Improvements in the Resistance of the Banana Species to Fusarium Wilt: A Systematic Review of Methods and Perspectives

Anelita de Jesus Rocha 1,†, Julianna Matos da Silva Soares 1,†, Fernanda dos Santos Nascimento 1,†, Adriana Souza Santos 2,†, Vanusia Batista de Oliveira Amorim 3, Claudia Fortes Ferreira 3, Alfredo Souza Santos 2, Vanusia Batista de Oliveira Amorim 3, Claudia Fortes Ferreira 3, Fernando Haddad 3, Janay Almeida dos Santos-Serejo 3 and Edson Perito Amorim 3,∗

1 Department of Biological Sciences, State University of Feira de Santana, Feira de Santana 44036-900, Bahia, Brazil; anelitarocha@gmail.com (A.d.J.R.); juliannamatos91@gmail.com (J.M.d.S.S.); feel.20@hotmail.com (F.d.S.N.)
2 Bahia Education Secretary, Salvador 41745-004, Bahia, Brazil; adriadna_souza@yahoo.com.br
3 Embrapa Cassava and Fruit, Cruz das Almas 44380-000, Bahia, Brazil; vanusiaamorim50@gmail.com (V.B.d.O.A.); claudia.ferreira@embrapa.br (C.F.F.); fernando.haddad@embrapa.br (F.H.); janay.serejo@embrapa.br (J.A.d.S.-S.)
∗ Correspondence: edson.amorim@embrapa.br; Tel.: +55-75-3312-8058; Fax: + 55-75-3312-8097
† Authors contributed equally to this manuscript.

Abstract: The fungus Fusarium oxysporum f. sp. cubense (FOC), tropical race 4 (TR4), causes Fusarium wilt of banana, a pandemic that has threatened the cultivation and export trade of this fruit. This article presents the first systematic review of studies conducted in the last 10 years on the resistance of Musa spp. to Fusarium wilt. We evaluated articles deposited in different academic databases, using a standardized search string and predefined inclusion and exclusion criteria. We note that the information on the sequencing of the Musa sp. genome is certainly a source for obtaining resistant cultivars, mainly by evaluating the banana transcriptome data after infection with FOC. We also showed that there are sources of resistance to FOC race 1 (R1) and FOC TR4 in banana germplasms and that these data are the basis for obtaining resistant cultivars, although the published data are still scarce. In contrast, the transgenics approach has been adopted frequently. We propose harmonizing methods and protocols to facilitate the comparison of information obtained in different research centers and efforts based on global cooperation to cope with the disease. Thus, we offer here a contribution that may facilitate and direct research towards the production of banana resistant to FOC.

Keywords: Musa spp.; Fusarium oxysporum f. sp. cubense; genetic improvement; resistance; state-of-the-art

1. Introduction

Dessert bananas and plantains are very popular fruits worldwide. In 2018, approximately 116 million tons of bananas and 40 million tons of plantains were produced [1]. In terms of exports, bananas are among the most traded fruits globally, with almost 23 million tons (except for plantains) exported in 2017, representing almost 20% of global production [1]. Approximately 11.3 million hectares are dedicated to banana and plantain production worldwide, and there are more than 1000 varieties produced and consumed locally [2]. The Cavendish banana, which accounts for about 47% of global production, is the most traded [2]. In African regions, plantains comprise a significant and essential component, contributing considerably to food security and income generation for more than 70 million Africans [3–5]. Similarly, in Latin America and the Caribbean, 62% of total banana and plantain production (20 million tons) is consumed locally, and approximately
6.8 million tons of plantains are produced, of which 72% are traded on international markets, indicating the enormous importance of these crops for local food and food security throughout the region [6,7].

Among banana improvement programs’ objectives are achieving cultivars resistant to abiotic stressors, such as salinity [8,9] and drought [10–12]. Another major challenge for the global production of Musaceae species is the development of cultivars resistant to biotic stressors, represented by their primary pests, the banana root borer (Cosmopolites sordidus) and the nematodes Meloidogyne spp., Pratylenchus coffeae, and Radopholus similis [13–19], and disease-causing pathogens, including banana bunchy top virus (BBTV) [20,21], Xanthomonas vasicola pv. musacearum causing bacterial wilt [22–25], Pseudocercospora fijiensis causing black Sigatoka [26–29], and Fusarium oxysporum f. sp. cubense (FOC) causing Fusarium wilt [30–33].

