Gibberella fujikuroi isolate GCF	372/374 (99%)
Fall	OF201N1	FD_01299_EF-1a [*Fusarium globosum*]	315 / 323 (97.52%)	Gibberella fujikuroi isolate GCF	327/328 (99%)
Fall	OF201N3	FD_01320_EF-1a [*Fusarium pallidoroseum*]	351 / 386 (90.93%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	385/386 (99%)
Fall	IF202N1	FD_01321_EF-1a [*Fusarium sp.*]	586 / 610 (96.06%)	Fusarium sp. NRRL 36318	621/623 (99%)
Fall	OF202N3	FD_01268_EF-1a | F. oxysporum species complex 88 NRRL26961	573 / 574 (99.82%)	Fusarium oxysporum f. sp. melonis partial tef1a gene	573/574 (99%)
Fall	OF202N2	FD_01320_EF-1a [*Fusarium pallidoroseum*]	579 / 624 (92.78%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt142	596/637 (94%)
Fall	OF202N5	FD_01321_EF-1a [*Fusarium sp.*]	425 / 446 (95.29%)	Fusarium cf. incarnatum MLST 3-b clone spt072	444/446 (99%)
Fall	IF203N5	FD_01320_EF-1a [*Fusarium pallidoroseum*]	606 / 615 (98.53%)	Fusarium sp. NRRL 31167	625/628 (99%)
Fall	IF203N2	FD_01321_EF-1a [*Fusarium sp.*]	541 / 577 (93.76%)	Fusarium equiseti EF-1alpha gene	621/622 (99%)
Fall	IF204N4	FD_00805_EF-1a | F. oxysporum species complex 99 NRRL40182	365 / 366 (99.72%)	Fusarium oxysporum strain NRRL28359	368/371 (99%)
Fall	IF204N1	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	388 / 388 (100%)	Fusarium subglutinans clone spt144	388/388 (100%)
Fall	IF204N6	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	621 / 652 (95.24%)	Fusarium subglutinans clone spt144	630/662 (95%)

Fall	IF204N2	FD_01320_EF-1a [*Fusarium pallidoroseum*]	257 / 260 (98.84%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt142	271/273 (99%)
Fall	OF204N3	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	613 / 614 (99.83%)	Fusarium subglutinans clone spt144	613/614 (99%)
Fall	OF204N7	FD_01319_EF-1a [*Fusarium sp.*]	580 / 627 (92.5%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	635/638 (99%)
Fall	OF204N1	FD_01320_EF-1a [*Fusarium pallidoroseum*]	608 / 615 (98.86%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt134	626/628 (99%)
Fall	OF204N5	FD_01378_EF-1a [*Fusarium proliferatum*]	626 / 633 (98.89%)	Gibberella intermedia clone spt067	633/634 (99%)
Fall	OF204N6	FD_01378_EF-1a [*Fusarium proliferatum*]	611 / 619 (98.7%)	Gibberella intermedia clone spt067	623/626 (99%)
Fall	OF204N2	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	621/623 (99%)
Fall	IF205N1	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	619/621 (99%)
Fall	IF206N3	FD_01388_EF-1a [*Fusarium verticillioides*]	564 / 565 (99.82%)	Gibberella moniliformis isolate B4	569/571 (99%)
Fall	OF206N3	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	590 / 604 (97.68%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	615/617 (99%)
Fall	OF206N5	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	594 / 608 (97.69%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	614/615 (99%)
Fall	OF206N6	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	279 / 285 (97.89%)	Gibberella cf. fujikuroi Trap_3_24_hr_Med_5 clone spt136	296/298 (99%)
Fall	OF206N2	FD_01388_EF-1a [*Fusarium verticillioides*]	621 / 622 (99.83%)	Gibberella moniliformis isolate B4	621/622 (99%)
Fall	OF206N4	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	625/628 (99%)
Fall	IF207N70	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	591 / 594 (99.49%)	Gibberella intermedia clone spt067	595/596 (99%)
Fall	IF207N15	FD_01119_EF-1a	614 / 615 (99.83%)	Gibberella zeae isolate G5S	618/619 (99%)
Fall	IF207N9	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	321/323 (99%)	Gibberella intermedia strain F1129	324/324 (100%)
Fall	IF207N16	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	368 / 370 (99.45%)	Gibberella intermedia clone spt067	370/370 (100%)
Fall	IF207N18	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	606 / 610 (99.34%)	Fusarium proliferatum isolate 001B	621/623 (99%)
Fall	IF207N29	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	604 / 610 (99.01%)	Fusarium proliferatum partial tef-1 gene	619/622 (99%)
Fall	IF207N53	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	369 / 371 (99.46%)	Gibberella intermedia strain F1129	370/371 (99%)
Fall	IF207N61	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	608 / 613 (99.18%)	Fusarium proliferatum partial tef-1 gene	621/623 (99%)
Fall	IF207N62	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	324 / 325 (99.69%)	Gibberella intermedia strain F1129	324/325 (99%)
Fall	IF207N69	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	591 / 594 (99.49%)	Gibberella intermedia clone spt067	619/623 (99%)
Fall	IF207N71	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	606 / 610 (99.34%)	Fusarium proliferatum isolate 001B	614/615 (99%)
