Original article

Genetic diversity of the pathogenic banana Fusarium wilt in northern Viet Nam

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Short running head: Fusarium wilt in northern Viet Nam

Abstract

Fusarium is one of the most important fungal genera of plant pathogens that affect the cultivation of a wide range of crops. Agricultural losses caused by *Fusarium oxysporum* f. sp. *cubense (Foc)* have a direct effect on the income, subsistence and nourishment of thousands of smallholder farmers worldwide. In addition, also commercial growers are strongly affected. For Viet Nam, predictions on the impact of *Foc* for the future are dramatic with an estimated loss in banana production area of 8% within the next 5 years and up to 71% within the next 25 years. In the current study we applied a combined morphological - molecular approach to assess the taxonomic identity and phylogenetic position of the different *Foc* isolates that were collected in northern Viet Nam. In addition, we aim to estimate the proportion of the different *Fusarium* races that are infecting bananas in northern Viet Nam. The morphology of the isolates was investigated by growing the collected *Fusarium* isolates on four distinct nutritious media (PDA, SNA, CLA, and OMA). Molecular phylogenetic relationships were inferred by sequencing partial *rpb1*, *rpb2* and *tef1a* genes and adding the obtained sequences into a large phylogenetic framework. The present study showed that *Foc* Race 1 is the most common strain in northern Viet Nam, causing 74% of all the infections. A more in-depth molecular characterization shows that of the *Foc* Race 1 infections, 92% are caused by *Fusarium tardichlamydosporum* and 8% by *F. duoseptatum*. Compared to *Foc* Race 1, *Foc* TR4 (represented by *F. odoratissimum*) account for only 10.5% of the Fusarium wilting in northern Viet Nam demonstrating that *Foc* TR4 is not yet a dominant strain in the region. *Foc* Race 2 infections of Vietnamese bananas also account for 10.5% of the Fusarium wilting in northern Viet Nam. One of the isolates cultured from diseased bananas collected in northern Viet Nam was phylogenetically not positioned within the *F. oxysporum* species complex (FOSC), but in contrast fell within the *Fusarium fujikuroi* species complex (FFSC). As a result, it is possible that a new pathogen for bananas has been found. Besides being present on several ABB ‘Tay banana’, *Foc* Race 1 was also found as pathogen on wild *Musa lutea*, showing the importance of wild bananas as possible sink for *Foc*.

Key words: *Fusarium* wilt, *Musa lutea*, ABB Tay banana, AAA Cavendish, *Foc*-TR4, *Foc*-Race 1, Viet Nam, banana disease, fungal diversity

Introduction

The ascomycete genus *Fusarium* comprises one of the most important fungal plant pathogens impacting the cultivation of numerous agricultural crops (e.g., rice, coffee, tomato, melon, wheat; Dean et al. 2012). *Fusarium* has a considerable economic, social and biological impact on the daily livelihood of millions of people worldwide. *Fusarium oxysporum* is one of the two most devastating pathogens in the genus, besides *F. gramineum*. The *Fusarium oxysporum* species complex is responsible for wilt diseases of various crops (e.g. cotton and tomato wilt), but is mainly known from its massive impact on the banana industry (Panama disease). For more than 100 years, the fungus has affected banana production worldwide (Ploetz and Pegg 1997; Ploetz 2015a). For millions of people, bananas are an important food crop. With an annual global production of 153 million tons produced on 5.6 million hectares of land, a revenue of more than 26.5 billion Euro was generated in 2017 (FAO 2018). Particularly in Asia, Africa, Latin America and the Caribbean bananas support rural livelihood as most of the grown bananas are self-consumed or locally traded. As a result, any reduction in crop harvest caused by for example *Foc* infections has a direct effect on the income, subsistence and nourishment of thousands of smallholders. Additionally, also the worldwide banana export is seriously affected by *Foc*, as most of its current production depends on the cultivation of members of the Cavendish subgroup (Buddenhagen 2009, Ploetz 2009). Although these triploid 'AAA' Cavendish cultivars were selected in the past century for their resistance against *F. oxysporum* f. sp. *cubense* Race 1 (*Foc*-Race 1), to which the initially grown Gros Michel cultivars were highly susceptible (Stover 1962a), Cavendish cultivars (e.g., Grand Naine, Williams) are highly susceptible to *Foc*-TR4. All *Foc* strains currently known (e.g., Race 1, Race 2, STR4, TR4) pose a huge treat for banana cultivation worldwide. Moreover, knowing that nearly half of the global banana production is derived from Cavendish clones, and that they also become more popular for domestic use, a *Foc*-TR4 pandemic is still not averted to date (Ploetz 2015b; Zheng et al. 2018).

In the near future, *Foc* will further intensively spread in Asia, thereby significantly affecting important banana producing countries such as China, the Philippines, Pakistan and Viet Nam (Scheerer et al. 2018). For Viet Nam, the predictions are dramatic, estimating a loss in banana production area for the country of 8% within the next 5 years and up to 71% within the next 25 years (Scheerer et al. 2018).

As a soil-borne fungus, *Foc* invades the rooting system from where it subsequently moves into the vascular tissue that gradually deteriorates. When reaching the corm, wilting takes place eventually resulting in the death of the contaminated plant (Stover 1962a). A particular problem that arises with *Foc* infections is the remaining presence of *Foc* spores (microconidia, macroconidia and chlamydospores) in the soil surrounding the infected plants for at least 20 years after the complete removal of all infected plants or plant tissue (Stover 1962b; Buddenhagen 2009; Dita et al. 2018). As a result, reinfection of new banana accessions in the same area is very likely to happen in the absence of a complete soil disinfection or if one has not waited long enough for planting new *Musa* cultivars (Moore et al. 2001, Huang et al. 2012). Therefore, *Fusarium* wilt not only has an impact on the overall yield during the time of infection, but also on the land use for banana cultivars during the coming 20 years.

In 1968, Vakili and coworkers published a first survey on the presence of *Fusarium* infected bananas in Southern Viet Nam (Vakili et al. 1968). Later studies showed that by the end of the 20th century, *Foc* infections were omnipresent in the whole country (Mai Van Tri 1997; Bentley et al. 1998; Vinh et al. 2001). Characterization of the *Fusarium* isolates in the above-mentioned studies demonstrated that *Fusarium* wilting on bananas in Viet Nam was derived from different *Foc* strains (e.g., VCG 0123, VCG 0124, VCG 0124/5, VCG 0125). Hung et al. (2017) reported the first observation of *Foc*-TR4 (VCG 01213/16) on Cavendish bananas in Viet Nam using a combined molecular (PCR approach) and morphological characterization. However, Zheng et al. (2018) claimed that they made the earliest collected records of *Foc*-TR4 in Viet Nam in 2016, by assessing the pathogenicity of the collected strains and characterizing them molecularly using whole genome sequencing methodology. The study of Mostert et al. (2017) also made use of a molecular-morphological characterization approach to determine the origin of the different *Fusarium* infections in Viet Nam. Their results showed the presence of at least five different *Foc* strains (VCG 0123, VCG 0124, VCG 0124/5, VCG 0128, VCG 01221) of which the latter two were not yet detected in earlier studies.

Whereas pathogenic *Foc* lineages were usually classified into three races (*Foc* 1, 2 & 4) based on the different *Musa* cultivars they had infected, the development of the Vegetative Compatibility Group (VCG) system resulted in a more in-depth identification tool of *Foc* strains into 24 unique entities (Fourie et al. 2011; O'Donnell et al. 2009; Perez-Vicente et al. 2014; Mostert et al. 2017). The fact that isolated *Foc* lineages could already be split up in compatible vegetative groups already indicated that there are more natural lineages in the FOSC (*Fusarium oxysporum* species complex) than can be reflected by the number of races. In addition, the polyphyletic nature of *Fusarium oxysporum* f. sp. *cubense* isolates is also demonstrated by Maryani et al. (2019a), who used a combined molecular phylogenetic approach to delineate natural lineages within the *Fusarium oxysporum* species complex (FOSC; O'Donnell and Cigelnik 1997), thereby describing 11 new *Fusarium* species which were formerly considered as *Fusarium oxysporum*. A side result of the study of Maryani et al. (2019) also indicated that the VCG system is perhaps slightly prone to an oversimplification of the categorization of different *Foc* strains that cause *Fusarium* wilting in bananas and plantains. As a result, in the current study we aim to assess the overall diversity of *Foc* wilting in northern Viet Nam by using combined morphological - molecular phylogenetic approach in which also the different VCG's are included. With this approach we provide the overall species identity and phylogenetic position of *Foc* infections in the northern Vietnamese region and examine the genetic diversity between the different *Foc* isolates (from wild and cultivated bananes) that were collected from various provinces in northern Viet Nam. Furthermore, our results will give an indication of the proportion of the different *Foc* strains (and linked VCG's) that are currently infecting bananas in northern Viet Nam.

Material and methods

Sampling

From April 2018 until December 2019, several field trips were carried out focusing on the presence of banana *Fusarium* wilt in northern Viet Nam. During these surveys, banana *Fusarium* wilt samples were collected at 19 locations situated in three large geographic regions (North-eastern region, Red River Delta and North Central region; Table 1, Fig. 1). *Fusarium* infected banana plants were identified by following a set of diagnostic characters in which (mostly older) leaves were clearly yellow (initiated from the leaf margin) or even completely collapsed, halfway the petiole forming a ring of dead leaves around a dying plant, combined with brown discoloration and longitudinally fissuring of the pseudostems leaf sheaths (Fig. 2). From symptomatic plants observed in the field, discoloured brownish vascular tissue was collected from pseudostems and roots. Subsequent to collection, infected tissue samples were stored in paper bags and put in a refrigerator or cooling box to avoid quality loss upon further analysis in the molecular lab. For each sample collected, notes were taken about the altitude, longitude and latitude, site location and the host specimen. Collected *Fusarium* samples were stored at the Plant Resources Center (PRC), Ha Noi, Viet Nam. Of the 19 collected *Fusarium* samples, 17 were found in the triploid *Musa* ABB variety 'Tay banana', one in the triploid *Musa* AAA variety 'Cavendish', and one on a wild *Musa lutea* specimen (Table 1).

Isolate cultivation

In order to observe possible morphological differences between the *Fusarium* wilt isolates that were collected from the wild and cultivated northern Vietnamese *Musa* accessions, we followed the approach of Groenewald et al. (2006) in which different *Foc* isolate were grown on different growing media. All 19 *Fusarium* isolates were cultured prior to further analysis.

Infected discoloured pseudostem tissue samples were cut into 2-3 cm pieces and placed on the Komada medium (Komada 1975). After a few days, fungal *Fusarium* colonies were transferred to plates with different medium and were then put in a growing chamber at 25° C until the colonies reached a size of 2-3 cm. The different isolates were grown on four distinct nutritious media to observe the *Fusarium* wilting in different culture conditions: PDA (Potato Dextrose Agar), SNA (Spezieller Nährstoffarmer Agar), CLA (Carnation Leaf Agar), and OMA (Oatmeal Agar)(Nirenberg 1976). The PDA medium consisted of 200g potato dextrose, 20g D-glucose and 20g agar dissolved in 1000ml distilled water, whereas the SNA medium consisted of 1g KH_2PO_4, 1g KNO_3, 0.5g $MgSO_4{\bullet}7H_2O$, 0.5g KCl, 0.2g D-glucose and 0.2g D-sucrose dissolved in 1000ml distilled water. The CLA medium contained aseptic carnation leaves and 20g agar dissolved in 1000ml distilled water. The OMA medium consisted of 50g oatmeal and 20g agar dissolved in 1000ml distilled water. Growth of the *Fusarium* isolates on the different media took place under in-vitro conditions with the optimal grow temperature between 23 and 27°C (Pérez et al.