FOC is one of the main biotic stress factors affecting bananas and _Fusarium_ wilt is considered the most destructive and widely spread disease in the banana-producing regions around the world [34,35]. The causal agent is a soilborne fungus apparently considered hemibiotrophic; therefore, it initially establishes in a biotrophic relationship interacting with live plant cells of the host, and then in its necrotrophic phase, the host’s tissues are dead [30]. Frequently FOC persists in cultivated areas for years due to it is survival phase when it then interacts as saprophytic in cultural remains or produces resting spores known as chlamydospores besides surviving and multiplying in alternative hosts [30,35,36]. The disease is characterized by yellowing of the young leaves, and pseudostem splitting, and eventually death of the plant [30,37,38].

_Fusarium_ wilt epidemics caused by race 1 (FOC R1), which occurred in Central America, caused the devastation of the susceptible “Gros Michel” cultivar plantations and was one of the most severe in the history of the crop in the Americas. For this reason, Gros Michel was replaced by cultivars of the subgroup Cavendish that are resistant to FOC R1 [39–41]. However, in the late 1980s, a highly virulent strain of FOC-infected Cavendish cultivars and spread to Asia, Africa, Indonesia, and more recently to South America [30,41,42]. Currently, _Fusarium_ wilt can be considered a pandemic disease because of the spread of the tropical race 4 (FOC TR4) strain [43,44].

Chemical control is unfeasible and minimally effective, and it can be harmful to human health and the environment. Although still in its initial stages, biological control demonstrates promising results [31,45]. Low efficacy of the biological control is attributed to inherent factors to the dynamics of the disease’s primary inoculum, especially production of chlamydospores, which persists in cultivated areas, such as the capacity to survive in crop remains as an endophytic fungus in alternative hosts [30,36,46]. In addition, the genetic variability of the pathogen, resulting in new strains capable of infecting resistant cultivars, is another factor that limits the use of methods of disease management and control [47–49]. Therefore, efforts on the genetic improvement to achieve resistance to FOC R1 and FOC TR4 have been focused on finding resistant cultivars through traditional methods of germplasm selection or the generation of new cultivars by hybridization, genetic transformation, somaclonal variation, or mutation induction [31,50,51].

Until now, there are reviews available in the literature about _Fusarium_ wilt related to epidemiology and disease management [30,35,41,52–54], biological control [45,55], genetic breeding for resistance [56,57] and one review about genomic aspects of _Musa_ spp. for stress resistance [58].

The systematic reviews were mainly developed because of the need for rapid responses to human health issues, and nowadays, this tool has contributed to several study areas [59–61]. However, to our best knowledge, no systematic reviews on the genetic improvement of _Musa_ spp. to resist Fusarium wilt have been published; only studies related to water stress in _Musa_ spp. [62] and banana consumption [63]. Therefore, to provide detailed information on the subject and to collaborate with the information gathered so far, we propose a systematic approach to the studies on _Musa_ spp., with a focus on genetic improvement for resistance to the FOC pathogen, through a systematic review of studies conducted over the last 10 years.
2. Materials and Methods

The free software State of the Art by Systematic Review (StArt) v.3.3 beta 03, developed by the Federal University of São Carlos (UFSCar), was used to perform a systematic review. This tool offers systematized answers to questions directed toward the objective of the review. The review process was performed in three stages—planning, execution, and summarization—according to the review flowchart in Figure 1, which followed the model proposed by Santos et al. [62].