Fall	IF207N4	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	592 / 608 (97.36%)	Gibberella intermedia EF-1alpha gene	618/621 (99%)
Fall	IF207N23	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	589 / 604 (97.51%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	610/613 (99%)
Fall	IF207N49	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	588 / 604 (97.35%)	Gibberella fujikuroi isolate V22	609/611 (99%)
Fall	IF207N10	FD_01319_EF-1a	577 / 626 (92.17%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	618/632 (98%)
Fall	IF207N76	FD_01319_EF-1a	577 / 626 (92.17%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	624/640 (98%)
Fall	IF207N77	FD_01319_EF-1a	577 / 626 (92.17%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	622/637 (98%)

Fall	IF207N11	FD_01320_EF-1a	296 / 320 (92.5%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	321/329 (98%)
Fall	IF207N64	FD_01320_EF-1a	606 / 615 (98.53%)	Fusarium cf. incarnatum MLSTs 18-a and 18-b clone spt116	629/633 (99%)
Fall	IF207N26	FD_01321_EF-1a	585 / 610 (95.9%)	Fusarium sp. NRRL 36318	619/622 (99%)
Fall	IF207N65	FD_01321_EF-1a	530 / 619 (85.62%)	Fusarium cf. incarnatum 30-a DPGS-2011 strain FRC R10113	546/629 (87%)
Fall	IF207N72	FD_01321_EF-1a	571 / 596 (95.8%)	Fusarium sp. NRRL 43637	593/597 (99%)
Fall	IF207N6	FD_01378_EF-1a	609 / 616 (98.86%)	Gibberella intermedia clone spt067	624/627 (99%)
Fall	IF207N8	FD_01378_EF-1a	226 / 230 (98.26%)	Gibberella intermedia strain E1163	235/237 (99%)
Fall	IF207N12	FD_01378_EF-1a	613 / 620 (98.87%)	Gibberella intermedia clone spt067	625/627 (99%)
Fall	IF207N14	FD_01378_EF-1a	608 / 616 (98.7%)	Gibberella intermedia clone spt067	620/623 (99%)
Fall	IF207N17	FD_01378_EF-1a	609 / 616 (98.86%)	Gibberella intermedia strain E1163	624/628 (99%)
Fall	IF207N20	FD_01378_EF-1a	609 / 616 (98.86%)	Gibberella intermedia strain E1163	618/621 (99%)
Fall	IF207N28	FD_01378_EF-1a	613 / 621 (98.71%)	Gibberella intermedia clone spt067	620/622 (99%)
Fall	IF207N36	FD_01378_EF-1a	610 / 618 (98.7%)	Gibberella intermedia clone spt067	617/619 (99%)
Fall	IF207N37	FD_01378_EF-1a	602 / 609 (98.85%)	Gibberella intermedia clone spt067	614/616 (99%)
Fall	IF207N38	FD_01378_EF-1a	607 / 614 (98.85%)	Gibberella intermedia clone spt067	619/621 (99%)
Fall	IF207N41	FD_01378_EF-1a	608 / 616 (98.7%)	Gibberella intermedia clone spt067	623/627 (99%)
Fall	IF207N42	FD_01378_EF-1a	539 / 546 (98.71%)	Gibberella intermedia clone spt067	550/553 (99%)
Fall	IF207N46	FD_01378_EF-1a	613 / 620 (98.87%)	Gibberella intermedia clone spt067	625/627 (99%)
Fall	IF207N51	FD_01378_EF-1a	571 / 578 (98.78%)	Gibberella intermedia clone spt067	583/585 (99%)
Fall	IF207N55	FD_01378_EF-1a	609 / 616 (98.86%)	Gibberella intermedia clone spt146	624/628 (99%)
Fall	IF207N74	FD_01378_EF-1a	617 / 624 (98.87%)	Gibberella intermedia clone spt067	629/631 (99%)
Fall	IF207N75	FD_01378_EF-1a	610 / 616 (99.02%)	Gibberella intermedia clone spt146	621/623 (99%)
Fall	IF207N78	FD_01378_EF-1a	608 / 616 (98.7%)	Gibberella intermedia clone spt067	615/617 (99%)
Fall	IF207N79	FD_01378_EF-1a	609 / 616 (98.86%)	Gibberella intermedia clone spt146	620/623 (99%)
Fall	IF207N1	FD_01378_EF-1a [*Fusarium proliferatum*]	348 / 352 (98.86%)	Gibberella intermedia clone spt146	357/359 (99%)
Fall	IF207N2	FD_01378_EF-1a [*Fusarium proliferatum*]	376 / 382 (98.42%)	Gibberella intermedia strain E1163	382/383 (99%)
Fall	IF207N30	FD_01379_EF-1a	660 / 669 (98.65%)	Gibberella intermedia	689/693 (99%)
Fall	IF207N19	FD_01380_EF-1a	325 / 329 (98.78%)	Gibberella intermedia clone spt141	328/329 (99%)
Fall	IF207N33	FD_01380_EF-1a	541 / 547 (98.9%)	Gibberella intermedia strain NRRL 25089	560/561 (99%)
Fall	IF207N39	FD_01380_EF-1a	631 / 638 (98.9%)	Fusarium proliferatum isolate 001B	641/641 (100%)
Fall	IF207N52	FD_01380_EF-1a	146 / 155 (94.19%)	Fusarium proliferatum isolate LJC10023	150/159 (94%)

Fall	IF207N56	FD_01380_EF-1a	639 / 647 (98.76%)	Gibberella intermedia clone spt141	652/653 (99%)
Fall	IF207N59	FD_01380_EF-1a	603 / 615 (98.04%)	Gibberella intermedia clone spt141	615/620 (99%)
Fall	IF207N5	FD_01388_EF-1a	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	621/623 (99%)
Fall	IF207N7	FD_01388_EF-1a	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	626/630 (99%)
Fall	IF207N13	FD_01388_EF-1a	648 / 649 (99.84%)	Gibberella moniliformis clone spt086	649/650 (99%)
Fall	IF207N21	FD_01388_EF-1a	616 / 618 (99.67%)	Gibberella moniliformis isolate B4	621/624 (99%)
Fall	IF207N22	FD_01388_EF-1a	644 / 648 (99.38%)	Fusarium verticillioides partial tef-1 gene	644/645 (99%)
Fall	IF207N24	FD_01388_EF-1a	581 / 586 (99.14%)	Gibberella moniliformis clone spt078	584/586 (99%)
Fall	IF207N25	FD_01388_EF-1a	353 / 353 (100%)	Gibberella moniliformis isolate B4	353/353 (100%)
Fall	IF207N31	FD_01388_EF-1a	589 / 589 (100%)	Gibberella moniliformis isolate B4	594/595 (99%)