2003). After 7 days of incubation, the developing colonies were morphologically investigated under a light microscope (400x magnification). Coloration of the colony, the morphology and size of the conidia were determined. The colony reverse colour was determined on PDA medium after incubation at room temperature. Colony colours were assessed with the colour charts of Rayner (1970). In addition to colony colour, also the aroma of the different cultures was assessed as a strong rank odour generated by mature cultures is a typical characteristic for TR4 infections. In the first stage of culturing, we characterized the isolates as *Fusarium* spp. emanated from mycelium morphology and the presence of different types of conidia. The study of Maryani et al. (2019a) was used to further classify the Foc lineages into different sublineages. All obtained *Fusarium* isolates were stored in the Plant Resources Center (PRC), Ha Noi, Viet Nam.

Molecular protocols

In order to extract high-quality DNA from the *Fusarium* wilt isolates collected and cultured, we used the pure mycelium cultures that were generated for the morphological characterization of the banana wilt. Total genomic DNA was isolated using a modified TNE protocol based on the study of Lin et al. (2008) and Dellaporte et al. (1983). After the addition of 5ml TNE buffer (100 mM Tris-HCl, 50 mM EDTA, 50 mM NaCl, 8 μM β-mercaptoethanol, 1% SDS, pH 8.0) to the sampled mycelium, the samples were incubated for 1h (65°C). Subsequent to the lysis phase, 1.66ml NaOAc (5M) was added and centrifuged. Chloroform-isoamylalcohol (24/1 v/v) extraction was done twice, followed by an isopropanol precipitation at -32°C for 12h. After centrifugation at 4°C, the pellet was washed twice (75% ethanol), air-dried, and dissolved in 100µl TE buffer (10mM TrisHCl, 0.1mM EDTA; pH 8)

Amplification reactions of *rpb1*, *rpb2* and *tef1a* were carried out using standard PCR (20µl). Reactions were initiated with a 3 min heating at 95°C followed by 30 cycles consisting of 95°C for 30s, 55-65°C (*rpb1* and *rpb2*) and 53°-59°C (*tef1a*) for 60s, and 72°C for 60s. Reactions ended with a 3 min incubation at 72°C. Primers designed by O'Donnell et al. (1998) were used to sequence *tef1a*, whereas primers for *rpb1* and *rpb2* were adopted from O'Donnell et al. (2010). PCR products were purified using an ExoSap purification protocol. Purified amplification products were sequenced by the Macrogen sequencing facilities (Macrogen, Seoul, South Korea).

Phylogenetic analyses

Raw sequences were assembled using Geneious Prime (Biomatters, New Zealand). Automatic alignment was conducted with MAFFT (Katoh et al. 2002) using an E-INS-i algorithm, a 100PAM/k=2 scoring matrix, a gap open penalty of 1.3 and an offset value of 0.123. Manual fine-tuning of the aligned dataset was performed in Geneious Prime.

Fusarium sequence data of *rpb1*, *rpb2* and *tef1a* was extracted from GenBank (September 20, 2020) using the 'NCBI Nucleotide extraction' tool in Geneious Prime. Together with the newly generated sequences for the 19 Vietnamese *Fusarium* wilt accessions, the total sequence data matrix consisted of 542 specimens divided over 210 species (Suppl. Table S1). Of those, 11 species belonging to different closely related genera of *Fusarium* within the Nectriaceae family were chosen as outgroup (*Cosmospora*, *Cylindrocarpon*, *Fusicolla*, *Macroconia* and *Microcera*). Newly generated sequences were deposited in the GenBank sequence database (Table 1). Furthermore, in order to compare the newly collected Vietnamese *Foc* accessions with the known Vegetative Compatibility Groups (VGC's), the sequence dataset included *Foc* samples representing all VCG's (see Table S1; Ordonez et al. 2015), except for VCG01212 and VCG0129. For the latter two, only one locus was available causing phylogenetic biases due to the occurrence of too much missing data.

Possible incongruency between the different datasets was inferred by conducting an ILD test (Farris et al. 1995) as implemented in PAUP* v.4.0b10 (Swofford 2003) with following parameters applied: simple taxon addition, TBR branch swapping and heuristic searches of 1000 repartitions of the data. Despite the well-known sensitivity of the ILD test (Barker and Lutzoni 2002), the results of this test were compared in light of the resolution and support values for each of the single gene topologies. As a result, possible conflict between data matrices was visually inspected by searching for conflicting relationships within each topology (obtained per single sequence data matrix) that were supported by a Maximum Likelihood (ML) support value >70% (hard vs. soft incongruence; Johnson and Soltis 1998; Pirie 2015). A conflict was assumed to be significant if two different relationships for the same set of taxa (one being monophyletic and the other non-monophyletic) were observed in rival trees. ML analyses were conducted under the RAxML search algorithm (Stamatakis 2014) with the GTRGAMMAI approximation of rate heterogeneity for each gene. ML bootstrapping was carried out on five hundred bootstrapped datasets using the RAxML Rapid bootstrap algorithm (ML-BS).

The best-fit nucleotide substitution model for each dataset was selected using jModelTest 2.1.4. (Posada 2008) out of 88 possible models under the Akaike information criterion (AIC). The GTR+I+G model was determined as best fit for *rpb1*, while the TVM+G model was calculated as best substitution model for *tef1a* and HKY+I+G as best substitution model for *rpb2*. Consequently, we used a mixed-model approach to apply different evolutionary models on each DNA region of the combined dataset (Ronquist and Huelsenbeck 2003). Bayesian inference analyses were conducted with MrBayes v3.2.6 (Ronquist et al. 2012) on three individual data partitions and a combined data matrix. Each analysis was run two times for 20 million generations. Trees were sampled every 5000th generation. Chain convergence and ESS parameters were inspected with TRACER v.1.4 (Rambaut and Drummond 2007). Only nodes with Bayesian posterior probabilities (BPP) above 0.95 were considered as well supported by the data (Suzuki et al. 2002).

Results

Pathogenic *Fusarium* wilt infections are prevalent in most of northern Viet Nam as they have been observed in all provinces of northern Viet Nam that were sampled in this study. The 19 *Fusarium* wilt infections collected based on the typical plant Fusariosis symptoms (old leaves turning yellow, leaves gradually collapsing, petioles broken close to the midrib with dead leaves remaining attached to the pseudostem, pseudostem sheaths longitudinally splitting near the base, vascular necrosis) were cultured and further morphologically and molecularly analysed.

Morphological characterization of the cultured pathogenic *Fusarium* wilt isolates showed that when the isolates were grown on CLA medium, they produced macroconidia that were uniform in size and form. On SNA medium, the morphology of the macroconidia was sometimes less uniform in size compared to when SLA medium was used. Except for two accessions (FOC56 and FOC61), no aroma was observed among the pathogenic *Fusarium* isolates collected in northern Viet Nam. In general, for all isolates, we observed that macroconidia are sickle-shaped, 3-7 septate, and thin-walled. Microconidia are oval to kidney-shaped, 0-1 septate. Chlamydospores were round and thick-walled. Subtle differences have been observed in the colony morphology and coloration. Based on these morphological differences, we tried to identify different groups within the *Fusarium* isolates analysed. The first group, consisting of 14 isolates (FOC1, 2, 5, 6-1, 7, 11, 16, 18, 21, 23-2, 24, 25-1, 25-2, 38), is characterized by a purple reverse in the centre, white-greyish towards the periphery. The colony surface is dry and is filamentous at the edge. On CLA medium, it produces ample macroconidia, yet only little microconidia. On PDA and SNA medium, it produces prolific microconidia. The second group has a reverse colony colour containing a small touch of dark purple in the centre, gradually discolouring to white towards the edge. This type is observed for isolates FOC 4 and 10. The surface of these colonies is also dry and filamentous at the margin. On CLA medium, ample macroconidia are produced whereas on PDA and SNA medium, the presence of macroconidia is less profound. On the latter two media, prolific microconidia are produced. A third group of isolates (FOC56 and 61) is characterized by an unpigmented, white colony reverse and a dry colony surface with filamentous margin. On CLA medium, a large number of macroconidia is produced while on PDA and SNA medium macroconidia are hardly formed. On PDA and SNA prolific microconidia are produced, whereas on CLA medium only few microconidia were observed. In addition, FOC 56 and 61 isolates are characterized by a typical strong odour of the older cultures. FOC 58 falls a bit amidst the first and second group, containing a pale purple colony reverse colour that becomes whitish towards the periphery and with a dry colony surface appearance.

Phylogenetic analyses of pathogenic *Fusarium* wilt isolates

Sequence characteristics of all data matrices analysed are summarized in Table 2. Despite the fact that sometimes not all gene markers could be sequenced, their absence did not influence the overall phylogenetic results, as sufficient nucleotide variation was present. No significant incongruence between all three sequence datasets (with all *P*-value being larger than 0.05) was found using the partition homogeneity test. Visual examination of the two different partitions of the combined dataset corroborates this congruency analysis.

Phylogenetic analyses of the 19 pathogenic *Fusarium* wilt isolates that were found on various northern Vietnamese bananas showed that although overall morphological characterization pointed towards *Fusarium oxysporum* f. sp. *cubense*, it was clear that they had various evolutionary origins (Fig. 3c, d). Of the 19 accessions analysed, two (FOC61 and FOC56) were placed within the *Fusarium odoratissimum* clade (as defined by Maryani et al. 2019a, Fig. 3d) and for which pathogenicity tests by Maryani et al. (2019a) showed that the members of this group caused infections in Cavendish and Gros Michel AAA banana varieties. In addition, VCG 01213 and VCG 01216 are positioned close to FOC61 and FOC56. As a result, two of the 19 (10.5%) northern Vietnamese pathogenic *Fusarium* wilt isolates are assumed to be *Foc*-TR4 (also taking the morphological characterization into account). Interestingly, one of the two isolates characterized as *Foc*-TR4 (FOC61) infected a Cavendish plantation in Vinh Phuc province, whereas the other infection of *Foc*-TR4 (FOC56) took place on ABB Tay banana cultivars situated on a smallholder farm in Nam Dinh province (Table 1). The largest group (13 accessions; 68.5%) of pathogenic *Fusarium* wilt isolates in northern Vietnamese bananas belong to the recently delineated *Fusarium tardichlamydosporum* clade (Fig. 3d). Pathogenicity tests carried out for this clade by Maryani et al. (2019a) have indicated a large infection rate in Gros Michel cultivars for this lineage and therefore members of the *Fusarium tardichlamydosporum* clade are consequently classified as *Foc*-Race 1. Furthermore, the isolates that fell within the *Fusarium tardichlamydosporum* were also most closely related to VCG 0125, a known *Foc*-Race 1 representative. In northern Viet Nam, infections of *Foc*-Race 1 occurred both on wild and cultivated accessions. For the cultivated accessions, the *Foc*-Race 1 was only found on the ABB Tay banana cultivar, yet was clearly spread in northern Viet Nam as it was found in eight different provinces (Ha Giang, Yen Bai, Lao Cai, Bac Giang, Nam Dinh, Ha Nam, Tuyen Quang, Ha Noi; Table 1). Most interestingly, *Foc*-Race 1 was also identified (isolate FOC5) in an individual of the wild banana *Musa lutea* (section Callimusa). Here the infected accession grew sympatrically with other individuals of *Musa lutea* as well as with *Musa itinerans*. The area where this infection occurred was a steep, abandoned rice terrace in Yen Bai province where hundreds of individuals of both wild species co-occurred and was rather close to one of the smallholder farms where *Foc*-Race 1 was also detected (isolate FOC6-1). In addition to the *Foc*-Race 1 infections caused by *Fusarium tardichlamydosporum*, also *F. duoseptatum* is classified as a *Foc*-Race 1 *Fusarium* wilt (see Maryani et al. 2019). An infection of this latter *Foc* isolate (FOC38) was found only once in northern Viet Nam (Nghe An province; c. 5% of the *Fusarium* wilt infections) where it infected the ABB Tay banana cultivars that where grown on a smallholder farm. The VCG's that occurred in the same clade as FOC38 are VCG 01223 and VCG 01217, with the latter being known as a *Foc*-Race 1 representative (e.g. Katan 1999, Fraser-Smith et al. 2014).