![Figure 1. General systematic literature review flowchart. Source: author’s compilation.](image)

2.1. Planning

A protocol to be followed during the review process was formulated, in which the title, objective, keywords, research questions, research sources, and inclusion/exclusion criteria of articles were defined during their selection and extraction. The StArt protocol is available for download at [https://doi.org/10.5281/zenodo.4555385](https://doi.org/10.5281/zenodo.4555385) (accessed on 22 February 2021). The research questions of the review are listed in Table 1.

| Research Questions                                                                 |
|-----------------------------------------------------------------------------------|
| Q1: What are the known sources of resistance (germplasm) to *Fusarium oxysporum* f. sp. *cubense*? |
| Q2: Which breeding programs work on the resistance to *Fusarium* wilt with respect to cultivar development? |
| Q3: Which genes are reported associated with resistance to *Fusarium oxysporum* f. sp. *cubense* in *Musa* spp. |
| Q4: What breeding techniques are associated with overcome *Fusarium* wilt? |
| Q5: Which biotechnological tools are used for assisted selection for resistance to *Fusarium oxysporum* f. sp. *cubense*? |
| Q6: Which germplasm collections have information with the potential for genetic improvement to *Fusarium* wilt? |
| Q7: What is the frequency of studies by country, and which programs of improvement work with crossbreeding in order to develop resistant cultivars? |
| Q8: Are there scales to assess the disease? What is the difference between them? |
| Q9: How often is the banana genome used? |

Table 1. List of questions about the genetic improvement of *Musa* for resistance to *Fusarium* wilt to be answered by a systematic review of studies carried out in the last ten years.

To answer question 7, when there was no mention in the text of the location where the study was conducted, the search criteria within the article were standardized to the corresponding author’s mailing address to obtain information from which country the studies originated.
2.2. Execution: Search

Electronic surveys were conducted on the following databases, aiming to identify publications made available between January 2010 and December 2020: Scopus (http://www.scopus.com/), Web of Science (http://apps.isiknowledge.com), PubMed Central (https://www.ncbi.nlm.nih.gov/pmc/about/intro/), Springer (https://www.springer.com/br); Coordination for the Improvement of Higher Education Personnel Portal Journal (http://www.periodicos.capes.gov.br/), and Google Scholar (https://scholar.google.com.br/schhp?hl=en&as_sdt=0,5), using a standardized search string with the following keywords: *Musa* spp. and bananas and plantains and *Fusarium* wilt or *Fusarium oxysporum* f. sp. cubense or Panama disease and genetic resistance and markers and genes. This set of terms was used for research in all fields within the articles. The Boolean operators AND and OR were used to differentiate the search terms. Search results in each base were imported into BIBTEX, MEDLINE, or RIS formats, compatible with StArt. Relevant documents not found or published after the selection stage started were added manually. We did not consider using the name *Fusarium odoratissimum* proposed by Maryani et al. [64] in our standardized search due to the low number of published articles using this new suggested nomenclature, and this would limit the number of recovered articles in the database.

2.3. Execution: Selection and Extraction

In the selection stage, the articles that contained the terms adopted in the search string in the title, abstract, or keywords were accepted. In the extraction stage, where the number of articles was restricted, a single criterion to include articles was adopted, as follows: (I) articles that answer the protocol’s questions (Table 1). The criteria used to exclude articles in the extraction stage were (E) review articles, (E) theses, dissertations, manuals, and book chapters, (E) articles outside the subject, (E) articles published in event annals, (E) articles on genetic diversity of FOC, (E) articles on disease management strategies, and (E) articles on first reports of FOC. These criteria were considered to restrict the selected articles to the focus of this review since they do not answer the proposed questions about improving the resistance of *Musa* spp. to FOC. The preferred reporting items for systematic reviews and meta-analyses (PRISMA) checklist is presented for download at https://doi.org/10.5281/zenodo.4313617 (accessed on 9 December 2020).

2.4. Analysis of the Articles

The process of analyzing the articles was based on the calculation of the frequencies of articles related to each of the research questions. Subsequently, graphs, word clouds, and tables were prepared.

3. Results

3.1. Screening of Studies

The article screening process is represented by the flow chart in Figure 2. PubMed Central contributed the largest number of articles to this review, with 806 (50%) of the total, followed by Web of Science with 361 (22%) and Google Scholar with 319 (20%). The other databases, namely Scopus, Springer, and Coordination for the Improvement of Higher Education Personnel Portal Journal, contributed 69 (4%), 26 (2%), and 8 (0.5%) articles, respectively. Moreover, 22 (1.2%) articles that were not obtained automatically were added manually (Figure 2).
We identified 1612 articles from the database tracking, of which 234 were duplicated, and 1377 were eliminated in the selection process by reading the title, abstracts, and keywords, which did not fit the purposes of the research. In the extraction stage, 308 articles were analyzed. After reading the articles entirely, 213 were eliminated; hence, 95 were selected to compose the systematic review (Figure 2). The articles selected to compose the systematic review are available for consultation and download at https://doi.org/10.5281/zenodo.4555343 (accessed on 22 February 2021) and its origin and database in Table S2.

