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Genetic Diversity of Fusarium Wilt Disease of Banana

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Abstract

Bananas and plantains (*Musa* spp.) represent the fourth most important crop in the world. In 2017, an area of 5,637,508 hectares and a production of 153 million tons were reported. Fusarium wilt caused by the fungus *Fusarium oxysporum* f. sp. *cubense* (Foc), is considered one of the most destructive diseases of bananas and plantains worldwide. The pathogen *Foc* causes a typical wilt syndrome on infected plants, it has a saprophytic and parasitic phase in its life cycle. Fusarium wilt is a “polycyclic” disease. This pathogen shows a relatively diverse population genetic structure for a fungus apparently of asexual reproduction and is composed of different evolutionary lineages, which has 24 groups of vegetative compatibility (VCGs), two clades and nine clonal lineage. Foc is a genetically diverse pathogen, although the available evidence so far indicates that it does not use the mechanisms of sexual reproduction, such as recombination, to increase its genetic diversity. Furthermore, the population of this fungus in Southeast Asia shows a high degree of variation, suggesting that Foc lineages evolved together with their hosts in Southeast Asia. Alternatively, it has been suggested that Foc has multiple independent evolutionary origins, both within and outside of the Musaceae origin center.

Keywords: genetics, diversity, fusarium wilt disease, banana

1. Introduction

Bananas and plantains (*Musa* spp.) represent the fourth most important crop in the world, since only rice, wheat and corn surpass it [1]. The fruit has a high content of carbohydrates, potassium, phosphorus, magnesium, vitamins A and C, folic acid and tannins [2]. This fruit is produced throughout the year. Therefore, we can always consume bananas, regardless of the month we are in.

These crops are produced in 135 countries in the tropical and subtropical regions. India contributes 31% of the total, followed by China with 10% and the Philippines with 9% of world production. In 2017, an area of 5,637,508 hectares and a production of 153 million tons were reported, with the main exporting countries being Ecuador, Costa Rica, the Philippines, Guatemala and Colombia, who ship their products to the United States, Canada, Europe, Russia, and the Asian Pacific region. The commercialization of this fruit represents an important source of income for the Latin American region. Most of the producers are farmers

who grow it for domestic consumption or for local markets and only 15 percent of production is for export [3].

The production of bananas and plantains is seriously affected by various phytopathogenic agents, such as fungi, nematodes, viruses, bacteria, and insects. Some of the pathogens spread during the distribution of Musaceae germplasm native to Southeast Asia occurred in the 20th century to new agricultural areas (Latin America and the Caribbean), since by nature their spread occurs on a smaller scale and hardly at long distances [1].

Fusarium wilt caused by the fungus *Fusarium oxysporum* f. sp. *cubense* (Foc), is considered one of the most destructive diseases of bananas and plantains worldwide [4, 5]. The disease greatly hinders the production mainly of the genotypes of *Musa acuminata*, *M. balbisiana*, *M. schizocarpa* and *M. textilis* and their hybrids [4, 6].

Once Foc enters the fields, it is difficult to control; this is due to the fact that the pathogen persists in the soil for long periods. This is the reason because the use of plants derived from tissue culture have been considered as one of the disease management strategies, this in order to avoid the introduction of Foc in pathogen-free fields; as well as the implementation of safety practices to avoid its dispersion [5]. However, the most effective means of controlling the disease is the replacement of susceptible cultivars by those who are resistant, although today the main markets demand the 'Giant Dwarf' clone from the Cavendish subgroup.

History indicates that the pathogen probably originated in Southeast Asia; however, the first report was in Australia in 1876 affected by the cultivar 'Silk', also known as 'Manzano' (AAB) [4] and in 1890 it occurred in plantations in Costa Rica and Panama. About 30,000 hectares were lost in this country between 1940 and 1960 [4]. In total, it was estimated that more than 40,000 hectares of bananas were lost in a 50-year period in Central and South America [4, 7]. Also, epidemics have been reported on other continents. For example, in Bali, banana production decreased from 134,000 to 54,000 tons in 1997, due to the disease [8].