In addition to the *Foc*-Race 1 and *Foc*-TR4 infections, two pathogenic *Foc* isolates (FOC4 and FOC10) were found in northern Viet Nam (10.5%) that belong to the recently described *F. cugenangense* (Maryani et al. 2019a; Fig. 3d). Up to now, this *Fusarium* species was considered to be strictly Indonesian (see Maryani et al. 2019a). Pathogenicity tests conducted for representatives of *F. cugenangense* by Maryani et al. (2019a) have demonstrated that it only causes a mild infection in Gros Michel and Cavendish and were regarded as non-pathogenic for the above-mentioned AAA cultivars. However, our results clearly show that the infection of this isolate also occurred on ABB Tay banana cultivars in northern Viet Nam, where it had a large impact on the fitness of the infected host plants. Although additional confirmation is needed, Maryani et al (2019a) assume that representatives of the *F. cugenangense* clade should be considered as *Foc*-Race 2 (Maryani et al. 2019a; Fig. 3d), yet more thorough analyses need to be carried out in order to further confirm this hypothesis. The VCG that occurred in the same clade as FOC4 and FOC10 is VCG 01221.

A final pathogenic *Fusarium* wilt infection (FOC58) that was regarded upon collection in the field and during morphological screening as a *Foc* infection (c. 5% of the *Fusarium* wilt infections observed in this study), was in fact not situated in the *Fusarium oxysporum species complex* (FOSC) but was a distinct lineage sister to *Fusarium fujikuroi* (Fig. 3c), a well-known pathogen of rice (e.g. Wulff et al. 2010; Choi et al. 2018). This pathogenic *Fusarium* isolate was the prime infection source of ABB Tay bananas that were cultivated on a small plantation for local use in Nam Dinh province (Fig. 1).

Discussion

Fusarium wilting in Vietnam: lineage identification

To better manage the significant threat of *Foc* dispersion in the northern Viet Nam, the correct identification and abundancy of the *Foc* strains that cause Fusarium wilting in bananas in the region is necessary. This is the basis for eradication-confinement and suppression-contention measures (Perez-Vicente et al. 2014). Since the survey of Vakili et al. (1968), *Foc* Race 1 has been considered as the main *Foc* infecting edible bananas in Viet Nam. With the emergence of *Foc* TR4 it remained unclear how abundant this new pathogenic *Foc* strain had become in Viet Nam. Although officially present in Viet Nam for a few years (Hung et al. 2017; Zheng et al. 2018), *Foc* TR4 was already observed on Cavendish bananas in 1998 in Southern China (Hu et al. 2006). A few years later, in 2002, *Foc* TR4 was also found in Chinese regions adjacent to northern Viet Nam (Hu et al. 2006; Li et al. 2013). With the current shift of Cavendish cultivation in Asia from China to its neighbouring countries Laos, Myanmar and Viet Nam, there is also an active spread of *Fusarium* pathogens through transportation of planting material, farming equipment and contaminated soil from China (Zheng et al. 2018), so that *Foc* TR4 can quickly become the most dominant *Foc* race in Viet Nam affecting banana cultivation.

The present study applies the FOSC species delimitation concept of Maryani et al. (2019) in order to more thoroughly delineate the *Foc* lineages that were sampled in northern Viet Nam. Furthermore, the incorporation of the different VCG's in the current phylogenetic dataset allowed us to link the Vietnamese *Foc* isolates with the one of the currently known VCG's that have been assessed in the past. Based on the compatibility of the novel material with the VCG's that are present in the same clade, as well as with ther specific species allocation following the species delineation concept of Maryani et al. (2019), we classified the northern Vietnamese *Foc* isolates into one of the known *Foc* Races. Accordingly, our results shows that *Foc* Race 1 is the most common isolate in northern Viet Nam, causing 74% of all the infections. A more in-depth molecular characterization shows that among these *Foc* Race 1 infections, 13 out of 14 isolates are caused by the species *Fusarium tardichlamydosporum* and one by the species *F. duoseptatum*. Interestingly, *Foc* Race 1 *Fusarium* wilting caused by *F. tardichlamydosporum* occurred in different provinces than *Foc* Race 1 *Fusarium* wilting caused by *F. duoseptatum* (Fig. 1). Whereas *F. tardichlamydosporum* is commonly present throughout the northernly oriented Northeastern region and Red River Delta, *F. duoseptatum* is not present in these more northerly oriented geographic regions but occurs in the more centrally oriented North Central region in Viet Nam. Also, from a global distributional perspective, *F. tardichlamydosporum* is much more widespread than *F. duoseptatum*, with the first species located in Australia, Indonesia, Malaysia, Honduras and Brazil, and the latter only known to date from Indonesia and Malaysia (Maryani et al. 2019a). Compared to *Foc*-Race 1, *Foc*-TR4 infections (*F. odoratissimum*; Maryani et al. 2019a) account for only 10% of the Fusarium wilting in northern Viet Nam demonstrating that *Foc-TR4* has not yet become a dominant banana pathogen, unlike other countries in Asia where there is a tendency to grow Cavendish cultivars as large monocultures, such as in China, the Philippines and Taiwan. The *Foc*-TR4 isolates that were found in the current study were located in the River Delta region of northern Vietnam, provinces Vinh Phuc and Nam Dinh, which are rather distant from *Foc*-TR4 infected regions in Southern China. This indicates a gradual spreading in Viet Nam of *F. odoratissimum* (=*F. oxysporum* f. sp. *cubense* TR4) towards the south as the TR4 isolates analysed by Zheng et al. (2018) were collected in the upper North of Viet Nam in the Lao Cai province at only few kilometres from the border with China (Yunnan). At the moment it is unclear whether the occurrence of *Foc*-TR4 in Viet Nam is still in an initial lag phase, with the potential of largely increasing its distribution range in the country if conditions would improve for the disease to spread (Pegg et al. 2019). Especially the replacement of citrus plantations and maize fields by Cavendish monocultures provides an ideal basis for *Foc*-TR4 to rapidly spread as plants available for infection become less limited. A more worrying observation is that *Foc*-TR4 is not only found in Cavendish bananas in Viet Nam, but that it also poses a threat to local banana varieties as is observed in the current study where ABB Tay banana cultivars seem to be prone to *Fusarium* wilting caused by *Foc*-TR4.

The current study demonstrates that *Foc*-Race 2 infections of Vietnamese bananas also account for 10% of the *Fusarium* wilting in northern Viet Nam. In general, *Foc*-Race 2 infections occur on triploid ABB Bluggoe varieties and its closely related cooking cultivars (Jones, 2000). Besides Bluggoe cooking bananas, *Foc*-Race 2 also infects the tetraploid AAAA Bodles Altafort hybrid between Gros Michel (AAA) and Pisang Lilin (AA)(Stover and Simmonds 1987). In addition, experimental infection of

Ensete ventricosum demonstrated that this important Ethiopian crop is highly susceptible to *Foc*-Race 2 (Ploetz, 2005). With the confirmation of a *Foc*-Race 2 infection affecting also representatives of the ABB Tay banana cultivar, it is clear that *Fusarium* wilting caused by *Foc*-Race 2 is potentially more widespread than has often been assumed.

Fusarium cf. fujikuroi as a novel pathogen of bananas

In addition to the pathogenic *Fusarium* isolates collected from northern Vietnamese bananas belonging to the FOSC, an infection with symptoms similar to *Foc* wilting was observed, yet the cultured isolate did not belong to FOSC. The morphological colony characteristics were very comparable to those observed for FOSC cultures by having a pale purple colony reverse colour that became whitish towards the periphery with a dry colony surface appearance. However, when genetically assessing within the *Fusarium* genus, this isolate did not fall within *F. oxysporum* representatives, but was member of the *Fusarium fujikuroi* species complex (FFSC) where it is the sister lineage of *F. fujikuroi*. It is not uncommon that several *Fusarium* species cause the same disease pattern as this phenomenon has also been identified in mango deformity (Lima et al. 2009) and sugar beet wilting (Burlakoti et al. 2012). Within the FFSC, some species are known to be pathogenic for some *Musa* cultivars (*F. proliferatum, F. verticillioides, F. sacchari, F. lumajangense, F. desaboruense* and *F. musae*; Maldonado-Bonilla et al. 2019, Van Hove et al. 2002, Huang et al. 2019, Maryani et al. 2019b), yet to date no other species of the *Fusarium fujikuroi* species complex - except for the abovementioned - was identified as pathogen for *Musa*. From a phylogenetic point of view, the novel pathogenic *Fusarium* isolate that infected a triploid ABB Tay banana cultivar in Nam Dinh province is sister to *F. fujikuroi*. *Fusarium fujikuroi* is a widespread phytopathogen causing the bakanae disease in various *Oryza sativa* cultivars (rice), but is also known to have a major impact on many other economically important crops (e.g., maize, wheat). However, to date, no infection of *F. fujikuroi* or a close relative has been detected in bananas. This result increases our knowledge on the diversity of *Fusarium* species that cause wilting symptoms on bananas. More importantly, it also demonstrates the urgent need for an accurate identification of plant pathogens that are morphologically very difficult to distinguish from each other in the field.

Fusarium wilting on wild bananas

Although mainly observed on cultivated bananas, *Foc* has also been rarely recorded on wild Musa species (Ploetz and Pegg 2000). Waite (1954) noticed that *Fusarium* wilting also occurred on *M. acuminata*, *M. balbisiana*, *M. schizocarpa* and *M. textilis*. Since these specific *Musa* species belong to different sections in the genus - section *Musa* and *Callimusa* (*Australimusa*) - it is therefore likely that *Foc* can also infect other wild bananas. The current finding of a *Foc*-Race 1 infection on a wild representative of *Musa lutea*, could indicate that wild species are perhaps more susceptible to *Fusarium* wilting than previously assumed. Besides this one individual showing visual symptoms of *Fusarium* wilting, none of the hundreds of individuals of *Musa itinerans* and *Musa lutea* surveyed in the same population showed any sign of *Foc* infection. This lack of visual symptoms either implies that *F. oxysporum* f. sp. *cubense* could have been absent from all those other wild accessions or that the *Foc*-Race 1 pathogen was present but failing to cause the disease in the other wild bananas. If the latter assumption is true, this could indicate that the pathogen not necessarily co-evolved together with its host in Southeast Asia as postulated by Vakili, (1965) but that *Fusarium oxysporum* is omnipresent throughout the native distribution range of the *Musa* genus and that infections take place when the plant is weakened due to external biotic of abiotic stressors and the endophytic equilibrium is disturbed.

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Author Contribution

LLT, AM, DTV and SBJ conceptualized the manuscript. LLT, SdB, AM and SBJ carried out the experimental work. SBJ, AM and LLT wrote the original manuscript. MA, SG and CD optimized the morphological analyses. RS, FV, DTV and SBJ acquired funding for the project. All other authors optimized the initial draft and provided helpful contributions to the finalization of the paper.