A word cloud was generated from the keywords of the 95 articles for this review. As expected, there was a predominance of the articles with the keywords, “Fusarium oxysporum f. sp. cubense”, “Fusarium wilt”, “Musa”, “banana”, “disease”, “resistance”, “race”, tropical, and TR4 (Figure 3). Other keywords that had a remarkable frequency in the word cloud were “gene”, “Panama”, “transformation or transgenesis”, “plant”, “infection, green fluorescent protein (GFP)”, “protein”, “SCAR”, “Acuminata”, “species”, “Cavendish”, and “polymerase chain reaction (PCR)” (Figure 3).
3.2. Known Origin Sites

Among the 95 articles, 53% were from China, followed by India (15%), Australia (12%), Brazil (7%), Malaysia (5%), Indonesia (4%), Uganda (4%), and other countries with a contribution of 1% (Figure 4). In the selected articles, 10 improvement programs located in different countries were mentioned, containing information with the potential for genetic improvement for the resistance of Musa spp. to Fusarium wilt (Figure 4).

Figure 3. Word cloud generated from article keywords of selected articles to compose a systematic review on breeding Musa to Fusarium wilt. The word cloud was created in a free online generator (https://www.wordclouds.com/, accessed on 16 August 2020), based on the frequency of each keyword.

Figure 4. Frequency of articles on genetic improvement of Musa spp. to Fusarium wilt published in the last ten years in different countries and genetic breeding programs of the banana mentioned. The light yellow tones indicate a frequency below 10% of the articles considered in this review; the intermediate tones indicate frequencies between 10 and 30%, and the intense red tones indicate frequencies above 40%. The location icons indicate the locations of Musa breeding programs identified by the colors. The map was plotted in R, using the packages maps, ggmap, geosphere, Eurostat, GADMTools, country code and ggplot2. lat: latitude; long: longitude.
Among the improvement programs cited, those that worked with crossbreeding to develop resistant cultivars were as follows: Honduras Foundation for Agricultural Research (Fundación Hondureña de Investigación Agrícola—FHIA), located in Honduras; Centre Africain de Recherches sur Bananiers et Plantains (CARBAP) in Cameroon; the International Institute of Tropical Agriculture (IITA) in Nigeria and Uganda; National Improvement Program of the Brazilian Agricultural Research Corporation (EMBRAPA) in Brazil; National Banana Research Center (NCRB) in India; National Research Organization (NARO) in Uganda; and Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD) in Guadeloupe, French Antilles (Figure 4). In contrast, the improvement programs Taiwan Banana Research Institute (TBRI) and Guangdong Academy of Agricultural Sciences (GDAAS) in China worked with somaclonal variants and biotechnology.

3.3. Main Methods and Tools

Concerning the fungal races, the highest number of articles addressed specific studies with FOC TR4 (57%), 25.8% of the studies dealt only with FOC R1, and 10.1% of the articles performed comparative studies between FOC TR4 and FOC R1 (Figure 5A). Other studies with lower numbers conducted studies on subtropical race 4 (FOC STR4) (3.2%), FOC subtropical race 4 (STR4) and Foc TR4 (2.2%), and FOC R1 and FOC STR4 (1%) (Figure 5A). The highest frequency of articles was related to in silico (42.1%) and in vitro (32.6%) studies, followed by studies performed only in the greenhouse (12.6%), in the greenhouse and the field (5.3%), in the field only (4.2%), in the glasshouse (2.1%), and in other places (1%) (Figure 5B).

Figure 5. Stacked bar chart of the frequency of articles with different races of *Fusarium oxysporum* f. sp. *cubense* in the past ten years (a). Places of achievement of work in articles on the improvement of banana plants to *Fusarium* wilt carried out in the last 10 years (b). R1: race 1; STR4: subtropical race 4; TR4: tropical race 4.