Fall	IF207N32	FD_01388_EF-1a	612 / 613 (99.83%)	Gibberella moniliformis isolate B4	617/619 (99%)
Fall	IF207N35	FD_01388_EF-1a	618 / 618 (100%)	Gibberella moniliformis isolate B4	623/624 (99%)
Fall	IF207N40	FD_01388_EF-1a	613 / 617 (99.35%)	Gibberella moniliformis clone spt078	621/623 (99%)
Fall	IF207N43	FD_01388_EF-1a	617 / 620 (99.51%)	Gibberella moniliformis isolate B1	624/626 (99%)
Fall	IF207N44	FD_01388_EF-1a	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	624/627 (99%)
Fall	IF207N47	FD_01388_EF-1a	615 / 617 (99.67%)	Gibberella moniliformis isolate B4	620/623 (99%)
Fall	IF207N48	FD_01388_EF-1a	630 / 633 (99.52%)	Gibberella moniliformis clone spt086	635/639 (99%)
Fall	IF207N50	FD_01388_EF-1a	617 / 617 (100%)	Gibberella moniliformis isolate B4	625/627 (99%)
Fall	IF207N54	FD_01856_EF-1a [Fusarium sp.]	614 / 617 (99.51%)	Fusarium verticillioides	614/614(100%)
Fall	IF207N57	FD_01388_EF-1a	643 / 650 (98.92%)	Gibberella moniliformis clone spt086	643/650 (99%)
Fall	IF207N58	FD_01388_EF-1a	615 / 617 (99.67%)	Gibberella moniliformis isolate B4	620/623 (99%)
Fall	IF207N60	FD_01388_EF-1a	576 / 576 (100%)	Gibberella moniliformis isolate B4	581/582 (99%)
Fall	IF207N63	FD_01388_EF-1a	648 / 648 (100%)	Gibberella moniliformis clone spt086	648/648 (100%)
Fall	IF207N66	FD_01388_EF-1a	587 / 588 (99.82%)	Gibberella moniliformis isolate JD4	587/588 (99%)
Fall	IF207N67	FD_01388_EF-1a	610 / 636 (95.91%)	Gibberella moniliformis clone spt086	612/637 (96%)
Fall	IF207N68	FD_01388_EF-1a	584 / 587 (99.48%)	Gibberella moniliformis clone spt086	584/587 (99%)
Fall	IF207N73	FD_01388_EF-1a	594 / 595 (99.83%)	Gibberella moniliformis isolate B4	594/595 (99%)
Fall	IF207N80	FD_01388_EF-1a	617 / 617 (100%)	Gibberella moniliformis isolate B4	622/623 (99%)
Fall	IF207N3	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	621/623 (99%)
Fall	OF207N5	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	594 / 597 (99.49%)	Fusarium proliferatum isolate 001B	615/620 (99%)
Fall	OF207N9	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	609 / 614 (99.18%)	Gibberella intermedia clone spt146	625/628 (99%)

Fall	OF207N14	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	620 / 624 (99.35%)	Gibberella intermedia clone spt146	641/644 (99%)
Fall	OF207N29	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	524 / 524 (100%)	Gibberella intermedia clone spt146	551/556 (99%)
Fall	OF207N27	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	590 / 605 (97.52%)	Gibberella intermedia EF-1alpha gene	616/618 (99%)
Fall	OF207N11	FD_01319_EF-1a [*Fusarium sp.*]	583 / 632 (92.24%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	625/639 (98%)
Fall	OF207N21	FD_01319_EF-1a [*Fusarium sp.*]	580 / 628 (92.35%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	622/637 (98%)
Fall	OF207N26	FD_01319_EF-1a [*Fusarium sp.*]	576 / 625 (92.16%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	618/632 (98%)
Fall	OF207N1	FD_01378_EF-1a [*Fusarium proliferatum*]	613 / 621 (98.71%)	Gibberella intermedia clone spt067	625/628 (99%)
Fall	OF207N4	FD_01378_EF-1a [*Fusarium proliferatum*]	609 / 617 (98.7%)	Gibberella intermedia clone spt067	626/631 (99%)
Fall	OF207N13	FD_01378_EF-1a [*Fusarium proliferatum*]	612 / 620 (98.7%)	Gibberella intermedia clone spt067	624/627 (99%)
Fall	OF207N16	FD_01378_EF-1a [*Fusarium proliferatum*]	609 / 617 (98.7%)	Gibberella intermedia clone spt141	626/629 (99%)
Fall	OF207N17	FD_01378_EF-1a [*Fusarium proliferatum*]	618 / 626 (98.72%)	Gibberella intermedia clone spt141	631/633 (99%)
Fall	OF207N18	FD_01378_EF-1a [*Fusarium proliferatum*]	612 / 620 (98.7%)	Gibberella intermedia clone spt067	619/621 (99%)
Fall	OF207N23	FD_01378_EF-1a [*Fusarium proliferatum*]	608 / 617 (98.54%)	Gibberella intermedia clone spt141	621/624 (99%)
Fall	OF207N24	FD_01378_EF-1a [*Fusarium proliferatum*]	613 / 620 (98.87%)	Gibberella intermedia clone spt067	620/621 (99%)
Fall	OF207N32	FD_01378_EF-1a [*Fusarium proliferatum*]	611 / 619 (98.7%)	Gibberella intermedia clone spt067	623/626 (99%)
Fall	OF207N19	FD_01380_EF-1a [*Fusarium proliferatum*]	640 / 646 (99.07%)	Gibberella intermedia clone spt146	648/648 (100%)
Fall	OF207N31	FD_01380_EF-1a [*Fusarium proliferatum*]	638 / 646 (98.76%)	Gibberella intermedia clone spt146	644/646 (99%)
Fall	OF207N25	FD_01387_EF-1a [*Fusarium verticillioides*]	613 / 617 (99.35%)	Gibberella moniliformis strain NRRL 25102	622/628 (99%)
Fall	OF207N2	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	625/628 (99%)
Fall	OF207N6	FD_01388_EF-1a [*Fusarium verticillioides*]	617 / 617 (100%)	Gibberella moniliformis isolate B4	622/623 (99%)
Fall	OF207N7	FD_01388_EF-1a [*Fusarium verticillioides*]	634 / 637 (99.52%)	Gibberella moniliformis clone spt086	639/643 (99%)