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Tables

Table 1. List of collected *Fusarium* (*Foc*) wilt samples on bananas in northern Viet Nam

Isolate	**Locality**	**Cultivar or Species**	**Altitude (m)**	**Latitude**	**Longitude**
FOC1	Yen Binh town, Quang Binh district, Ha Giang province	Tay banana (ABB)	78	22°23’5.28"	104°32’54.0"
FOC2	Dong Cay village, Yen Thang commune, Luc Yen district, Yen Bai province	Tay banana (ABB)	188	22°05'46.2"	104°45'34.0"
FOC4	Khe Chao village, Ngoi A commune, Van Yen district, Yen Bai province	Tay banana (ABB)	76	21°54'21.4"	104°43'48.3"
FOC5	No 7 village, Dai Son commune, Van Yen district, Yen Bai province	*Musa lutea*	351	21°48'17.6"	104°36'01.0"
FOC6-1	No 4 village, Dai Son commune, Van Yen district, Yen Bai province	Tay banana (ABB)	352	21°48'16.9"	104°36'02.5"
FOC7	No 18 village, Lam Giang commune, Van Yen district, Yen Bai province	Tay banana (ABB)	137	22°02'35.3"	104°30'52.3"
FOC10	Hai Son 1 village, Phu Nhuan commune, Bao Thang district, Lao Cai province	Tay banana (ABB)	370	22°13'58.6"	104°08'14.9"
FOC11	Khanh Yen town, Van Ban district, Lao Cai province	Tay banana (ABB)	383	22°06'53.9"	104°14'37.9"
FOC16	Hoang An commune, Hiep Hoa district, Bac Giang province	Tay banana (ABB)	20	21°23'00.2"	105°58'40.5"
FOC18	Hoang Thanh commune, Hiep Hoa district, Bac Giang province	Tay banana (ABB)	18	21°23'22.1"	106°00'24.9"
FOC21	Thinh Long town, Hai Hau district, Nam Dinh province	Tay banana (ABB)	4	20°01'59"	106°12'49.0"
FOC23-2	Thanh Chau commune, Phu Ly district, Ha Nam province	Tay banana (ABB)	7	20°31'24.2"	105°55'31.1"
FOC24	Hung Thanh commune, Tuyen Quang city, Tuyen Quang province	Tay banana (ABB)	26	21°48'19.4"	105°11'39.7"

FOC25-1	Le Chi commune, Gia Lam district, Ha Noi province	Tay banana (ABB)	11	21°18'20.5"	106°00'24.6"
FOC25-2	Le Chi commune, Gia Lam district, Ha Noi province	Tay banana (ABB)	11	21°18'20.5"	106°00'24.6"
FOC38	Quan Mia village, Nghia Tan commune, Nghia Dan district, Nghe An province	Tay banana (ABB)	85	19°19'07.5"	105°21'53.7"
FOC56	Agriculture University,Trau Quy town, Gia Lam district, Ha Noi province	Tay banana (ABB)	11	21°18'20.5"	106°00'24.6"
FOC58	Nui Ngam, Minh Tan commune, Vu Ban district, Nam Dinh province	Tay banana (ABB)	3	20°21'59.1"N	106°04'02.9"E
FOC 61	Hong Chau commune, Yen Lac district, Vinh Phuc province	Cavendish (AAA)	3	21°10'17.1"N	105°34'37.0"E

Table 2. Alignment and sequence characteristics of the different partitions (including outgroup specimens).

	rpb1	*rpb2*	*tef1a*
N° taxa	469	539	273
Sequence length range	558-1574	597-859	343-636
Aligned sequence range	1578	917	797
Variable characters	1106 (70%)	573 (62%)	529 (66%)
Constant characters	472	344	268

Supplementary Tables

Supplementary Table S1. List of accessions used for the phylogenetic analyses, including voucher information and GenBank numbers. Asterisks indicate accessions for which new sequences were generated in the current study.

Species	Accession n°	*rpb1*	*rpb2*	*tef1a*
Cosmospora arxii	NRRL 54560	JX171554	JX171666	-
Cosmospora coccinea	NRRL 53583	JX171545	JX171657	-
Cosmospora cymosum	NRRL 54561	JX171555	JX171667	-
Cylindrocarpon candidum	NRRL 20485	JX171588	JX171474	-
Cylindrocarpon cylindroides	NRRL 22505	JX171499	JX171612	-
Cylindrocarpon heteronema	NRRL 20487	JX171475	JX171589	-
Cylindrocarpon sp.	NRRL 6149	JX171445	JX171559	-
Fusarium acaciae/mearnsii	NRRL 26755	KM361640	KM361658	-
Fusarium acuminatum	NRRL 28449	MG282373	MG282402	-
Fusarium acuminatum	NRRL 28652	MG282384	MG282414	-
Fusarium acutatum	CBS 402.97	MT010947	KT154005	MT010989
Fusarium acutatum	NRRL 13308	MN193911	MN193883	-
Fusarium aethiopicum	NRRL 46718	KM361652	KM361670	-
Fusarium agapanthi	NRRL 31653	KU900619	KU900624	-
Fusarium agapanthi	NRRL 54464	KU900622	KU900627	-
Fusarium albidum	NRRL 22152	JX171492	JX171605	-
Fusarium albosuccineum	NRRL 20459	JX171585	JX171585	-
Fusarium algeriense	NRRL 66647	MF120488	MT409451	-
Fusarium ambrosium	NRRL 20438	JX171470	JX171584	-
Fusarium ambrosium	NRRL 22345	KC691586	KC691618	-
Fusarium ambrosium	NRRL 36510	KC691588	KC691619	-
Fusarium anguioides	NRRL 25385	JX171624	JX171624	-
Fusarium anthophilum	CBS 119858	MT010940	KU604275	MT010997
Fusarium anthophilum	NRRL 25214	KU171696	KF466403	-
Fusarium arcuatisporum	NRRL 32997	HM347164	GQ505802	-
Fusarium armeniacum	NRRL 43641	HM347192	GQ505494	-
Fusarium armeniacum	NRRL 6227	JX171446	HQ154480	-
Fusarium arthrosporioides	NRRL 26416	MG282383	MG282413	-
Fusarium asiaticum	NRRL 13818	JX171459	JX171573	-

Fusarium astromatum	NRRL 22566	JX171500	JX171613	-
Fusarium atrovinosum	CBS 130394	MN120714	MN120734	-
Fusarium atrovinosum	NRRL 13444	JX171454	JX171568	-
Fusarium atrovinosum	NRRL 34016	HM347170	GQ505475	-
Fusarium austroafricanum	NRRL 53441	MH742536	MH742615	-
Fusarium austroafricanum	NRRL 66741	MH742537	MH742616	-
Fusarium austroamericanum	NRRL 28585	KM361643	KM361661	-
Fusarium avenaceum	INRA495	MH667523	MH667549	-
Fusarium avenaceum	INRA496	MH667524	MH667550	-
Fusarium avenaceum	NRRL 36374	MG282366	MG282395	-
Fusarium aywerte	NRRL 25410	JX171513	JX171626	-
Fusarium azukicola	NRRL 54364	KJ511276	KJ511287	-
Fusarium azukicola	NRRL 54366	KJ511277	KJ511288	-
Fusarium babinda	NRRL 25539	JX171632	JX171632	-
Fusarium babinda	NRRL 53470	MH742548	MH742627	-
Fusarium babinda	NRRL 53488	MH742552	MH742631	-
Fusarium bactridioides	CBS 100057	MT010939	MT010963	MT010995
Fusarium begoniae	CBS 452.97	MT010936	MT010964	MT010998
Fusarium begoniae	NRRL 25300	MN193914	MN193886	-
Fusarium beomiforme	NRRL 25174	JX171506	JX171619	-
Fusarium boothii	NRRL 26916	KM361641	GQ915487	-
Fusarium brachygibbosum	NRRL 13829	JX171460	JX171574	-
Fusarium brachygibbosum	NRRL 31008	JX171529	MH845433	-
Fusarium brachygibbosum	NRRL 34033	HM347172	GQ505482	-
Fusarium brasilicum	NRRL 31238	KM361645	KM361663	-
Fusarium brasiliense	NRRL 31779	KJ511272	KJ511283	-
Fusarium brasiliense	NRRL 43350	KJ511274	KJ511285	-
Fusarium brevicatenulatum	CBS 404.97	MT010948	MT010979	MT011005
Fusarium brevicatenulatum	NRRL 25447	MN193915	MN193887	-
Fusarium brevicaudatum	NRRL 43694	HM347193	GQ505846	-
Fusarium buharicum	NRRL 13371	JX171449	JX171563	-
Fusarium buharicum	NRRL 25488	KX302920	KX302928	-
Fusarium bulbicola	NRRL 13618	KF466394	KF466404	-
Fusarium bulbicola	NRRL 22947	KU171679	KU171699	-
Fusarium burgessii	NRRL 66654	MF120495	MT409450	-
Fusarium burgessii	RBG5319	KJ716217	HQ646392	-
Fusarium buxicola	NRRL 36148	JX171534	HM068357	-
Fusarium caatingaense	NRRL 34003	HM347166	GQ505805	-
Fusarium californicum	BL24	MK878580	MK878565	-
Fusarium californicum	BL28	MK878582	MK878567	-
Fusarium californicum	BL30	MK878584	MK878569	-
Fusarium cerealis	NRRL 13721	KM361638	KM361656	-
Fusarium cerealis	NRRL 25491	MG282371	MG282400	-

Fusarium cf. fujikuroi *	Foc 58	XX000000	XX000000	XX000000
Fusarium chlamydosporum	CBS 145.25	MN120715	MN120735	-
Fusarium circinatum	NRRL 25331	JX171510	HM068354	-
Fusarium citri	MoPo1	-	LT970750	LT970778
Fusarium citri	MoPo2	-	LT970751	LT970779
Fusarium citri	MoSm29	-	LT970754	LT970782
Fusarium citricola	CPC 27067	LT746287	LT746307	LT746194
Fusarium citricola	CPC 27069	LT746288	LT746308	LT746195
Fusarium citricola	CPC 27709	LT746289	LT746309	LT746196
Fusarium clavum	ITEM 10393	-	LN901601	LN901566
Fusarium clavum	ITEM 10445	-	LN901603	LN901568
Fusarium clavum	NRRL 34032	HM347171	GQ505813	-
Fusarium coffeatum	CBS 635.76	MN120717	KU604328	-
Fusarium coicis	RBG5368	KP083269	KP083274	-
Fusarium commune	NRRL 28387	JX171638	HM068356	-
Fusarium compactum	FiPo2=FiPoR	-	LT970748	LT970776
Fusarium compactum	NRRL 28029	HM347150	GQ505780	-
Fusarium concentricum	CBS 450.97	MT010942	MT010981	MT010992
Fusarium concolor	NRRL 53455	MH742506	MH742583	-
Fusarium concolor	NRRL 53480	MH742513	MH742591	-
Fusarium concolor	NRRL 53493	MH742535	MH742614	-
Fusarium continuum	F201030	KM520387	KM236782	-
Fusarium continuum	F201127	KM520386	KM236779	-
Fusarium continuum	F201129	KM520385	KM236781	-
Fusarium cortaderiae	NRRL 29297	KM361644	KM361662	-
Fusarium crassistipitatum	NRRL 46170	KJ511275	KJ511286	-
Fusarium cugenangense	InaCC F983	LS479559	LS479307	LS479756
Fusarium cugenangense	InaCC F984	LS479560	LS479308	LS479757
Fusarium cugenangense	NRRL 25433	LS479462	LS479202	LS479648
Fusarium cugenangense	NRRL 36118 (VCG01221)	LS479477	LS479221	LS479669
Fusarium cugenangense	BRIP29094	KX434922	KX434957	-
Fusarium cugenangense	BRIP45952	KX434923	KX434958	-
Fusarium cugenangense	NRRL 25387	JX171625	HM347209	-
Fusarium cugenangense *	Foc 10	-	XX000000	XX000000
Fusarium cugenangense *	Foc 4	-	XX000000	XX000000
Fusarium culmorum	NRRL 25475	JX171515	JX171628	-
Fusarium culmorum	NRRL 66294	MG282380	MG282410	-
Fusarium cuneirostrum	NRRL 31157	KJ511271	FJ240389	-
Fusarium cyanescens	NRRL 37625	HM347175	-	-
Fusarium cyanostomum	NRRL 53998	JX171546	JX171658	-
Fusarium cyanostomum	NRRL 54603	JX171553	JX171665	-
Fusarium dactylidis	NRRL 29298	KM361654	KM361672	-
Fusarium dactylidis	NRRL 29380	KM361653	KM361671	-