To evaluate *Fusarium* wilt symptoms, 26 scales were cited, divided among rhizome-discoloration symptoms, leaf-yellowing symptoms, and pseudostem division (Table 2). We found that 37% (n = 36) of studies adopted a scoring scale for external or internal *Fusarium* wilt symptoms (Table 2). According to the highest frequency of articles, the most-used scoring grades were from 1 to 6 for rhizome-discoloration and leaf-yellowing symptoms.
and from 1 to 3 for pseudostem division (Table 2). The most frequently cited scales were those of [65–68].

**Table 2.** Scales of grades for assessing symptoms of *Fusarium oxysporum* f. sp. *cubense* reported in articles on banana breeding to *Fusarium* wilt conducted in the last ten years.

| Article                  | Internal Symptoms | External Symptoms | Scale Reference |
|--------------------------|-------------------|-------------------|-----------------|
|                          | Rhizome           | Yellowing of the Leaf | Pseudostem Division |               |
|                          | Discoloration     |                   |                 |                |
| Yip et al. [69]          | 0–3               |                   |                 | [69] *         |
| Orr et al. [70]          | 1–6               |                   |                 | [71]           |
| Chen et al. [72]         | 1–8               |                   |                 | [68]           |
| Warman and Aitken [46]   | 1–6               |                   |                 | [66]           |
| Baharum et al. [73]      | 1–8               |                   |                 | [68]           |
| Zhang et al. [74]        | 0–4               | 0–4               |                 | [75,76]        |
| Zuo et al. [77]          | 1–5               |                   |                 | [77] *         |
| Ribeiro et al. [78]      | 0–5               | 0–4               |                 | [67,79]        |
| Wei et al. [80]          |                   | 0–4               |                 | [80] *         |
| Garcez et al. [81]       | 0–5               | 0–5               |                 | [67,82]        |
| Li et al. [75]           | 0–3               | 0–3               |                 | [75] *         |
| Ghag et al. [83]         | 1–6               |                   |                 | [66]           |
| Smith et al. [84]        | 1–6               |                   |                 | [65,85]        |
| Mohandas et al. [86]     | 1–6               | 0–5               |                 | [65,87]        |
| Ting et al. [88]         |                   | 0–5               |                 | [88] *         |
| Paul et al. [89]         | 1–5               | 1–3               |                 | [89] *         |
| Sun et al. [90]          | 1–5               | 1–5               |                 | [64,91]        |
| Wu et al. [92]           | 1–6               |                   |                 | [92] **        |
| Ssali et al. [93]        | 1–6               |                   |                 | [94]           |
| Li et al. [95]           | 0–4               | 0–5               |                 | [95] *         |
| Ghag et al. [96]         | 1–6               |                   |                 | [96] *         |
| Saraswathi et al. [97]   | 1–5               | 1–5               |                 | [66,91]        |
| Ghag et al. [98]         | 1–6               |                   |                 | [83]           |
| Sun et al. [76]          |                   | 0–4               |                 | [76] *         |
| Wu et al. [99]           | 1–6               |                   |                 | [99] **        |
| Magambo et al. [100]     | 1–5               | 1–3               |                 | [68]           |
| Smith et al. [101]       | 1–6               |                   |                 | [65]           |
| García-Bastidas et al. [102] | 1–6             | 1–4               |                 | [102] *        |
| Arinaitwe et al. [31]    | 1–5               | 1–6               | 1–3             | [71]           |
| Cheng et al. [103]       | 1–8               |                   |                 | [68]           |
| Gonçalves et al. [33]    | 1–5               | 1–6               |                 | [67,104]       |
| Buregyeya et al. [105]   | 1–6               |                   | 1–3             | [94]           |
| Sunisha et al. [106]     |                   | 1–5               | 1–3             | [89]           |
| Rocha et al. [107]       | 1–5               | 1–4               |                 | [104]          |
| Ahmad et al. [108]       | 1–6               | 1–4               |                 | [102]          |

* use their own scale; ** in vitro.
Among the main methods used for obtainment or characterization of plants resistant to *Fusarium* wilt, gene expression analysis represented 33% of the selected articles, followed by transgenesis (16%), symptomatology (13%), and resistance induction (11%) (Figure 6). In related articles, the other methods were classified as molecular markers (5%), symptomatology associated with the agronomic characterization of banana genotypes (5%), in vitro mutagenesis (4%), enzyme activity (3%), protein analysis and expression (3%), hybridization by crossbreeding (2%), and methods of somaclonal variation, clone selection, and somatic embryogenesis, each with a 1% frequency (Figure 6).