Given the damage caused by Fusarium wilt, there is a probability that the pathogen could be distributed through the planting material (corms or suckers) of 'Gros Michel', since this was used for use in new plantations [4, 9]. At that time, large shipments of suckers and rhizomes may also have been transported between countries by transnational companies to supplement local stocks of commercial cultivars, thereby promoting the spread of disease. The stage was set for a major epidemic to emerge [10].

2. Banana importance

Banana and plantain (*Musa* spp.) are believed to have originated in Southeast Asia and are cultivated in a wide variety of environments in the tropics and subtropics regions of the world. *Musa*, including the dessert banana and the cooking types or plantains are produced in 155 countries.

Throughout history *Musa* has provided humans with food, medicine, clothing, tools, shelter, furniture, paper, and handicrafts. *Musa* are rich in vitamin C, B6, minerals (particularly potassium), and dietary fiber. They are also a rich energy source, with carbohydrates accounting for 22% and 32% of fruit weight for banana and plantain, respectively. It is cholesterol free, high in fiber, and low in sodium.

In terms of total fruit crops production, the banana ranks after oranges, grapes, and apples, but when plantain production is added, it becomes the world's number one fruit crop. According to the Food and Agriculture Organization of the United Nations (FAO), in 2018 more than 11.3 million hectares of banana and plantain were harvested worldwide and were produced a total of 155.2 million tonnes:

Rank	Country/territory	Production (tonnes)
1	India	30,808,000
2	China	11,221,700
3	Philippines	9,358,785
4	Colombia	7,287,997
5	Indonesia	7,264,383
6	Ecuador	7,157,603
7	Brazil	6,752,171
8	Cameroon	5,144,258
9	Congo, Democratic Republic of the	5,066,203
10	Uganda	4,337,747
11	Guatemala	4,294,121
12	Ghana	4,264,258
13	Tanzania	4,045,568
14	Angola	3,492,184
15	Nigeria	3,093,872
16	Costa Rica	2,633,788
17	Mexico	2,354,479
18	Peru	2,329,480
19	Cote d'Ivoire	2,280,368
20	Dominican Republic	2,224,403

Source: <http://www.promusa.org/Banana-producing+countries+portal>

Table 1.
Top 20 of banana-producing countries and overseas territories.

115.7 million tonnes under their bananas crop item (75%) and 39.5 million tonnes under their plantains crop item (25%). However, the estimated production for the same year published by [11] is 139.5 million tonnes: 79.6 million tonnes of Cavendish (57%), 17.5 million tonnes of other dessert bananas (13%), 20.9 million tonnes of Plantain (15%), and 21.4 million tonnes of other cooking bananas (15%).

In the **Table 1**, the list of top 20 of banana-producing countries and overseas territories and the number of tonnes they each produced in 2018 is showed. Production is measured in tonnes and represent the total of the bananas and plantains categories into, according FAO statistics.

3. Fusarium wilt caused by the fungus *Fusarium oxysporum* f. sp. *cubense* (Foc)

Fusarium is a genus comprises several species of filamentous ascomycetes, including pathogenic and non-pathogenic species for agricultural crops. One of the best known is *F. oxysporum*, this causes vascular wilt and root rot in more than 100 plant species [12].

In the *Fusarium* system, Foc belongs to the *Fusarium oxysporum* species complex (FOSC), four clades have been identified from this, using the translational elongation factor 1-alpha (*tef1*) and the rDNA of the mitochondrial subunit (*mtssu*), in Foc isolates, which were grouped as baseline lineage [13].

The pathogenic isolates of *F. oxysporum* have been classified in more than 100 special forms. Members of a special form usually cause disease in a particular range of host species, with some special forms capable of colonizing a wider range of plants [14]. A special form can be subdivided into races based on characteristic virulence patterns in differential host cultivars [15].