Fusarium decemcellulare	KNU01	LC212975	LC214751	-
Fusarium decemcellulare	NRRL 13412	JX171567	JX171567	-
Fusarium delphinoides	NRRL 36160	HM347204	HM347219	-
Fusarium denticulatum	CBS 407.97	MT010953	MT010970	MT011002
Fusarium dimerum	NRRL 20691	JX171478	JX171592	-
Fusarium dimerum	NRRL 36140	HM347203	HM347218	-
Fusarium dlaminii	NRRL 13164	KU171681	KU171701	-
Fusarium domesticum	NRRL 29976	JX171528	JX171641	-
Fusarium duoseptatum	FocMal43 (VCG01217)	-	LS479207	LS479653
Fusarium duoseptatum	InaCC F828	LS479520	LS479266	LS479715
Fusarium duoseptatum	InaCC F829	LS479528	LS479274	LS479723
Fusarium duoseptatum	InaCC F831	LS479538	LS479285	LS479734
Fusarium duoseptatum	InaCC F835	LS479567	LS479315	LS479764
Fusarium duoseptatum	InaCC F911	-	LS479234	LS479683
Fusarium duoseptatum	InaCC F915	LS479494	LS479238	LS479687
Fusarium duoseptatum	InaCC F916	LS479495	LS479239	LS479688
Fusarium duoseptatum	InaCC F920	LS479499	LS479244	LS479693
Fusarium duoseptatum	InaCC F921	LS479500	LS479245	LS479694
Fusarium duoseptatum	InaCC F975	LS479549	LS479296	LS479745
Fusarium duoseptatum	InaCC F976	LS479550	LS479297	LS479746
Fusarium duoseptatum	InaCC F977	LS479551	LS479298	LS479747
Fusarium duoseptatum	InaCC F978	LS479552	LS479299	LS479748
Fusarium duoseptatum	InaCC F979	LS479553	LS479300	LS479749
Fusarium duoseptatum	Indo80	LS479619	LS479387	LS479829
Fusarium duoseptatum	NRRL 36115 (VCG01224)	LS479475	LS479218	LS479666
Fusarium duoseptatum	NRRL 36116 (VCG01223)	-	LS479219	LS479667
Fusarium duoseptatum *	Foc 38	-	XX000000	XX000000
Fusarium ensiforme	CPC 27190	-	LT746312	LT746199
Fusarium ensiforme	CPC 27191	-	LT746313	LT746200
Fusarium equiseti	FUS18	MN692709	MN692731	-
Fusarium equiseti	FUS28	MN692714	MN692736	-
Fusarium equiseti	FUS42	MN692718	MN692740	-
Fusarium equiseti	ITEM 10675	-	LN901607	LN901573
Fusarium equiseti	ITEM 11363	-	LN901609	LN901574
Fusarium equiseti	NRRL 43636	HM347189	GQ505841	-
Fusarium euwallaceae	NRRL 54724	JQ038023	JQ038030	-
Fusarium euwallaceae	NRRL 54725	JQ038024	JQ038031	-
Fusarium euwallaceae	NRRL 54726	JQ038025	JQ038032	-
Fusarium falciforme	MIW 58	MN242937	MN725019	-
Fusarium falciforme	NRRL 43529	JX171541	JX171653	-
Fusarium falciforme	NRRL 43529	JX171541	JX171653	-
Fusarium ficicrescens	CBS 125178	MT010950	KT154002	MT011004
Fusarium flagelliforme	ITEM 11296	-	LN901606	LN901572

Fusarium flocciferum	NRRL 25473	JX171514	JX171627	-
Fusarium flocciferum	NRRL 45999	HM347195	GQ505497	-
Fusarium floridanum	NRRL 62608	KC691592	KC691623	-
Fusarium floridanum	NRRL 62628	KC691593	KC691624	-
Fusarium floridanum	NRRL 62629	KC691594	KC691625	-
Fusarium foetens	CBS 110286	MT010945	MT010984	MT011001
Fusarium foetens	NRRL 38302	JX171652	JX171652	-
Fusarium fujikuroi	NRRL 13566	JX171456	JX171570	-
Fusarium fujikuroi	NRRL 5538	MN193916	MN193888	-
Fusarium fujikuroi	NRRL 66288	MG282385	MG282415	-
Fusarium gaditjirrii	NRRL 45417	JX171654	JX171654	-
Fusarium globosum	NRRL 26132	LT746301	LT746343	-
Fusarium globosum	NRRL 26133	LT746302	LT746344	-
Fusarium globosum	NRRL 26134	LT746303	LT746345	-
Fusarium gracilipes	NRRL 43635	HM347188	GQ505840	-
Fusarium graminearum	SP100	-	MN625698	MK611901
Fusarium graminearum	SP102	-	MN625699	MK611900
Fusarium graminearum	SP99	-	MN625697	MK611899
Fusarium graminum	NRRL 20692	JX171479	JX171593	-
Fusarium grosmichelii	InaCC F832	LS479542	LS479289	LS479738
Fusarium grosmichelii	InaCC F833	LS479548	LS479295	LS479744
Fusarium grosmichelii	InaCC F848	LS479588	LS479338	LS479786
Fusarium grosmichelii	InaCC F849	LS479589	LS479339	LS479787
Fusarium grosmichelii	InaCC F850	-	LS479340	LS479788
Fusarium grosmichelii	InaCC F851	-	LS479341	LS479789
Fusarium grosmichelii	InaCC F852	-	LS479342	LS479790
Fusarium grosmichelii	InaCC F853	-	LS479343	LS479791
Fusarium grosmichelii	InaCC F854	LS479591	LS479345	LS479793
Fusarium grosmichelii	InaCC F855	LS479592	LS479346	LS479794
Fusarium grosmichelii	InaCC F861	LS479597	LS479351	LS479797
Fusarium grosmichelii	InaCC F862	LS479598	LS479352	LS479798
Fusarium grosmichelii	InaCC F863	LS479599	LS479353	LS479799
Fusarium grosmichelii	InaCC F867	-	LS479360	LS479806
Fusarium grosmichelii	InaCC F868	-	LS479361	LS479807
Fusarium grosmichelii	InaCC F884	LS479616	LS479382	LS479824
Fusarium grosmichelii	InaCC F887	LS479620	LS479388	LS479830
Fusarium grosmichelii	InaCC F888	LS479621	LS479389	LS479831
Fusarium grosmichelii	Indo83	-	LS479390	-
Fusarium grosmichelii	NRRL 36120 (VCG01218)	LS479478	LS479222	LS479670
Fusarium guilinense	NRRL 32865	HM347161	GQ505792	-
Fusarium guttiforme	CBS 409.97	MT010938	MT010967	MT010999
Fusarium guttiforme	NRRL 2294	MN193917	MN193889	-
Fusarium guttiforme	NRRL 22945	JX171505	JX171618	-

Fusarium hainanense	NRRL 26417	JX171522	GQ505776	-
Fusarium heterosporum	NRRL 20693	JX171480	JX171594	-
Fusarium hexaseptatum	InaCC F866	-	LS479359	LS479805
Fusarium hostae	NRRL 29888	MT409435	MT409445	-
Fusarium hostae	NRRL 29889	JX171640	JX171640	-
Fusarium humicola	CBS 124.73	MN120718	MN120738	-
Fusarium illudens	NRRL 22090	JX171488	JX171601	-
Fusarium incarnatum	ITEM 6748	-	LN901618	LN901582
Fusarium incarnatum	ITEM 7155	-	LN901617	LN901581
Fusarium incarnatum	NRRL 32866	HM347162	GQ505793	-
Fusarium ipomoeae	NRRL 43640	HM347191	GQ505845	-
Fusarium irregulare	NRRL 32175	JX171532	GQ505787	-
Fusarium irregulare	NRRL 34006	HM347169	GQ505808	-
Fusarium kalimantanense	InaCC F917	LS479497	LS479241	LS479690
Fusarium kalimantanense	InaCC F918	-	LS479242	LS479691
Fusarium kalimantanense	InaCC F922	-	LS479246	LS479695
Fusarium keratoplasticum	ATS92	MF179712	KY512536	-
Fusarium keratoplasticum	ATS94	MF179714	KY512538	-
Fusarium kyushuense	NRRL 66296	MG282364	MG282393	-
Fusarium lacertarum	NRRL 20423	JX171581	GQ505771	-
Fusarium lactis	CBS 411.97	MT010954	MT010969	MT011010
Fusarium langsethiae	NRRL 54940	JX171550	JX171662	-
Fusarium lateritium	NRRL 13622	JX171457	HM068350	-
Fusarium lateritium	NRRL 25197	HM347140	HM347207	-
Fusarium longipes	NRRL 13368	JX171448	JX171562	-
Fusarium longipes	NRRL 13374	JX171450	JX171564	-
Fusarium longipes	NRRL 20723	JX171483	JX171596	-
Fusarium luffae	NRRL 32522	HM347158	GQ505790	-
Fusarium lunatum	NRRL 36168	JX171536	JX171648	-
Fusarium lunulosporum	NRRL 13393	KM361637	KM361655	-
Fusarium lyarnte	NRRL 54252	JX171661	MN193908	-
Fusarium macrosporum	CPC 28191	-	LT746331	LT746218
Fusarium macrosporum	CPC 28192	-	LT746332	LT746219
Fusarium macrosporum	CPC 28193	-	LT746333	LT746220
Fusarium mangiferae	MUCL 54671	-	LT575059	LT574978
Fusarium mangiferae	NRRL 25226	JX171509	HM068353	-
Fusarium mangiferae	UMAF 910	KP753434	KP753441	-
Fusarium meridionale	NRRL 28436	KM361642	KM361660	-
Fusarium mesoamericanum	NRRL 25797	KM361639	KM361657	-
Fusarium mexicanum	MICMW 32.13a	MN242900	MN724975	-
Fusarium mexicanum	MICMW 3A	MN242905	MN724980	-
Fusarium miscanthi	NRRL 26231	JX171634	JX171634	-
Fusarium multiceps	NRRL 43639	HM347190	GQ505844	-

Fusarium mundagurra	RBG5717	KP083272	KP083276	-
Fusarium musae	CBS 624.87	MT010957	MT010973	MT010991
Fusarium nanum	NRRL 32868	HM347163	GQ505795	-
Fusarium napiforme	CBS 748.97	MT010958	KU604233	MT011011
Fusarium napiforme	F111	KU974338	KU974364	-
Fusarium napiforme	NRRL 25196	MN193919	MN193891	-
Fusarium nectrioides	NRRL 20689	JX171477	JX171591	-
Fusarium nelsonii	NRRL 13338	JX171447	GQ505466	-
Fusarium nematophilum	NRRL 54600	JX171552	JX171664	-
Fusarium neocosmosporiellum	NRRL 22436	JX171497	JX171610	-
Fusarium newnesense	RBG5443	KJ397218	KJ397254	-
Fusarium nisikadoi	NRRL 25179	JX171620	JX171620	-
Fusarium nisikadoi	NRRL 25203	MG282388	MG282418	-
Fusarium nisikadoi	NRRL 25308	MG282391	MG282421	-
Fusarium nodosum	CBS 200.63	MN120724	MN120742	-
Fusarium nodosum	CBS 201.63	MN120725	MN120743	-
Fusarium nodosum	CBS 698.74	MN120726	MN120744	-
Fusarium nurragi	NRRL 36452	JX171538	JX171650	-
Fusarium nygamai	CBS 749.97	MT010955	KU604262	MT011009
Fusarium nygamai	NRRL 66291	MG282368	MG282397	-
Fusarium nygamai	NRRL 66293	MG282367	MG282396	-
Fusarium obliquiseptatum	NRRL 62610	KC691605	KC691636	-
Fusarium obliquiseptatum	NRRL 62611	KC691606	KC691637	-
Fusarium odoratissimum	InaCC F1000	LS479575	LS479323	LS479772
Fusarium odoratissimum	InaCC F816	LS479485	LS479228	LS479677
Fusarium odoratissimum	InaCC F817	LS479556	LS479304	LS479753
Fusarium odoratissimum	InaCC F818	LS479584	LS479333	LS479782
Fusarium odoratissimum	InaCC F819	LS479600	LS479354	LS479800
Fusarium odoratissimum	InaCC F821	LS479609	LS479374	LS479818
Fusarium odoratissimum	InaCC F822	LS479618	LS479386	LS479828
Fusarium odoratissimum	InaCC F824	LS479486	LS479229	LS479678
Fusarium odoratissimum	InaCC F825	LS479496	LS479240	LS479689
Fusarium odoratissimum	InaCC F836	LS479577	LS479325	LS479774
Fusarium odoratissimum	InaCC F837	LS479578	LS479326	LS479775
Fusarium odoratissimum	InaCC F838	LS479579	LS479327	LS479776
Fusarium odoratissimum	InaCC F839 Indo25 (VCG01219)	LS479580	LS479328	LS479777
Fusarium odoratissimum	InaCC F840	-	LS479329	LS479778
Fusarium odoratissimum	InaCC F846	-	LS479336	LS479785
Fusarium odoratissimum	InaCC F857	LS479594	LS479348	LS479795
Fusarium odoratissimum	InaCC F864	-	LS479356	LS479802
Fusarium odoratissimum	InaCC F870	LS479602	LS479363	LS479809
Fusarium odoratissimum	InaCC F871	-	LS479365	LS479811
Fusarium odoratissimum	InaCC F873	LS479604	LS479369	LS479814