**Figure 6.** Banana plant breeding techniques used to supplant *Fusarium* wilt in articles published in the last 10 years.

Among the tools used for the analysis and characterization of plants resistant to *Fusarium* wilt, the frequency of articles that employed analysis of reverse transcription-PCR (RT–qPCR) and PCR was the highest (35%). Analyses using bioinformatics tools were in 23% of the articles, and tissue culture represented 13% (Figure 7). Other tools adopted included the genetic transformation of the fungus with the GFP gene, the infection process by FOC strains (7%), banana transcriptome (7%), and phylogenetic analysis (7%). In addition to these tools, there was also a portion of articles using histochemistry and/or histology (6%) and other tools with a lower frequency (Figure 7).

**Figure 7.** Frequency of articles associated with the main tools used in studies on banana plant breeding to *Fusarium* wilt in the last 10 years. The frequency considered that more than one tool was used per article. RT–qPCR/PCR: reverse transcription-PCR/polymerase chain reaction/ GFP: green fluorescent protein.
Some articles used molecular markers associated with wilting resistance: Silva et al. [109], Wang et al. [110], and Wang et al. [51]. Among the markers associated with the resistance to FOC TR4, seven were from sequence characterized amplified region (SCAR)-type. One marker was associated with the susceptibility to FOC R1 [111] (Table 3). One random amplified polymorphic DNA (RAPD) molecular marker associated with the resistance to FOC R1 was found by Ghag et al. [98] (Table 3).

Table 3. Molecular markers associated with banana breeding strategies to *Fusarium* wilt in articles carried out in the last ten years.

| Name            | Type     | Function                  | Citation |
|-----------------|----------|---------------------------|----------|
| ScaU1001        | SCAR     | Resistance to FOC TR4     | [109]    |
| SuscPD          | SCAR     | Susceptibility to FOC 1   | [111]    |
| Lipoxygenase (gene) | RAPD | Resistance to FOC 1 | [98] |
| ScaU1001        | SCAR     | Resistance to FOC TR4     | [110]    |
| ScaS0901        | SCAR     | Resistance to FOC TR4     | [51]     |
| SC1/SC2         | SCAR     | Resistance to FOC TR4     | [51]     |
| SC3/SC4         | SCAR     | Resistance to FOC TR4     | [51]     |
| SC5/SC6         | SCAR     | Resistance to FOC TR4     | [51]     |
| SC7/SC8         | SCAR     | Resistance to FOC TR4     | [51]     |

SCAR: sequence characterized amplified region; RAPD: random amplified polymorphic DNA.

### 3.4. Resistance Sources

In the set of selected articles, many sources of resistance to *Fusarium* wilt were found for different FOC races (Table 4). Of the sources reported as resistant, 38% were triploid (AAA genome), 33% were diploid (AA genome), 12% were triploid (AAB genome), and 8% were tetraploid (AAAB genome); other genomes reported had a frequency of less than 5% (Figure 8 and Table 4).

Table 4. Sources of resistance to *Fusarium oxysporum* f. sp. *cubense* characterized in articles on the improvement of banana to *Fusarium* wilt carried out in the last ten years.

| Musa Germplasm | Musa Genome | Race | Level of Tolerance or Resistance to Races | Institution and Location/Country Where Germplasm Was Screened | Known Use to Mitigate Fusarium Impact | References |
|----------------|-------------|------|-------------------------------------------|---------------------------------------------------------------|--------------------------------------|------------|
| M53            | AA          | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [33,78,107]     |            |
| Birmanie       | AA          | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78,107]        |            |
| PA Songkla     | AA          | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]            |            |
| Pirua          | AAA         | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | Brazil                              | [78]       |
| Imperial       | AAA         | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | Brazil                              | [78]       |
| Poyo           | AAA         | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil [78], DAFF, Australia [84] | Brazil, Africa [78,84]               |            |
| BRS Vitória    | AAAB        | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | Brazil                              | [107]      |
| Ambei          | AA          | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]            |            |
| Walebo         | AAA         | Race 1 | R                                         | Embrapa cassava and fruit growing, Brazil                      | Brazil                              | [78]       |
Table 4. Cont.