Taxonomic classification:

Domain: Eukaryota

Kingdom: Fungi

Phylum: Ascomycota

Class: Ascomycetes

Subclass: Sordariomycetidae

Order: Hypocreales

One of the most devastating special forms is responsible for Fusarium wilt of bananas and plantains [9], which is caused by *Fusarium oxysporum* Schlecht. f. sp. *cubense* (E.F. Smith) Snyder & Hansen, who lives in the soil. The sexual phase (teleomorphic) of the fungus is unknown and cannot be distinguished morphologically between different strains. This pathogen produces three types of asexual spores, these are macroconidia, microconidia and chlamydospores, which function as mechanisms of dispersal, reproduction and survival [16].

The microconidia ($5\text{--}16 \times 2.4\text{--}3.5 \mu\text{m}$) are oval in shape and consist of a single cell, generally without septa, may be oval, elliptical to reniform, and develop abundantly on false heads on short monophialides. While macroconidia ($27\text{--}55 \times 3.3\text{--}5.5 \mu\text{m}$) are abundant, slightly curved, and relatively thin, they have 4–8 cells, with 3–5 septa (generally 3 septa) see **Figure 1A**. The apical cell is attenuated or hook-shaped in some isolates. The basal cells are shaped like a foot. Macroconidia develop into single hyphal fialids (**Figure 1B**). Micro and macroconidia occur on branched or unbranched monophial cuts [17, 18].

Chlamydospores ($7\text{--}11 \mu\text{m}$ in diameter) are generally globose and form individually or in pairs, they are abundantly formed in hyphae or conidia, single or in chains, generally in pairs, this type of spores constitutes resistance structures of the fungus, These have thick cell walls, and their production is abundant on infected tissues in advanced stages of the disease [4]. They can be interspersed or in the terminal part of the hyphae [17].

Figure 1.
Reproductive structure of *Fusarium oxysporum* f.sp. *cubense* (A) Microconidia y (B) Macroconidia.

Figure 2.
 Colony morphotypes of *Fusarium oxysporum* f. sp. cubense isolated from bananas and plantains in different states of Mexico.

In vitro development of the pathogen onto potato dextrose agar (PDA) culture medium, has a variable morphology, its growth is 4 to 7 mm per day at 24°C, forming colonies with abundant aerial mycelium and variable color pigmentation from white, salmon to pale violet. In general, the *F. oxysporum* strains cannot be morphologically distinguished between different races or groups of vegetative compatibility (VCGs). The fungus *F. oxysporum* generally produces black to violet sclerotia, while the pigmentation of the colonies is pale violet to dark red on PDA culture media [9, 19], as shown on **Figure 2**.

Some isolates rapidly mutate from pionnotal (with abundant fatty or shiny aggregates of conidia) to a flat, moist pale yellowish-white to peach mycelium grown on a PDA culture [9, 19].

4. Symptomatology

The pathogen *Fusarium oxysporum* f.sp. cubense causes a typical wilt syndrome on infected plants, it has a saprophytic and parasitic phase in its life cycle. It begins as a saprophyte in the soil as chlamydospores, which are dormant and immobile until plant exudates stimulate their germination to spread towards the roots [9]. These germinated chlamydospores develop a thallus that produces conidia after 6–8 hours. The conidia germinate and adhere to the roots of the host plant where they penetrate the epidermal cells and then invade and colonize the vascular system [20, 21].

After successfully infecting the roots, the pathogen grows towards the rhizome and pseudostem, causing a deficiency in the absorption of water and consequently an eventual wilting of the leaves and finally causing the death of the plant [9, 16]. This pathogen has the ability to invade all the organs of the plant with the exception of the fruit [16].

Externally, the first signs of the disease are usually wilting and yellowing of the older leaves around the margins (**Figure 3A**), the older chlorotic leaves collapse (**Figure 3B**), the old leaves hang down and dry forming a skirt (**Figure 3C**), the suckers are shown asymptomatic (**Figure 3D**), while internally the vascular bundles of the pseudostem turn reddish brown (**Figure 3E**), the corm shows an abnormal dark brown discoloration (**Figure 3F**), the base of the pseudostem shows fissures (**Figure 3G**) and the midrib of the leaves shows a dark brown discoloration (**Figure 3H**) [5, 6, 9].