Fall	OF207N8	FD_01388_EF-1a [*Fusarium verticillioides*]	620 / 621 (99.83%)	Gibberella moniliformis isolate B4	620/621 (99%)
Fall	OF207N10	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	620/622 (99%)
Fall	OF207N12	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	621/623 (99%)
Fall	OF207N15	FD_01388_EF-1a [*Fusarium verticillioides*]	623 / 624 (99.83%)	Gibberella moniliformis isolate B4	623/624 (99%)
Fall	OF207N20	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	621/623 (99%)
Fall	OF207N22	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	616/617 (99%)
Fall	OF207N28	FD_01388_EF-1a [*Fusarium verticillioides*]	614 / 618 (99.35%)	Gibberella moniliformis isolate B4	619/624 (99%)
Fall	OF207N30	FD_01388_EF-1a [*Fusarium verticillioides*]	485 / 512 (94.72%)	Fusarium oxysporum isolate FSY0951	488/516 (95%)
Fall	IF208N1	FD_01388_EF-1a	538 / 552 (97.46%)	Gibberella moniliformis isolate JD4	557/574 (97%)
Fall	IF208N2	FD_01389_EF-1a [Fusarium proliferatum]	608 / 608 (100%)	Fusarium proliferatum	608/608(100%)

Fall	IF208N3	FD_01856_EF-1a [Fusarium sp.]	600 / 602 (99.66%)	Gibberella moniliformis	602/602(100%)
Fall	IF208N4	FD_01856_EF-1a [Fusarium sp.]	609 / 610 (99.83%)	Gibberella moniliformis	609/610(99%)
Fall	IF208N5	FD_01856_EF-1a [Fusarium sp.]	567 / 568 (99.82%)	Gibberella moniliformis	574/576(99%)
Fall	IF208N6	FD_01857_EF-1a [Fusarium sp.]	591 / 592 (99.83%)	Gibberella intermedia	592/592(100%)
Fall	IF208N7	FD_01856_EF-1a [Fusarium sp.]	601 / 601 (100%)	Gibberella moniliformis	606/607(99%)
Fall	IF208N8	FD_00801_EF-1a | F. oxysporum species complex 231 NRRL38885	603 / 605 (99.66%)	Fusarium oxysporum	617/620(99%)
Fall	IF208N9	FD_01856_EF-1a [Fusarium sp.]	616 / 618 (99.67%)	Gibberella moniliformis	622/624(99%)
Fall	IF208N10	FD_01857_EF-1a [Fusarium sp.]	610 / 610 (100%)	Gibberella cf. fujikuroi	615/616(99%)
Fall	IF208N11	FD_01635_EF-1a | F. incarnatum-equiseti species complex 18-b NRRL32522	613 / 615 (99.67%)	Fusarium cf. incarnatum	623/626(99%)
Fall	IF208N12	FD_01858_EF-1a [Fusarium sp.]	593 / 594 (99.83%)	Gibberella intermedia	606/608(99%)
Fall	OF208N1	FD_01388_EF-1a [*Fusarium verticillioides*]	617 / 619 (99.67%)	Gibberella moniliformis isolate B4	622/625 (99%)
Fall	OF208N2	FD_01388_EF-1a [*Fusarium verticillioides*]	625 / 625 (100%)	Gibberella moniliformis isolate B4	625/625 (100%)
Fall	OF208N3	FD_01380_EF-1a [*Fusarium proliferatum*]	610 / 617 (98.86%)	Gibberella intermedia clone spt146	622/623 (99%)
Fall	OF208N4	FD_01378_EF-1a [*Fusarium proliferatum*]	593 / 600 (98.83%)	Gibberella intermedia clone spt067	603/605 (99%)
Fall	OF208N5	FD_01380_EF-1a [*Fusarium proliferatum*]	624 / 630 (99.04%)	Gibberella intermedia clone spt146	631/631 (100%)
Fall	OF208N6	FD_01388_EF-1a [*Fusarium verticillioides*]	596 / 600 (99.33%)	Gibberella moniliformis strain NRRL 25113	604/606 (99%)
Fall	OF208N7	FD_01388_EF-1a [*Fusarium verticillioides*]	589 / 592 (99.49%)	Gibberella moniliformis clone spt078	597/598 (99%)
Fall	OF208N8	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	567 / 581 (97.59%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	592/594 (99%)
Fall	OF208N9	FD_01380_EF-1a [*Fusarium proliferatum*]	612 / 619 (98.86%)	Gibberella intermedia clone spt146	622/623 (99%)
Fall	OF208N10	FD_01319_EF-1a [*Fusarium sp.*]	575 / 621 (92.59%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	635/646 (98%)
Fall	OF208N11	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	605 / 610 (99.18%)	Fusarium proliferatum partial tef-1 gene	620/622 (99%)
Fall	OF208N12	FD_01388_EF-1a [*Fusarium verticillioides*]	613 / 618 (99.19%)	Gibberella moniliformis clone spt078	621/624 (99%)
Fall	OF208N13	FD_01388_EF-1a [*Fusarium verticillioides*]	647 / 649 (99.69%)	Gibberella moniliformis clone spt086	650/652 (99%)
Fall	OF208N14	FD_01378_EF-1a [*Fusarium proliferatum*]	608 / 617 (98.54%)	Gibberella intermedia clone spt141	621/624 (99%)
Fall	OF208N15	FD_01378_EF-1a [*Fusarium proliferatum*]	608 / 617 (98.54%)	Gibberella intermedia clone spt141	621/624 (99%)
Fall	OF208N16	FD_01304_EF-1a [*Fusarium sp.*]	633 / 636 (99.52%)	Fusarium sporotrichioides strain F627	653/656 (99%)
Fall	OF208N17	FD_01319_EF-1a [*Fusarium sp.*]	575 / 623 (92.29%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	617/632 (98%)
Fall	OF208N18	FD_01380_EF-1a [*Fusarium proliferatum*]	107 / 110 (97.27%)	Fusarium proliferatum isolate ASHCFp5	105/107 (98%)
Fall	OF208N19	FD_01319_EF-1a [*Fusarium sp.*]	577 / 626 (92.17%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	622/637 (98%)
Fall	OF208N20	FD_01378_EF-1a [*Fusarium proliferatum*]	612 / 619 (98.86%)	Gibberella intermedia clone spt146	623/626 (99%)
Fall	OF208N21	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	618 / 619 (99.83%)	Fusarium subglutinans clone spt144	618/619 (99%)