| Musa Germplasm | Musa Genome | Race | Level of Tolerance or Resistance to Races | Institution and Location/Country Where Germplasm Was Screened | Known Use to Mitigate Fusarium Impact | References |
|----------------|-------------|------|------------------------------------------|---------------------------------------------------------------|---------------------------------------|------------|
| Kongo FRF 1286 | AAA         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | Brazil [78]                           |            |
| Pisang Nangka  | AAB         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | Brazil, Africa, Australia [78]        |            |
| Pisang Jaran   | AA          | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| Tjau Lagada    | AA          | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil [33,78]              | In breeding programs [33,78]          |            |
| Mangana        | AA          | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| Pisang Pipit   | AAA         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| Pisang Rojo Uter | AA      | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| 2803-01        | AA          | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| GN. P. Formoso | AAA         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [109]            |            |
| Pisang Tongat  | AA          | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| Mchare cultivars | AA      | Race 1 | R                                        | Stellenbosch University, South Africa (Arusha, Tanzania)      | Africa [112]                          |            |
| Mchare hybrids | AA          | Race 1 | R                                        | Stellenbosch University, South Africa (Arusha, Tanzania)      | Africa [112]                          |            |
| NARITA hybrids | AA          | Race 1 | R                                        | Stellenbosch University, South Africa (Kawanda, Uganda)       | Africa [112]                          |            |
| Figo Cinza     | ABB         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | Brazil [78,111]                       |            |
| M-61           | AAA         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| Nanicão Magario | AAA       | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | Brazil [78]                           |            |
| Buitenzorg     | AA          | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| BRS Platina    | AAAB        | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil [33,78,107]         | Brazil [33,78,107,111]                |            |
| Nanicã         | AAA         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | Brazil [78,107,109]                  |            |
| Pisang Ustrali | AAB         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| Markatooa      | AAA         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| Robusta        | AAA         | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | In breeding programs [78]             |            |
| BRS Pacovan Ken | AAAB      | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | Brazil [78,107]                       |            |
| BRS Princesa   | AAAB        | Race 1 | R                                        | Embrapa cassava and fruit growing, Brazil                      | Brazil [33,81,107]                   |            |
Table 4. Cont.