To better understand the process of the Foc-banana interaction, some investigations have emerged using isolates transformed from Foc with the gene for the

Figure 3. External and internal symptoms caused by *Fusarium oxysporum f.sp. cubense* in banana and plantain plants (*Musa spp.*). Chlorosis in older leaves around the margins (A). Older leaves collapsed (B). Hanging and dried leaves forming a skirt (C). Asymptomatic children (D). Reddish-brown vascular bundles of the pseudostem (E). Corm with abnormal dark brown discoloration (F). Fissures at the base of the pseudostem (G). Central rib with dark brown discoloration (H).

green fluorescent pigment (GFP), with the aim of studying the movement of the pathogen from the soil towards the roots and rhizome [22, 23].

Recently [24], using GFP they demonstrated the movement of the pathogen before the appearance of external symptoms, as well as the presence of inoculum on the external surface of the veins of senescent or decomposing leaves, followed by the substantial production of macroconidia and chlamydospores, these results demonstrate that there may be serious implications regarding the spread of the pathogen. In addition, chlamydospore production occurs inside and outside the veins of the leaves, which increases the risk of spores returning to the ground through leaf removal. Also, it was possible to identify the progress of the pathogen in the pseudostem before the development of external symptoms. The authors suggest that future studies are required on the possible wind-borne spread of inoculum and the potential of the pathogen to infect a healthy plant through aerial inoculation.

5. Epidemiology

Fusarium wilt is a “polycyclic” disease. However, several cycles of infection can occur in affected banana plantations. Losses can eventually develop, even when very small amounts of the pathogen inoculum manage to infest fields and the disease is initially of little concern to growers [6]. For example, the first outbreaks of TR4 reported in China and the Philippines were not taken with great importance; this resulted in devastation and uncontrollable problems in the affected plantations [25].

In addition to prevention, early recognition and rapid containment of a disease outbreak is necessary to prevent epidemic development. A good understanding of the key factors responsible for the development of the disease is required when designing practical protocols for the destruction of infected plants, the treatment of the surrounding infested soil, and the reduction of inoculum in plant residues and soil [26].

Foc was shown to have the ability to survive for decades in infested soil, as “Gros Michel” production was generally impossible in plantations previously affected by Foc [9]. Chlamydospores of Foc in dead host material play a role in their survival, but their persistence for long periods is probably due to their ability to infect weed species [6]. For example, in studies in tropical America and Australia, Foc was isolated from the roots of various weed species (*Chloris inflata*, *Euphorbia heterophylla*, *Tridax procumbens*, *Cyanthillium cinereum*, *Commelina diffusa*, *Ixophorus unisetus*, *Panicum purpurascens*, *Cyperus luzulae*, *Paspalum fasciculatum*), present in banana plantations that were affected by R1 and TR4 [27]; however, these are asymptomatic and their presence in banana fields could be of high risk and therefore it is important to carry out a targeted control to reduce their presence. Foc’s ability to survive in the absence of its host is an important factor in the management of this disease [6].

Foc has been shown to spread in various ways, with infected suckers being the most efficient, since they are the most used as vegetative material for new plantations [9]. In many cases, the suckers are washed and treated with fungicides. However, infected suckers were the main material before tissue culture seedlings were available [6], being practically impossible to establish plantations free of the pathogen. However, even after it was possible to produce tissue culture material, secondary contamination of plantations by Foc was common. For example, TR4-affected Cavendish plantations were routinely established with tissue culture seedlings [6].

Foc has the ability to spread in the soil, which indirectly contaminates in and around plantations, but unfortunately it is also used in nurseries for the propagation of seedlings used for field establishment [25]. Surface waters are easily polluted and use for irrigation of polluted river or pond water is highly risky. In addition, Foc is spread by contaminated tools (shovels, machetes, hoes, etc.), agricultural machinery, clothing and footwear [9, 28]. Any or all of these ways can facilitate the spread of Foc in and around a plantation, and may be possible through other means [6, 28].

Studies carried out in Australia detected TR4 spores in the exoskeletons of the banana weevil (*Cosmopolites sordidus*) and suggested that the insect could be a predisposing agent as a vector of the disease [29].