Fall	OF208N22	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	165 / 174 (94.82%)	Fusarium subglutinans clone spt144	165/174 (95%)
Fall	OF208N23	FD_01388_EF-1a [*Fusarium verticillioides*]	614 / 617 (99.51%)	Gibberella moniliformis isolate B1	621/623 (99%)
Fall	OF208N24	FD_01378_EF-1a [*Fusarium proliferatum*]	612 / 619 (98.86%)	Gibberella intermedia clone spt067	624/626 (99%)
Fall	OF208N25	FD_01378_EF-1a [*Fusarium proliferatum*]	614 / 622 (98.71%)	Gibberella intermedia clone spt141	627/629 (99%)
Fall	OF208N26	FD_01378_EF-1a [*Fusarium proliferatum*]	613 / 621 (98.71%)	Gibberella intermedia clone spt067	625/628 (99%)
Fall	OF208N27	FD_01295_EF-1a [*Fusarium bulbicola*]	603 / 614 (98.2%)	Fusarium subglutinans EF-1alpha gene	607/608 (99%)
Fall	OF208N28	FD_01388_EF-1a [*Fusarium verticillioides*]	619 / 620 (99.83%)	Gibberella moniliformis isolate B4	624/626 (99%)
Fall	OF208N29	FD_01319_EF-1a [*Fusarium sp.*]	579 / 627 (92.34%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	634/638 (99%)
Fall	OF208N30	FD_01378_EF-1a [*Fusarium proliferatum*]	607 / 614 (98.85%)	Gibberella intermedia clone spt067	624/627 (99%)
Fall	OF208N31	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	592 / 607 (97.52%)	Gibberella intermedia EF-1alpha gene	618/620 (99%)
Fall	OF208N32	FD_01319_EF-1a [*Fusarium sp.*]	580 / 627 (92.5%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	635/638 (99%)
Fall	OF208N33	FD_01388_EF-1a [*Fusarium verticillioides*]	614 / 618 (99.35%)	Gibberella moniliformis clone spt078	622/624 (99%)
Fall	OF208N34	FD_01388_EF-1a [*Fusarium verticillioides*]	647 / 649 (99.69%)	Gibberella moniliformis clone spt086	647/649 (99%)
Fall	OF208N35	FD_01119_EF-1a [*Fusarium graminearum*]	606 / 613 (98.85%)	Gibberella zeae partial tef1a gene	611/619 (99%)
Fall	OF208N36	FD_00986_EF-1a [*Fusarium graminearum*]	614 / 614 (100%)	Gibberella zeae clone spt132	619/620 (99%)
Fall	OF208N37	FD_01388_EF-1a [*Fusarium verticillioides*]	618 / 620 (99.67%)	Gibberella moniliformis isolate B4	623/626 (99%)
Fall	OF208N38	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	592 / 607 (97.52%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	612/614 (99%)
Fall	OF208N39	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	616/617 (99%)
Fall	OF208N40	FD_01319_EF-1a [*Fusarium sp.*]	580 / 628 (92.35%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	622/636 (98%)
Fall	OF208N41	FD_00986_EF-1a [*Fusarium graminearum*]	612 / 612 (100%)	Gibberella zeae clone spt132	612/612 (100%)
Fall	OF208N42	FD_01388_EF-1a [*Fusarium verticillioides*]	618 / 619 (99.83%)	Gibberella moniliformis isolate B4	623/625 (99%)
Fall	OF208N43	FD_01380_EF-1a [*Fusarium proliferatum*]	636 / 644 (98.75%)	Gibberella intermedia clone spt146	642/644 (99%)
Fall	OF208N44	FD_01319_EF-1a [*Fusarium sp.*]	579 / 627 (92.34%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	628/631 (99%)
Fall	OF208N45	FD_01388_EF-1a [*Fusarium verticillioides*]	613 / 618 (99.19%)	Gibberella moniliformis strain NRRL22172	619/625 (99%)
Fall	OF208N46	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	621/623 (99%)
Fall	OF208N47	FD_01319_EF-1a [*Fusarium sp.*]	583 / 631 (92.39%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	634/637 (99%)
Fall	OF208N48	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	586 / 588 (99.65%)	Gibberella intermedia clone spt146	626/631 (99%)
Fall	OF208N49	FD_01378_EF-1a [*Fusarium proliferatum*]	609 / 618 (98.54%)	Gibberella intermedia clone spt141	622/625 (99%)
Fall	OF208N50	FD_01388_EF-1a [*Fusarium verticillioides*]	604 / 615 (98.21%)	Fusarium verticillioides partial tef-1 gene	610/621 (98%)
Fall	0F208N51	FD_01388_EF-1a [*Fusarium verticillioides*]	620 / 621 (99.83%)	Gibberella moniliformis isolate B4	623/625 (99%)
Fall	0F208N52	FD_01388_EF-1a [*Fusarium verticillioides*]	617 / 620 (99.51%)	Gibberella moniliformis isolate B4	617/620 (99%)

Fall	0F208N53	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	623 / 628 (99.2%)	Fusarium subglutinans clone spt144	635/641 (99%)
Fall	0F208N54	FD_01378_EF-1a [*Fusarium proliferatum*]	594 / 636 (93.39%)	Gibberella intermedia	611/650 (94%)
Fall	0F208N55	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	601 / 610 (98.52%)	Fusarium proliferatum partial tef-1 gene	611/616 (99%)
Fall	0F208N56	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	606 / 610 (99.34%)	Fusarium proliferatum isolate 001B	624/627 (99%)
Fall	0F208N57	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	588 / 604 (97.35%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	613/617 (99%)
Fall	0F208N58	FD_01388_EF-1a [*Fusarium verticillioides*]	613 / 615 (99.67%)	Gibberella moniliformis isolate B4	619/623 (99%)