Fusarium odoratissimum	InaCC F875	LS479607	LS479372	LS479816
Fusarium odoratissimum	InaCC F876	LS479608	LS479373	LS479817
Fusarium odoratissimum	InaCC F877	LS479610	LS479375	LS479819
Fusarium odoratissimum	InaCC F879	LS479612	LS479377	LS479820
Fusarium odoratissimum	InaCC F880	-	LS479378	LS479821
Fusarium odoratissimum	InaCC F882	LS479614	LS479380	LS479822
Fusarium odoratissimum	InaCC F883	LS479615	LS479381	LS479823
Fusarium odoratissimum	InaCC F885	-	LS479384	LS479826
Fusarium odoratissimum	InaCC F891	-	LS479393	LS479833
Fusarium odoratissimum	InaCC F892	LS479624	LS479394	LS479834
Fusarium odoratissimum	InaCC F893	LS479625	LS479395	LS479835
Fusarium odoratissimum	InaCC F894	LS479626	LS479396	LS479836
Fusarium odoratissimum	InaCC F896	LS479629	LS479399	LS479839
Fusarium odoratissimum	InaCC F897	LS479630	LS479400	LS479840
Fusarium odoratissimum	InaCC F898	LS479631	LS479401	LS479841
Fusarium odoratissimum	InaCC F899	LS479632	LS479402	LS479842
Fusarium odoratissimum	InaCC F900	LS479633	LS479403	LS479843
Fusarium odoratissimum	InaCC F901	LS479634	LS479404	LS479844
Fusarium odoratissimum	InaCC F902	LS479635	LS479405	LS479845
Fusarium odoratissimum	InaCC F903	LS479636	LS479406	LS479846
Fusarium odoratissimum	InaCC F904	LS479637	LS479407	LS479847
Fusarium odoratissimum	InaCC F905	LS479638	LS479408	LS479848
Fusarium odoratissimum	InaCC F906	LS479639	LS479409	LS479849
Fusarium odoratissimum	InaCC F907	LS479487	LS479230	LS479679
Fusarium odoratissimum	InaCC F908	LS479488	LS479231	LS479680
Fusarium odoratissimum	InaCC F909	LS479489	LS479232	LS479681
Fusarium odoratissimum	InaCC F910	LS479490	LS479233	LS479682
Fusarium odoratissimum	InaCC F912	LS479491	LS479235	LS479684
Fusarium odoratissimum	InaCC F919	LS479498	LS479243	LS479692
Fusarium odoratissimum	InaCC F923	LS479501	LS479247	LS479696
Fusarium odoratissimum	InaCC F924	LS479502	LS479248	LS479697
Fusarium odoratissimum	InaCC F925	LS479503	LS479249	LS479698
Fusarium odoratissimum	InaCC F926	LS479504	LS479250	LS479699
Fusarium odoratissimum	InaCC F927	LS479506	LS479252	LS479701
Fusarium odoratissimum	InaCC F928	LS479507	LS479253	LS479702
Fusarium odoratissimum	InaCC F929	LS479508	LS479254	LS479703
Fusarium odoratissimum	InaCC F930	LS479509	LS479255	LS479704
Fusarium odoratissimum	InaCC F931	LS479510	LS479256	LS479705
Fusarium odoratissimum	InaCC F932	LS479511	LS479257	LS479706
Fusarium odoratissimum	InaCC F933	LS479512	LS479258	LS479707
Fusarium odoratissimum	InaCC F934	LS479514	LS479260	LS479709
Fusarium odoratissimum	InaCC F935	LS479515	LS479261	LS479710
Fusarium odoratissimum	InaCC F936	LS479516	LS479262	LS479711

Fusarium odoratissimum	InaCC F937	LS479517	LS479263	LS479712
Fusarium odoratissimum	InaCC F938	LS479518	LS479264	LS479713
Fusarium odoratissimum	InaCC F939	LS479519	LS479265	LS479714
Fusarium odoratissimum	InaCC F942	LS479521	LS479267	LS479716
Fusarium odoratissimum	InaCC F943	LS479522	LS479268	LS479717
Fusarium odoratissimum	InaCC F944	LS479523	LS479269	LS479718
Fusarium odoratissimum	InaCC F945	LS479524	LS479270	LS479719
Fusarium odoratissimum	InaCC F946	LS479525	LS479271	LS479720
Fusarium odoratissimum	InaCC F947	LS479526	LS479272	LS479721
Fusarium odoratissimum	InaCC F948	LS479527	LS479273	LS479722
Fusarium odoratissimum	InaCC F953	LS479529	LS479275	LS479724
Fusarium odoratissimum	InaCC F954	LS479530	LS479276	LS479725
Fusarium odoratissimum	InaCC F955	LS479531	LS479277	LS479726
Fusarium odoratissimum	InaCC F973	LS479547	LS479294	LS479743
Fusarium odoratissimum	InaCC F985	LS479562	LS479310	LS479759
Fusarium odoratissimum	InaCC F986	LS479563	LS479311	LS479760
Fusarium odoratissimum	InaCC F989	LS479566	LS479314	LS479763
Fusarium odoratissimum	InaCC F990	LS479568	LS479316	LS479765
Fusarium odoratissimum	InaCC F994	LS479569	LS479317	LS479766
Fusarium odoratissimum	InaCC F997	LS479572	LS479320	LS479769
Fusarium odoratissimum	InaCC F998	LS479573	LS479321	LS479770
Fusarium odoratissimum	InaCC F999	LS479574	LS479322	LS479771
Fusarium odoratissimum	Indo204	LS479561	LS479309	LS479758
Fusarium odoratissimum	Indo222	LS479576	LS479324	LS479773
Fusarium odoratissimum	Indo4	LS479590	LS479344	LS479792
Fusarium odoratissimum	Indo53	-	LS479357	LS479803
Fusarium odoratissimum	Indo61	-	LS479366	LS479812
Fusarium odoratissimum	Indo62	-	LS479367	-
Fusarium odoratissimum	Indo66	LS479605	LS479370	LS479815
Fusarium odoratissimum	Indo77	LS479617	LS479383	LS479825
Fusarium odoratissimum	Indo89	LS479627	LS479397	LS479837
Fusarium odoratissimum	JV11	LS479465	LS479205	LS479651
Fusarium odoratissimum	Leb1.2C	LS479466	LS479206	LS479652
Fusarium odoratissimum	NRRL 36102 (VCG0121)	LS479468	LS479209	LS479655
Fusarium odoratissimum	Pak1.1A	LS479479	LS479223	LS479671
Fusarium odoratissimum *	Foc 56	XX000000	XX000000	XX000000
Fusarium odoratissimum *	Foc 61	-	XX000000	XX000000
Fusarium odoratissimum	FocII5 (VCG01213)	LS479459	LS479198	LS479644
Fusarium penzigii	NRRL 20711	HM347202	HM347217	-
Fusarium pernambucanum	NRRL 32864	HM347160	GQ505791	-
Fusarium perseae	CPC 26829	-	LT991909	LT991902
Fusarium perseae	CPC 26830	-	LT991910	LT991903
Fusarium perseae	CPC 26832	-	LT991912	LT991905

Fusarium peruvianum	CBS 511.75	MN120728	MN120746	-
Fusarium petersiae	JW14004	MG386138	MG386149	-
Fusarium petersiae	JW14005	MG386139	MG386150	-
Fusarium phaseoli	CBS 265.50	KM232226	KM232375	HE647964
Fusarium phaseoli	NRRL 22276	JX171495	JX171608	-
Fusarium phaseoli	NRRL 22411	KJ511267	KJ511278	-
Fusarium phialophorum	FocIndo25	LS479464	LS479204	LS479650
Fusarium phialophorum	FocST4.98 (VCG0120)	LS479484	LS479227	LS479676
Fusarium phialophorum	InaCC F826	LS479505	LS479251	LS479700
Fusarium phialophorum	InaCC F827	LS479513	LS479259	LS479708
Fusarium phialophorum	InaCC F830	LS479536	LS479282	LS479731
Fusarium phialophorum	InaCC F834	LS479557	LS479305	LS479754
Fusarium phialophorum	InaCC F842	LS479582	LS479331	LS479780
Fusarium phialophorum	InaCC F843	LS479583	LS479332	LS479781
Fusarium phialophorum	InaCC F844	LS479585	LS479334	LS479783
Fusarium phialophorum	InaCC F845	LS479586	LS479335	LS479784
Fusarium phialophorum	InaCC F889 Indo84 (VCG01216)	LS479622	LS479391	LS479832
Fusarium phialophorum	InaCC F969	LS479543	LS479290	LS479739
Fusarium phialophorum	InaCC F970	LS479544	LS479291	LS479740
Fusarium phialophorum	InaCC F971	LS479545	LS479292	LS479741
Fusarium phialophorum	InaCC F972	LS479546	LS479293	LS479742
Fusarium phialophorum	InaCC F981	-	LS479303	LS479752
Fusarium phialophorum	InaCC F982	LS479558	LS479306	LS479755
Fusarium phialophorum	InaCC F987	LS479564	LS479312	LS479761
Fusarium phialophorum	InaCC F995	LS479570	LS479318	LS479767
Fusarium phialophorum	InaCC F996	LS479571	LS479319	LS479768
Fusarium phialophorum	NRRL 36101 (VCG0123)	LS479467	LS479208	LS479654
Fusarium phialophorum	NRRL 36103 (VCG0122)	LS479469	LS479210	LS479656
Fusarium phialophorum	NRRL 36109 (VCG01211)	LS479471	LS479214	LS479661
Fusarium phialophorum	NRRL 36112 (VCG01215)	LS479473	LS479216	LS479664
Fusarium phialophorum	R1.0124	LS479483	-	LS479675
Fusarium phyllophilum	NRRL 13617	KF466399	KF466410	-
Fusarium plagianthi	NRRL 22632	JX171501	JX171614	-
Fusarium poae	NRRL 13714	JX171458	JX171572	-
Fusarium poae	NRRL 66297	MG282363	MG282392	-
Fusarium praegraminearum	NRRL 39664	KX260125	KX260126	-
Fusarium proliferatum	ITEM2287	LT841251	LT841252	LT841245
Fusarium proliferatum	ITEM2400	LT841265	LT841266	LT841259
Fusarium proliferatum	NRRL 22944	JX171504	HM068352	-
Fusarium pseudensiforme	NRRL 46517	KC691615	KC691645	-
Fusarium pseudoanthophilum	CBS 414.97	MT010949	MT010980	MT011006
Fusarium pseudocircinatum	NRRL 22946	MG838070	MN724939	-
Fusarium pseudocircinatum	NRRL 31631	MG838073	MN724942	-