The recent transcontinental disseminations of TR4, suggest that something other than vegetative material (suckers) was responsible for these long-distance disseminations. Although these outbreaks may have been the result of something as simple as workers' boots impregnated with soil contaminated by Foc spores from plantations in Southeast Asia, or some other means could be responsible such as the entry of machinery from affected areas. Better knowledge is needed to understand the long-distance spread of this pathogen [6].

6. Genetic diversity and evolution of *Fusarium* wilt of bananas

Fusarium oxysporum Species Complex (FOSC) are widely distributed and it is mostly non-pathogenic and it is commonly found in roots and soil associated fungus in asymptomatic crop plants. It has been found to be associated with plants as endophyte, saprophyte or just latent in agro-ecosystems [30]. Both, studies on FOSC isolated from non-cultivated species and from cultivated crops have reported a considerable variability based on the morphology of the asexual reproductive structures [31] and latter at the DNA sequence [32, 33]. Understanding its genetic variability is relevant to implement an earlier detection system and implement a proper disease surveillance program.

Recent studies on molecular genetics of *Fusarium* from cultivated plants have shown a high diversity and this variation relays on environmental conditions and are classified in groups and vegetative compatible groups (VCG) as described latter in this chapter. *Fusarium* has evolved heavily depending on its interaction with plant genotypes, such is the case for both 'tropical' and 'subtropical' race 4, which attacks different cultivars, depending of the geographical region [34] as well as for those FOSC from non-cultivated species [30].

Knowledge of the genetic diversity of populations of phytopathogenic fungi and their mode of reproduction are important for the application of management strategies, this with the aim of reducing the impact of the disease [35]. In the case of Foc, this pathogen shows a relatively diverse population genetic structure for a fungus apparently of asexual reproduction and is composed of different evolutionary lineages [33], which has 24 groups of vegetative compatibility (VCGs, VCG0120 to VCG0126 and VCG0128 to VCG01224) distributed worldwide [34, 36–40].

However, in recent samplings in Latin America it was possible to identify 20 new VCGs (new VCG 1 to new VCG 20), these were distributed over the three main clades (clade 1, clade 2 and clade 3), these results show that the majority of the new VCG are grouped in clade 3 and these originate from Latin America [41], this supports the hypothesis on the evolution of Foc, in which it is mentioned that the local populations of *F. oxysporum* evolved and they became pathogenic in the introduced bananas [36, 42–44].

Studying VCGs has been a useful means of subdividing Foc into genetically isolated groups, but it does not, however, measure the genetic relationship between

the isolates. Furthermore, VCG are phenotypic markers that can undergo a selection process. Direct identification of VCG is a relatively objective, but time-consuming test, and the results indicate genetic similarity rather than genetic difference [31]. Therefore, VCGs represent good phenotypic traits for assessing diversity within populations, but the genetic relationships between VCGs must be assessed using other molecular tools.

Fourie and collaborators [39], classified Foc into two clades, clade 1 and clade 2, these based mainly on their evolutionary origins. In the case of clade A, the Foc groups that co-evolved with bananas of genome A belong, while those that belong to clade B evolved with their hosts having genome B or both genome A and genome B.

The teleomorph for Foc has never been reported and the pathogen is likely to manifest mutations or parasexualism, as the main basis for its genetic diversity. Although PCR analysis has shown the presence of both MAT idiomorphs, therefore the pathogen can potentially reproduce by sexual means.

The race concept has been widely used in the *F. oxysporum* classification system by plant pathologists. Based on the published data, it can be inferred that the Foc-TR4 isolates recently evolved from the predecessors in Foc-R1. Foc-R1 showed greater phylogenetic diversity than Foc-TR4. Once established, both races apparently co-evolved in the same region, which means that possible horizontal gene transfer could be involved in the high level of diversity seen in Foc-R1, as well as in the appearance of Foc-TR4.