Fall	0F208N59	FD_01378_EF-1a [*Fusarium proliferatum*]	606 / 617 (98.21%)	Gibberella intermedia clone spt141	619/624 (99%)
Fall	0F208N60	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	621/623 (99%)
Fall	0F208N61	FD_01388_EF-1a [*Fusarium verticillioides*]	620 / 622 (99.67%)	Gibberella moniliformis isolate B4	625/628 (99%)
Fall	0F208N62	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	585 / 604 (96.85%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	617/626 (99%)
Fall	0F208N63	FD_01388_EF-1a [*Fusarium verticillioides*]	640 / 641 (99.84%)	Gibberella moniliformis clone spt086	645/647 (99%)
Fall	0F208N64	FD_01388_EF-1a [Fusarium verticillioides]	639 / 641 (99.68%)	Gibberella moniliformis clone spt086	644/647 (99%)
Fall	0F208N65	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	608 / 614 (99.02%)	Fusarium proliferatum isolate 001B	623/627 (99%)
Fall	0F208N66	FD_01319_EF-1a [*Fusarium sp.*]	577 / 626 (92.17%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	618/632 (98%)
Fall	0F208N67	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	584 / 604 (96.68%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	613/622 (99%)
Fall	0F208N68	FD_01388_EF-1a [*Fusarium verticillioides*]	585 / 589 (99.32%)	Gibberella moniliformis isolate B4	585/589 (99%)
Fall	0F208N69	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	608 / 616 (98.7%)	Gibberella intermedia clone spt067	625/630 (99%)
Fall	0F208N70	FD_01319_EF-1a [*Fusarium sp.*]	576 / 624 (92.3%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	622/638 (97%)
Fall	0F208N71	FD_01857_EF-1a [Fusarium sp.]	596 / 604 (98.67%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	607/617 (98%)
Fall	0F208N72	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	605 / 610 (99.18%)	Fusarium proliferatum isolate 001B	624/628 (99%)
Fall	0F208N73	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	598 / 615 (97.23%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	616/620 (99%)
Fall	0F208N74	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	597 / 619 (96.44%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	611/619 (99%)
Fall	0F208N75	FD_01378_EF-1a [*Fusarium proliferatum*]	611 / 619 (98.7%)	Gibberella intermedia clone spt146	622/626 (99%)
Fall	0F208N76	FD_01378_EF-1a [*Fusarium proliferatum*]	608 / 616 (98.7%)	Gibberella intermedia clone spt146	623/628 (99%)
Fall	0F208N77	FD_01388_EF-1a [*Fusarium verticillioides*]	615 / 623 (98.71%)	Gibberella fujikuroi var. moniliformis partial tef-1 gene	621/629 (99%)
Fall	0F208N78	FD_01388_EF-1a [*Fusarium verticillioides*]	642 / 645 (99.53%)	Gibberella moniliformis clone spt086	642/645 (99%)
Fall	0F208N79	FD_01388_EF-1a [*Fusarium verticillioides*]	616 / 617 (99.83%)	Gibberella moniliformis isolate B4	616/617 (99%)
Fall	0F208N80	FD_01378_EF-1a [*Fusarium proliferatum*]	609 / 616 (98.86%)	Gibberella intermedia clone spt145	620/622 (99%)
Fall	0F208N81	FD_01388_EF-1a [*Fusarium verticillioides*]	621 / 622 (99.83%)	Gibberella moniliformis isolate B4	621/622 (99%)
Fall	0F208N82	FD_01388_EF-1a [*Fusarium verticillioides*]	619 / 622 (99.51%)	Gibberella moniliformis isolate B4	624/628 (99%)
Fall	0F208N83	FD_01388_EF-1a [*Fusarium verticillioides*]	605 / 609 (99.34%)	Gibberella moniliformis isolate B4	610/615 (99%)

Fall	0F208N84	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	602 / 609 (98.85%)	Fusarium proliferatum partial tef-1 gene	617/621 (99%)
Fall	0F208N85	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	613 / 615 (99.67%)	Fusarium subglutinans clone spt144	613/615 (99%)
Fall	0F208N86	FD_01378_EF-1a [*Fusarium proliferatum*]	608 / 616 (98.7%)	Gibberella intermedia clone spt146	623/628 (99%)
Fall	0F208N87	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	113 / 119 (94.95%)	Gibberella fujikuroi strain EF01	193/223 (87%)
Fall	0F208N88	FD_01380_EF-1a [*Fusarium proliferatum*]	102 / 106 (96.22%)	Fusarium proliferatum isolate ASHCFp5	111/116 (96%)
Fall	0F208N89	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	598 / 617 (96.92%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	616/622 (99%)
Fall	0F208N90	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	585 / 604 (96.85%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	610/617 (99%)
Fall	0F208N91	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	602 / 611 (98.52%)	Fusarium proliferatum isolate 001B	617/624 (99%)
Fall	0F208N92	FD_01378_EF-1a [*Fusarium proliferatum*]	610 / 619 (98.54%)	Gibberella intermedia clone spt141	623/626 (99%)
Fall	0F208N93	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	604 / 610 (99.01%)	Fusarium proliferatum partial tef-1 gene	619/622 (99%)
Fall	0F208N94	FD_01378_EF-1a [*Fusarium proliferatum*]	603 / 617 (97.73%)	Gibberella intermedia clone spt141	611/618 (99%)