Fusarium pseudocircinatum	NRRL 53570	MG838075	MN724944	-
Fusarium pseudograminearum	NRRL 28062	JX171524	JX171637	-
Fusarium pseudograminearum	NRRL 28065	MG282389	MG282419	-
Fusarium pseudonygamai	CBS 417.97	MT010951	MT010978	MT011008
Fusarium purpurascens	InaCC F823	LS479628	LS479398	LS479838
Fusarium purpurascens	InaCC F886	-	LS479385	LS479827
Fusarium purpurascens	InaCC F913	LS479492	LS479236	LS479685
Fusarium purpurascens	InaCC F914	LS479493	LS479237	LS479686
Fusarium purpurascens	InaCC F966	LS479539	LS479286	LS479735
Fusarium purpurascens	InaCC F967	LS479540	LS479287	LS479736
Fusarium purpurascens	InaCC F968	LS479541	LS479288	LS479737
Fusarium purpurascens	NRRL 36107 (VCG0126)	-	LS479213	LS479659
Fusarium ramigenum	CBS 418.97	MT010959	MT010975	MT011012
Fusarium ramigenum	NRRL 25208	KF466401	KF466412	-
Fusarium redolens	CBS 743.97	MT010935	MT010961	MT010987
Fusarium redolens	NRRL 22901	JX171616	JX171616	-
Fusarium redolens	NRRL 25600	MT409433	MT409443	-
Fusarium rusci	NRRL 22134	JX171490	JX171603	-
Fusarium sacchari	CBS 147.25	MT010941	MT010962	MT010988
Fusarium sacchari	NRRL 44901	HM347194	HM347212	-
Fusarium sacchari	YN BS37	MK983434	MK829737	-
Fusarium salinense	CPC 26403	LT746284	LT746304	LT746191
Fusarium salinense	CPC 26457	LT746285	LT746305	LT746192
Fusarium salinense	CPC 26973	LT746286	LT746306	LT746193
Fusarium sambucinum	NRRL 22187	JX171493	JX171606	-
Fusarium sangayamense	InaCC F961	-	LS479284	LS479733
Fusarium sarcochroum	CPC 28075	LT746296	LT746324	LT746211
Fusarium sarcochroum	CPC 28116	LT746297	LT746325	LT746212
Fusarium sarcochroum	NRRL 20472	JX171472	JX171586	-
Fusarium scirpi	NRRL 13402	JX171452	GQ505770	-
Fusarium setosum	NRRL 36526	JX171539	JX171651	-
Fusarium siculi	CPC 27188	LT746299	LT746327	LT746214
Fusarium siculi	CPC 27189	LT746300	LT746328	LT746215
Fusarium solani	FBF7	-	MK606410	MK606409
Fusarium solani	LEMM_110148	-	LN828050	LN827961
Fusarium solani	LEMM_110266	-	LN828053	LN827964
Fusarium solani melongenae	MIM 28	MN242938	MN725021	-
Fusarium solani melongenae	MIW 81	MN242939	MN724934	-
Fusarium solani melongenae	NRRL 22147	MG282390	MG282420	-
Fusarium spinosum	CBS 122438	MN120729	MN120747	-
Fusarium spinosum	NRRL 43631	HM347187	GQ505491	-
Fusarium sporodochiale	CBS 199.63	MN120730	MN120748	-
Fusarium sporodochiale	CBS 220.61	MN120731	MN120749	-

Fusarium sporotrichioides	NRRL 25479	HM347144	HM347210	-
Fusarium sporotrichioides	NRRL 3299	JX171444	DQ676587	-
Fusarium sporotrichioides	NRRL 66295	MG282378	MG282408	-
Fusarium staphyleae	NRRL 22316	JX171496	JX171609	-
Fusarium sterilihyphosum	NRRL 25623	LR792581	LR792617	-
Fusarium stilboides	HA 1 2	MK887361	MK887362	-
Fusarium stilboides	NRRL 20429	JX171468	JX171582	-
Fusarium subglutinans	NRRL 22016	JX171486	JX171599	-
Fusarium subglutinans	NRRL 54158	HM347201	HM347216	-
Fusarium subglutinans	NRRL 66333	MN193926	MN193898	-
Fusarium sublunatum	NRRL 13384	JX171451	JX171565	-
Fusarium subtropicale	NRRL 66764	MH706972	MH706973	-
Fusarium sulawesiense	NRRL 34004	HM347167	GQ505806	-
Fusarium tanahbumbuense	CBS 101138	MN120733	MN120751	-
Fusarium tanahbumbuense	NRRL 34005	HM347168	GQ505807	-
Fusarium tardichlamydosporum	BRIP44611	KX434927	KX434962	-
Fusarium tardichlamydosporum	BRIP62955	KX434936	KX434971	-
Fusarium tardichlamydosporum *	Foc 1	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 11	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 16	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 18	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 2	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 21	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 23-2	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 24	XX000000	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 25-1	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 25-2	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 5	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 6	-	XX000000	XX000000
Fusarium tardichlamydosporum *	Foc 7	-	XX000000	XX000000
Fusarium tardichlamydosporum	InaCC F956	LS479532	LS479278	LS479727
Fusarium tardichlamydosporum	InaCC F957	LS479533	LS479279	LS479728
Fusarium tardichlamydosporum	InaCC F958	LS479534	LS479280	LS479729
Fusarium tardichlamydosporum	InaCC F959	LS479535	LS479281	LS479730
Fusarium tardichlamydosporum	NRRL 36105 (VCG0124)	LS479470	LS479211	LS479657
Fusarium tardichlamydosporum	NRRL 36106 (VCG0125)	-	LS479212	LS479658
Fusarium tardichlamydosporum	NRRL 36111 (VCG0128)	LS479472	LS479215	LS479663
Fusarium tardichlamydosporum	NRRL 36117 (VCG01222)	LS479476	LS479220	LS479668
Fusarium tardicrescens	NRRL 36113 (VCG01214)	LS479474	LS479217	LS479665
Fusarium tardicrescens	NRRL 37622	LS479463	LS479203	LS479649
Fusarium tardicrescens	NRRL 54005	LS479482	LS479226	LS479674
Fusarium tardicrescens	NRRL 54008	LS479481	LS479225	LS479673
Fusarium temperatum	NRRL 25622	LR792582	LR792618	-

Fusarium thapsinum	NRRL 22045	JX171487	JX171600	-
Fusarium thapsinum	NRRL 22049	KU171713	MN193899	-
Fusarium tjaetaba	RBG5361	KP083267	KP083275	-
Fusarium tonkinense	CPC 27195	-	LT746340	LT746227
Fusarium torreyae	NRRL 54149	JX171548	HM068359	-
Fusarium torulosum	NRRL 22748	JX171502	JX171615	-
Fusarium torulosum	NRRL 52772	JF741003	MH582377	-
Fusarium tricinctum	NRRL 25481	JX171516	HM068327	-
Fusarium tuaranense	NRRL 22231	KC691600	KC691631	-
Fusarium tuaranense	NRRL 46518	KC691601	KC691632	-
Fusarium tuaranense	NRRL 46519	KC691602	KC691633	-
Fusarium tucumaniae	NRRL 31086	KJ511269	KJ511280	-
Fusarium tucumaniae	NRRL 34546	KJ511273	KJ511284	-
Fusarium tupiense	NRRL 53984	LR792583	LR792619	-
Fusarium tupiense	UMAF 0917	KP753436	KP753443	-
Fusarium tupiense	UMAF 0933	KP753437	KP753444	-
Fusarium udum	NRRL 25194	MN193928	MN193900	-
Fusarium ussurianum	NRRL 45681	KM361648	KM361666	-
Fusarium vanettenii	NRRL 45880	JX171543	JX171655	-
Fusarium venenatum	NRRL 22196	JX171494	JX171607	-
Fusarium ventricosum	NRRL 13953	JX171461	JX171575	-
Fusarium ventricosum	NRRL 20846	JX171484	JX171597	-
Fusarium ventricosum	NRRL 25729	JX171520	JX171633	-
Fusarium verticillioides	YN DH24	MK886821	MK886821	-
Fusarium verticillioides	YN DH28	MK983460	MK983384	-
Fusarium verticillioides	YN SJ46	MK983456	MK983397	-
Fusarium virguliforme	NRRL 31041	JX171643	FJ240386	-
Fusarium vorosii	NRRL 37605	KM361647	KM361665	-
Fusarium xylarioides	NRRL 25486	JX171630	HM068355	-
Fusarium xyrophilum	NRRL 62710	MN193931	MN193903	-
Fusarium xyrophilum	NRRL 62721	MN193933	MN193905	-
Fusarium xyrophilum	NRRL 66890	MN193932	MN193904	-
Fusarium zealandicum	NRRL 22465	JX171498	JX171611	-
Fusicolla aquaeductuum	NRRL 20686	JX171476	JX171590	-
Fusicolla sp.	NRRL 22136	JX171491	JX171604	-
Macroconia leptosphaeriae	NRRL 54562	JX171556	JX171668	-
Macroconia sp.	NRRL 54563	JX171557	JX171669	-
Microcera coccophila	NRRL 13962	JX171462	JX171576	-
Microcera diploa	NRRL 36545	JX171463	JX171577	-
Microcera larvarum	NRRL 20473	JX171473	JX171587	-

Figure Legends

Fig. 1. Distribution map of localities in northern Viet Nam where Fusarium wilting was observed. Colours indicate different *Fusarium* strains or species. Squares indicate *Fusarium* infections of wild bananas; circles indicate infections of cultivated bananas.

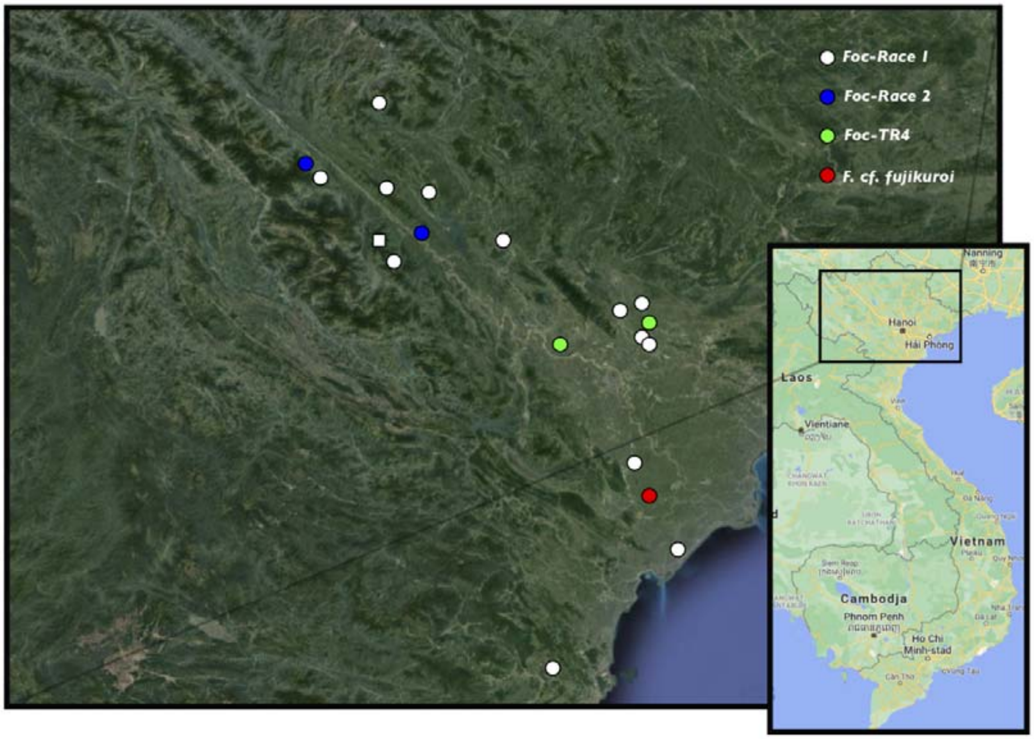

Fig. 2. A. Overall view of a banana plant infected by *Fusarium* wilt, B. Detailed view of wilted plant. C. Radial cutting of *Fusarium* infected banana pseudostem. D. Tangential cutting of *Fusarium* infected banana pseudostem.


A
B
C
D

Fig. 3. Maximum Likelihood topology obtained via heuristic search algorithm of the combined *rpb1*, *rpb2* and *tef1a* data matrix. Bootstrap support (ML-BS) values above 50 are indicated with a dot, ML-BS values above 75 are indicated with an asterisk. No indication above the branches indicates a ML-BS value below 50. Newly included accessions are indicated in red. FOSC: *Fusarium oxysporum* species complex, FFSC: *Fusarium fujikuroi* species complex.