Three races of Foc are known; but nevertheless, the term race is used in a less formal way in relation to this pathosystem (*Musa*-Foc), since the genetic bases of susceptibility and resistance have not yet been characterized. The Foc races currently described refer to strains of the pathogen, which have been found to be pathogenic to specific cultivars in the field [9, 38]. For example, race (R1) is pathogenic to cultivars of 'Silk', 'Manzano' (AAB) and 'Gros Michel' (AAA). While race 2 (R2) is pathogenic to cooking bananas such as 'Bluggoe' and 'Pear' (ABB) and race 4 (R4) affects all cultivars of the Cavendish subgroup (AAA) and those susceptible to R1 and R2 [4, 5, 45]. Previously, a population of *Fusarium oxysporum* in Central America was considered as race 3 causing wilt in *Heliconia* spp., but is no longer considered to be part of Foc [5].

A Foc race 4 variant was reported in Taiwan affecting Cavendish cultivars in the tropics in 1967 [4, 38]. Therefore, it was necessary to separate the populations that only affected Cavendish cultivars in the subtropics from those populations that affected in the tropics, so two divisions of Foc R4 were generated: race 4 subtropical (STR4) and race 4 tropical (TR4) [38], however, TR4 was pathogenic under tropical and subtropical conditions affecting Cavendish cultivars [25, 39]. In the case of VCGs, they have been associated with STR4 (0120, 01201, 01202, 01209, 01210, 01211, 01215, 0120/15; 0129/11), while only one VCG to TR4 (01213/16) [25, 40].

Visser and collaborators [46], carried out a study on the characterization of tropical Foc race 4 populations affecting 'Cavendish' plantations in South Africa. Only VCG 0120 and idiomorph MAT-2 could be identified, while phylogenetic analysis of the TEF sequence revealed that the isolates from South Africa were pooled with other isolates belonging to VCG 0120 from Australia and Asia. Suggesting, the introduction and dispersal mainly by infected material within the country.

In Latin America and the Caribbean, the composition of the populations has been limitedly studied. For example, the Cuban populations belong to VCG 01210 (mostly race 1), 0124, 0124/0125 and 0128 (mostly race 2); the isolates did not produce lacinias in K2 medium and the production of volatiles was independent of the race, while in Venezuela VCG 01215 and race 1 are reported. A study using AFLP markers grouped VCG 01210 into a subgroup and showed the presence of common

alleles with VCG 0124 [47]. On the other hand, the pathogenicity studies with representative isolates of each VCG in Cuba, showed a differentiated aggressiveness on different clones between VCG 0124 and 0128, belonging to race 2, indicating lack of genetic sense in the racial classification. It is required to determine in Latin America and the Caribbean the VCG present in the different countries and the pathogenic relationships between them.

In order to better understand how races 1 and 4 are related, genome and transcriptome analysis of *F. oxysporum* f. sp. *cubense* has shown common sequences of single-copy genes from Race 1 and Race 4, showing that there is a close relationship and suggesting that they share a common ancestor. Furthermore, a comparative genomics study among *F. oxysporum* f. sp. *licoperici*, *F. graminearum* and *F. verticillioides* showed that there is transfer of lineage-specific (LS) genomic regions that have pathogenicity related genes with distinct evolutionary profiles, indicative of horizontal acquisition and suggesting that there is transfer of LS chromosomes between genetically isolated *Fusarium* species. This is of high relevance and of particular concern for agricultural systems, because non-pathogenic *F. oxysporum* strains that are already endophytic to crop plants could suddenly become pathogenic [48] and give origin to new pathogenic lineages of *F. oxysporum*. It is clear that in the last decade a large amount of DNA sequence information has been published on *F. oxysporum*, but there is a lack of consistency in the data and a larger study needs to be conducted in which DNA sequences of isolates from non-cultivated species is included and even from *Fusarium* species that are thought not to be related.

Foc genetic diversity studies were initiated using various molecular methods, including random amplified polymorphic DNA markers (RAPDs) [49]; Restriction Fragment Length Polymorphisms (RFLP) [43]; Amplified fragment length polymorphism (AFLP) [50]; DNA sequence analysis [32, 44]; microsatellites or simple repetitive sequences [51]; simple repetitive inter sequence (ISSR) [52]. These studies showed that the population of this fungus in Southeast Asia shows a high degree of variation, suggesting that the Foc lineages evolved together with their hosts in Southeast Asia.