Fall	0F208N95	FD_01388_EF-1a [*Fusarium verticillioides*]	613 / 617 (99.35%)	Gibberella moniliformis isolate B4	617/622 (99%)
Fall	0F208N96	FD_01388_EF-1a [*Fusarium verticillioides*]	614 / 617 (99.51%)	Gibberella moniliformis isolate B4	622/627 (99%)
Fall	0F208N97	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	576 / 580 (99.31%)	Gibberella intermedia clone spt067	588/590 (99%)
Fall	0F208N98	FD_01319_EF-1a [*Fusarium sp.*]	590 / 637 (92.62%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	636/637 (99%)
Fall	0F208N99	FD_01388_EF-1a [*Fusarium verticillioides*]	604 / 606 (99.66%)	Gibberella moniliformis isolate B4	604/606 (99%)
Fall	0F208N100	FD_01388_EF-1a [*Fusarium verticillioides*]	624 / 625 (99.84%)	Gibberella moniliformis clone spt086	624/625 (99%)
Fall	0F208N101	FD_01319_EF-1a [*Fusarium sp.*]	565 / 615 (91.86%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	602/616 (98%)
Fall	0F208N102	FD_01319_EF-1a [*Fusarium sp.*]	567 / 614 (92.34%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	605/618 (98%)
Fall	0F208N103	FD_01378_EF-1a [*Fusarium proliferatum*]	600 / 609 (98.52%)	Gibberella intermedia strain NRRL 25092	605/610 (99%)
Fall	0F208N104	FD_01320_EF-1a [*Fusarium pallidoroseum*]	603 / 616 (97.88%)	Fusarium sp. NRRL 31167	615/621 (99%)
Fall	0F208N105	FD_01388_EF-1a [*Fusarium verticillioides*]	608 / 609 (99.83%)	Gibberella moniliformis isolate B4	612/614 (99%)
Fall	0F208N106	FD_01388_EF-1a [*Fusarium verticillioides*]	620 / 621 (99.83%)	Gibberella moniliformis isolate B4	625/627 (99%)
Fall	0F208N107	FD_01378_EF-1a [*Fusarium proliferatum*]	608 / 616 (98.7%)	Gibberella intermedia clone spt067	623/627 (99%)
Fall	0F208N108	FD_01160_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22016	613 / 614 (99.83%)	Fusarium subglutinans clone spt144	622/625 (99%)
Fall	0F208N109	FD_01388_EF-1a [*Fusarium verticillioides*]	609 / 616 (98.86%)	Gibberella moniliformis isolate B4	614/622 (99%)
Fall	0F208N110	FD_01378_EF-1a [*Fusarium proliferatum*]	613 / 622 (98.55%)	Gibberella intermedia clone spt141	626/629 (99%)
Fall	0F208N111	FD_01378_EF-1a [*Fusarium proliferatum*]	605 / 615 (98.37%)	Gibberella intermedia clone spt067	612/616 (99%)
Fall	0F208N112	FD_01378_EF-1a [*Fusarium proliferatum*]	608 / 616 (98.7%)	Gibberella intermedia clone spt067	620/623 (99%)
Fall	0F208N113	FD_01388_EF-1a [*Fusarium verticillioides*]	613 / 617 (99.35%)	Gibberella moniliformis isolate B4	622/628 (99%)
Fall	0F208N114	FD_01378_EF-1a [*Fusarium proliferatum*]	613 / 619 (99.03%)	Gibberella intermedia clone spt146	624/626 (99%)

Fall	0F208N115	FD_01378_EF-1a [*Fusarium proliferatum*]	613 / 620 (98.87%)	Gibberella intermedia clone spt146	619/621 (99%)
Fall	0F208N117	FD_01378_EF-1a [*Fusarium proliferatum*]	610 / 617 (98.86%)	Gibberella intermedia clone spt146	621/624 (99%)
Fall	OF208N118	FD_01858_EF-1a [Fusarium sp.]	608 / 610 (99.67%)	Gibberella intermedia	625/629(99%)
Fall	0F208N119	FD_01388_EF-1a [*Fusarium verticillioides*]	615 / 619 (99.35%)	Gibberella moniliformis isolate B1	622/625 (99%)
Fall	0F208N120	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	603 / 610 (98.85%)	Fusarium proliferatum partial tef-1 gene	618/622 (99%)
Fall	IF209N1	FD_01856_EF-1a [Fusarium sp.]	577 / 578 (99.82%)	Gibberella moniliformis	618/628(98%)
Fall	IF209N2	FD_01759_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22945	580 / 590 (98.3%)	Fusarium subglutinans	590/590(100%)
Fall	IF209N3	FD_01857_EF-1a [Fusarium sp.]	600 / 602 (99.66%)	Gibberella intermedia	612/615(99%)
Fall	IF209N4	FD_01389_EF-1a [Fusarium proliferatum]	609 / 610 (99.83%)	Gibberella intermedia	619/622(99%)
Fall	IF209N5	FD_01857_EF-1a [Fusarium sp.]	607 / 612 (99.18%)	Gibberella cf. fujikuroi	613/619(99%)
Fall	IF210N2	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a NRRL45996	611 / 613 (99.67%)	Fusarium equiseti	607/613(99%)
Fall	IF210N5	FD_01857_EF-1a [Fusarium sp.]	587 / 588 (99.82%)	Gibberella fujikuroi	597/599(99%)
Fall	IF210N6	FD_01614_EF-1a | F. incarnatum-equiseti species complex 8-a NRRL5537	610 / 612 (99.67%)	Fusarium equiseti	603/606(99%)
Fall	IF210N8	FD_01857_EF-1a [Fusarium sp.]	606 / 607 (99.83%)	Gibberella fujikuroi	617/619(99%)
Fall	OF210N5	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	603 / 610 (98.85%)	Gibberella intermedia clone spt146	622/628 (99%)
Fall	OF210N4	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	588 / 606 (97.02%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	613/619 (99%)
Fall	OF210N6	FD_01319_EF-1a [*Fusarium sp.*]	576 / 623 (92.45%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	613/626 (98%)
Fall	OF210N1	FD_01388_EF-1a [*Fusarium verticillioides*]	610 / 617 (98.86%)	Gibberella moniliformis isolate B4	610/617 (99%)