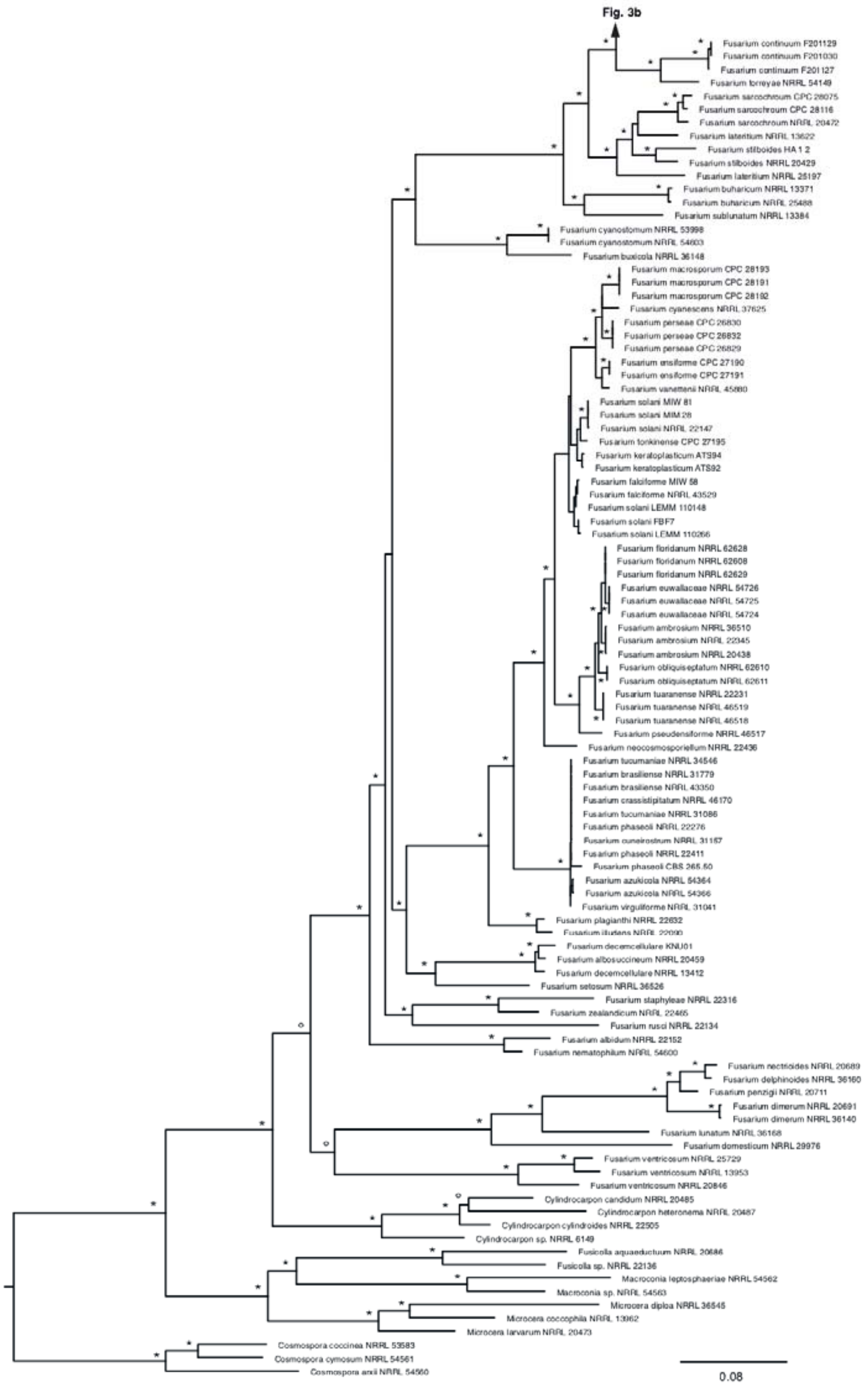
Fig. 3b
Fusarium continuum F201129
Fusarium continuum F201030
Fusarium continuum F201127
Fusarium torreyae NRRL 54149
Fusarium sarcochroum CPC 28075
Fusarium sarcochroum CPC 28116
Fusarium sarcochroum NRRL 20472
Fusarium lateritium NRRL 13622
Fusarium stilboides HA 1 2
Fusarium stilboides NRRL 20429
Fusarium lateritium NRRL 25197
Fusarium buharicum NRRL 13371
Fusarium buharicum NRRL 25488
Fusarium sublunatum NRRL 13384
Fusarium cyanostomum NRRL 53998
Fusarium cyanostomum NRRL 54603
Fusarium buxicola NRRL 36148
Fusarium macrosporum CPC 28193
Fusarium macrosporum CPC 28191
Fusarium macrosporum CPC 28192
Fusarium cyanescens NRRL 37625
Fusarium perseae CPC 26830
Fusarium perseae CPC 26832
Fusarium perseae CPC 26829
Fusarium ensiforme CPC 27190
Fusarium ensiforme CPC 27191
Fusarium vanettenii NRRL 45880
Fusarium solani MIW 81
Fusarium solani MIM 28
Fusarium solani NRRL 22147
Fusarium tonkinense CPC 27195
Fusarium keratoplasticum ATS94
Fusarium keratoplasticum ATS92
Fusarium falciforme MIW 58
Fusarium falciforme NRRL 43529
Fusarium solani LEMM 110148
Fusarium solani FBF7
Fusarium solani LEMM 110266
Fusarium floridanum NRRL 62628
Fusarium floridanum NRRL 62608
Fusarium floridanum NRRL 62629
Fusarium euwallaceae NRRL 54726
Fusarium euwallaceae NRRL 54725
Fusarium euwallaceae NRRL 54724
Fusarium ambrosium NRRL 36510
Fusarium ambrosium NRRL 22345
Fusarium ambrosium NRRL 20438
Fusarium obliquiseptatum NRRL 62610
Fusarium obliquiseptatum NRRL 62611
Fusarium tuaranense NRRL 22231
Fusarium tuaranense NRRL 46519
Fusarium tuaranense NRRL 46518
Fusarium pseudensiforme NRRL 46517
Fusarium neocosmosporiellum NRRL 22436
Fusarium tucumaniae NRRL 34546
Fusarium brasiliense NRRL 31779
Fusarium brasiliense NRRL 43350
Fusarium crassistipitatum NRRL 46170
Fusarium tucumaniae NRRL 31086
Fusarium phaseoli NRRL 22276
Fusarium cuneirostrum NRRL 31157
Fusarium phaseoli NRRL 22411
Fusarium phaseoli CBS 265.50
Fusarium azukicola NRRL 54364
Fusarium azukicola NRRL 54366
Fusarium virguliforme NRRL 31041
Fusarium plagianthi NRRL 22632
Fusarium illudens NRRL 22090
Fusarium decemcellulare KNU01
Fusarium albosuccineum NRRL 20459
Fusarium decemcellulare NRRL 13412
Fusarium setosum NRRL 36526
Fusarium staphyleae NRRL 22316
Fusarium zealandicum NRRL 22465
Fusarium rusci NRRL 22134
Fusarium albidum NRRL 22152
Fusarium nematophilum NRRL 54600
Fusarium nectrioides NRRL 20689
Fusarium delphinoides NRRL 36160
Fusarium penzigii NRRL 20711
Fusarium dimerum NRRL 20691
Fusarium dimerum NRRL 36140
Fusarium lunatum NRRL 36168
Fusarium domesticum NRRL 29976
Fusarium ventricosum NRRL 25729
Fusarium ventricosum NRRL 13953
Fusarium ventricosum NRRL 20846
Cylindrocarpon candidum NRRL 20485
Cylindrocarpon heteronema NRRL 20487
Cylindrocarpon cylindroides NRRL 22505
Cylindrocarpon sp. NRRL 6149
Fusicolla aquaeductuum NRRL 20686
Fusicolla sp. NRRL 22136
Macroconia leptosphaeriae NRRL 54562
Macroconia sp. NRRL 54563
Microcera diploa NRRL 36545
Microcera coccophila NRRL 13962
Microcera larvarum NRRL 20473
Cosmospora coccinea NRRL 53583
Cosmospora cymosum NRRL 54561
Cosmospora arxii NRRL 54560
0.08

Fig. 3. continuation

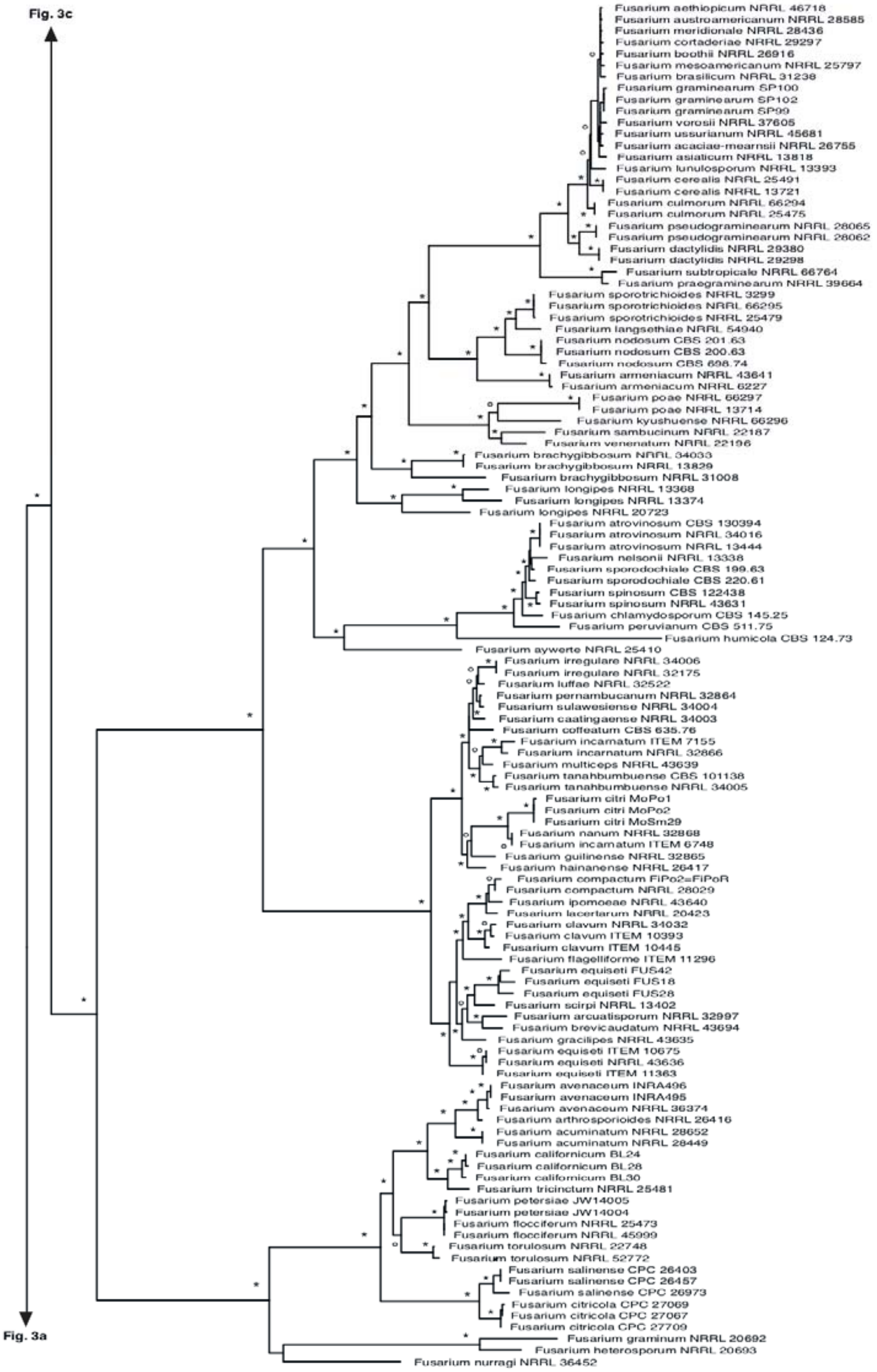

Fig. 3. continuation

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