Alternatively, Foc has been suggested to have multiple independent evolutionary origins, both within and outside the *Musa* genetic center [36]. Using the phylogenetic genealogical approach, [32] identified five Foc-independent genetic lineages in a global population. Using a similar approach and additional data, [44] found three additional lineages. However, none of these studies included Indonesian populations, and therefore there is only limited information available on Foc diversity at the center of origin of bananas.

F. oxysporum f.sp. *cubense* probably coevolved with its host species within its center of origin [32, 36, 44]. For example, various studies that have used deoxyribonucleic acid (DNA) markers have revealed the polyphyletic origin of Foc and the separation of two main clades and eight to ten lineages, as some VCGs are taxonomically closer to other special forms of *F. oxysporum* than some Foc VCGs [32, 36, 42, 44, 50, 53].

Furthermore, strains belonging to various VCGs infect particular banana cultivars and, therefore, were grouped in the same race, suggesting that the pathogenicity towards a specific cultivar evolved in a convergent way [32, 38, 44] or as a result of horizontal gene transfer between members of the *F. oxysporum* complex [48, 54].

High resolution genotyping sequencing analyzes using (DArTseq) validated and expanded these findings [55]. According to the DArTseq markers of 24 Foc strains (representing all the known VCG so far) they were divided into two groups. These results strongly corroborate the clades mentioned in previous studies, except VCG0123, VCG01210, VCG01212 and VCG01214, which were occasionally grouped into opposing clades, VCG 01221 and 01224, which were never classified before but now clearly belong to clade 2 [55].

In the advent of high throughput DNA sequencing technology [56] has allowed scientist to better understand the molecular weaponry used by this pathogen. The pathogen molecular tools include genes involved in root attachment, cell degradation, detoxification of toxins produced by the plant's defense mechanism and signal transduction, among others [16]. In Ref. [57], the authors have reported a predicted genome size for several *F. oxysporum* f. sp. *cubense* with a size of 48.56 Mb for Foc Race 1 and 48.81 for Foc Race 4, comprising and estimated of 15,865 and 14,506 genes, respectively. This genome information was compared and aligned to 11 of the 15 chromosomes contained in *F. oxysporum* f. sp. *licopersici*, including those regions reach in transposable elements; which might explain its high genetic variability and lack of chromosome stability [57].

Recently, in a study samples of musaceae with wilt symptoms were collected in the regions of Indonesia, Java, Sumatra, Kalimantan, Sulawesi, Papua and Nusa Tenggara, this demonstrated by phylogenetic analysis that the Foc lineages were genetically different, and it was achieved to identify 11 new species of *Fusarium* affecting musaceae, these were: *Fusarium cugenangense*, *F. duoseptatum*, *F. gros-michelii*, *F. hexaseptatum*, *F. kalimantanense*, *F. odoratissimum*, *F. phialophorum*, *F. purpurascens*, *F. sangayamense*, *F. tardichlamydosporum*, and *F. tardicrescens*, placing them in the Banana *Fusarium* Complex (FOBC), as well as showing that *F. odoratissimum* II-5 comprises TR4 [58].

7. Conclusions

Fusarium wilt disease of banana caused by soil-born pathogen *Fusarium oxysporum* f.sp. *cubense* (Foc) is considered of the most destructive diseases of bananas and plantains worldwide. Foc produces three types of asexual spores, these are macroconidia, microconidia and chlamydospores, which function as mechanisms of dispersal, reproduction and survival. Foc is a genetically diverse pathogen, although the available evidence so far indicates that it does not use the mechanisms of sexual reproduction, such as recombination, to increase its genetic diversity. Furthermore, the population of this fungus in Southeast Asia shows a high degree of variation, suggesting that Foc lineages evolved together with their hosts in Southeast Asia. Alternatively, it has been suggested that Foc has multiple independent evolutionary origins, both within and outside of the Musaceae origin center. Actually, more than 24 vegetative compatibility groups and three races have been reported. This genetic diversity is accommodated in two large clades and nine clonal lineages.

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