Fall	OF210N2	FD_01388_EF-1a [*Fusarium verticillioides*]	642 / 644 (99.68%)	Gibberella moniliformis clone spt086	645/648 (99%)
Fall	OF210N3	FD_01388_EF-1a [*Fusarium verticillioides*]	612 / 617 (99.18%)	Gibberella moniliformis isolate B1	618/622 (99%)
Fall	OF212N2	FD_01168_EF-1a | GFSC Gibberella fujikuroi species complex NRRL22944	590 / 594 (99.32%)	Gibberella intermedia clone spt067	617/623 (99%)
Fall	OF212N1	FD_01388_EF-1a [*Fusarium verticillioides*]	615 / 617 (99.67%)	Gibberella moniliformis isolate B4	619/622 (99%)
Fall	IF212N1	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a NRRL45996	614 / 616 (99.67%)	Fusarium equiseti	610/616(99%)
Fall	IF213N1	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a NRRL45996	609 / 614 (99.18%)	Fusarium equiseti	613/622(99%)
Fall	IF213N2	FD_01627_EF-1a | F. incarnatum-equiseti species complex 3-b NRRL28029	604 / 605 (99.83%)	Fusarium equiseti	605/613(99%)
Fall	IF213N4	FD_01628_EF-1a | F. incarnatum-equiseti species complex 26-b NRRL28714	575 / 592 (97.12%)	Fusarium equiseti	585/606(97%)
Fall	IF213N5	FD_00805_EF-1a | F. oxysporum species complex 99 NRRL40182	616 / 628 (98.08%)	Fusarium oxysporum	618/628(98%)
Fall	IF213N6	FD_01858_EF-1a [Fusarium sp.]	607 / 610 (99.5%)	Gibberella intermedia	614/617(99%)
Fall	IF213N7	FD_01858_EF-1a [Fusarium sp.]	608 / 611 (99.5%)	Gibberella intermedia	621/624(99%)
Fall	IF213N8	FD_01627_EF-1a | F. incarnatum-equiseti species complex 3-b NRRL28029	637 / 639 (99.68%)	Fusarium equiseti	634/642(99%)
Fall	OF213N9	FD_01169_EF-1a | GFSC Gibberella fujikuroi species complex NRRL13566	590 / 604 (97.68%)	Gibberella cf. fujikuroi Trap_1_5_min_Low_1 clone spt121	613/615 (99%)

Fall	OF213N8	FD_01319_EF-1a [*Fusarium sp.*]	579 / 627 (92.34%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	629/632 (99%)
Fall	OF213N6	FD_01321_EF-1a [*Fusarium sp.*]	531 / 563 (94.31%)	Fusarium sp. NRRL 5537	590/598 (99%)
Fall	OF213N7	FD_01321_EF-1a [*Fusarium sp.*]	601 / 635 (94.64%)	Fusarium sp. NRRL 5537	638/639 (99%)
Fall	OF213N2	FD_01857_EF-1a [Fusarium sp.]	612 / 615 (99.51%)	Gibberella intermedia	613/615(99%)
Fall	OF213N3	FD_01378_EF-1a [*Fusarium proliferatum*]	607 / 616 (98.53%)	Gibberella intermedia clone spt146	616/621 (99%)
Fall	OF214N4	FD_01319_EF-1a [*Fusarium sp.*]	579 / 627 (92.34%)	Fusarium cf. incarnatum MLSTs 25-a, 25-b, 25-c 26-a and 26-b clone spt045	625/627 (99%)
Fall	IF214N4	FD_01694_EF-1a | F. incarnatum-equiseti species complex 1-a NRRL45996	605 / 606 (99.83%)	Fusarium equiseti	608/614(99%)
Fall	OF215N3	FD_01321_EF-1a [*Fusarium sp.*]	565 / 610 (92.62%)	Fusarium cf. incarnatum MLSTs 1-a, 1-c and 4-b clone spt105	604/628 (96%)
Fall	IF217N3	FD_01321_EF-1a [*Fusarium sp.*]	603 / 628 (96.01%)	Fusarium cf. incarnatum MLST 3-b clone spt072	623/624 (99%)
Winter	F130N1	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	643 / 643 (100%)	Fusarium sp. NRRL 5537	648/649 (99%)
Winter	F130N2	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	642 / 643 (99.84%)	Fusarium sp. NRRL 5537	645/647 (99%)
Winter	F130N3	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	640 / 642 (99.68%)	Fusarium sp. NRRL 5537	640/642 (99%)
Winter	F131N2	F. incarnatum-equiseti species complex isolate NRRL 5537, MLST8-a	634 / 634 (100%)	Fusarium sp. NRRL 5537	637/638 (99%)
Winter	F131N3	F. solani species complex isolate NRRL 32821	133 / 144 (92.36%)	Neosartorya fischeri NRRL 181	267/271 (99%)
Winter	F131N1	FD_01321_EF-1a [Fusarium sp.]	633 / 656 (96.49%)	Fusarium sp. NRRL 45996	673/677 (99%)
Winter	F132N1	EQUAL MATCHES FOR MANY *Fusarium spp*.	142 / 149 (95.3%)	Clavicipitaceae sp. CV-2008a	170/181 (94%)
Winter	F132N2	FD_00785_EF-1a [*Fusarium sp.*]	677 / 682 (99.26%)	Fusarium oxysporum strain NRRL 46605	677/682 (99%)
Winter	F133N1	F. incarnatum-equiseti species complex isolate NRRL 5537	611 / 612 (99.83%)	Fusarium sp. NRRL 5537	627/631 (99%)
Winter	F133N3	F. incarnatum-equiseti species complex isolate NRRL 5537	638 / 640 (99.68%)	Fusarium sp. NRRL 5537	638/640 (99%)
Winter	F133N2	F. oxysporum species complex isolate NRRL 26960	622 / 624 (99.67%)	Fusarium oxysporum isolate SAT77	622/623 (99%)
Winter	OF222N1	FD_01389_EF-1a [Fusarium proliferatum]	605 / 606 (99.83%)	Gibberella intermedia	616/619(99%)
Winter	OF222N2	FD_01857_EF-1a [Fusarium sp.]	594 / 596 (99.66%)	Gibberella fujikuroi	600/602(99%)
Winter	OF222N3	FD_01856_EF-1a [Fusarium sp.]	600 / 602 (99.66%)	Gibberella moniliformis	602/602(100%)
Winter	OF222N5	FD_01857_EF-1a [Fusarium sp.]	558 / 560 (99.64%)	Gibberella fujikuroi	562/564(99%)
Winter	IF222N1	FD_00785_EF-1a | F. oxysporum species complex 191 NRRL38591	681 / 682 (99.85%)	Fusarium oxysporum	681/682(99%)
Winter	IF222N4	FD_00785_EF-1a | F. oxysporum species complex 191 NRRL38591	645 / 645 (100%)	Fusarium oxysporum	645/645(100%)