| Musa Germplasm | Musa Genome | Race | Level of Tolerance or Resistance to Races | Institution and Location/Country Where Germplasm Was Screened | Known Use to Mitigate Fusarium Impact | References |
|----------------|-------------|------|------------------------------------------|------------------------------------------------------------|--------------------------------------|------------|
| BRS Japira AAAB | Race 1 | R | Federal Institute of the Triangulo Mineiro, Brazil [81] Embrapa cassava and fruit growing, Brazil [107] | Brazil | Brazil | [81,107] |
| BRS Tropical AAAB | Race 1 | R | Federal Institute of the Triangulo Mineiro, Brazil | Brazil | Brazil | [81] |
| Grand Naine AAA | Race 1 | R | Embrapa cassava and fruit growing, Brazil [33,78,107,109], Federal University of Santa Catarina, Brazil [111] | Cavendish for export | Cavendish for export | [33,78,107,109,111] |
| Nanicão AAA | Race 1 | R | Embrapa cassava and fruit growing, Brazil [78,111], Federal University of Santa Catarina, Brazil [111] | Brazil | Brazil | [78,109,111] |
| SCS452 Corupá AAA | Race 1 | R | Federal University of Santa Catarina, Brazil | Brazil | Brazil | [111] |
| Zellig AAA | Race 1 | R | Federal University of Santa Catarina, Brazil | Brazil | Brazil | [111] |
| Figo ABB | Race 1 | R | Embrapa cassava and fruit growing, Brazil [78], Federal University of Santa Catarina, Brazil [111] | In breeding programs | In breeding programs | [78,111] |
| FHIA-17 AAAA | Race 1 | R | DAFF, Australia | Honduras, Brazil | Honduras, Brazil, Mozambique, Cameroon | [84] |
| SH-3640.10 AAAB | Race 1 | R | DAFF, Australia | Honduras, Brazil, Mozambique, Cameroon | Honduras, Brazil, Mozambique, Cameroon | [84] |
| Long Tavoy * | Race 1 | R | University of Malaya, Kuala Lumpur, Malaysia | In breeding programs | In breeding programs | [31] |
| Kasaska * | Race 1 | R | University of Malaya, Kuala Lumpur, Malaysia | In breeding programs | In breeding programs | [31] |
| Monyet * | Race 1 | R | University of Malaya, Kuala Lumpur, Malaysia | In breeding programs | In breeding programs | [31] |
| Mwitu Pemba * | Race 1 | R | University of Malaya, Kuala Lumpur, Malaysia | In breeding programs | In breeding programs | [31] |
| Hom Thong Mokho AAA | Race 1 | R | Department of Agriculture and Fisheries (DAF), Queensland, Australia | Australia | Australia | [101] |
| Mambee Thu AA | Race 1 | R | Embrapa cassava and fruit growing, Brazil | In breeding programs | In breeding programs | [78] |
| PV03-79 AAAB | Race 1 | R | Embrapa cassava and fruit growing, Brazil | In breeding programs | In breeding programs | [78] |
| Terra Maranhão AAB | Race 1 | R | Embrapa cassava and fruit growing, Brazil | Brazil | Brazil | [107] |
| Williams AAA | Race 1 | R | DAFF, Australia [101], Federal University of Santa Catarina, Brazil [111] | Cavendish for export | Cavendish for export | [101,111] |
| Williams AAA STR4 SS | University of Queensland, Australia | Cavendish for export | Cavendish for export | [72] |
| SH-3217 AA STR4 | University of Queensland, Australia | In breeding programs | In breeding programs | [72] |
| Ma250 AA STR4 | University of Queensland, Australia | In breeding programs | In breeding programs | [72] |
| Pisang Bangkahulu AA STR4 | University of Queensland, Australia | In breeding programs | In breeding programs | [72] |
| M61 Guadelupe * STR4 SS | University of Queensland, Australia | In breeding programs | In breeding programs | [72] |
### Table 4. Cont.

| Musa Germplasm | Musa Genome | Race | Level of Tolerance or Resistance to Races | Institution and Location/Country Where Germplasm Was Screened | Known Use to Mitigate Fusarium Impact | References |
|----------------|-------------|------|------------------------------------------|---------------------------------------------------------------|--------------------------------------|------------|
| CAM-020        | AAA         | STR4 | S                                        | University of Queensland, Australia                          | In breeding programs                 | [72]       |
| SH-3142        | AA          | TR4  | SS                                      | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                 | [77]       |
| FHIA-1 ("Gold Finger") | AAAB | TR4  | S                                        | GDAAS, Guangzhou, China                                      |                                      | [75]       |
| GCTCV-119      | AAA         | TR4  | HR                                      | Guangdong Academy of Agricultural Sciences, Guangzhou, China | In breeding programs                 | [77]       |
| M61 Guadeloupe | *           | TR4  | R                                        | University of Queensland, Australia                          | In breeding programs                 | [72]       |
| CAM-020        | AAA         | TR4  | R                                        | University of Queensland, Australia                          | In breeding programs                 | [72]       |
| Igbitsiri (Intuntu) | AAA  | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | EAHBs                               | [77]       |
| Ingagara       | AAA         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | EAHBs                               | [77]       |
| Inkira         | AAA         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | EAHBs                               | [77]       |
| Intokatoko     | AAA         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | EAHBs                               | [77]       |
| Kazirakwe      | AAA         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | EAHBs                               | [77]       |
| Mbwazirume     | AAA         | TR4  | HR                                      | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Akpakpak       | AAB         | TR4  | HR                                      | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Curare Enano   | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Obino l’Ewai   | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Obubit Ntanga  | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Orishele False Horn | AAB | TR4  | HR                                      | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Pisang Ceylan  | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Pisang Rajah   | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | Africa                               | [77]       |
| Musa itinerans | *           | TR4  | HR                                      | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                 | [77]       |
| CIRAD930/DH Pahang | AA | TR4  | HR                                      | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                 | [77]       |
| NBA 14         | AA          | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                 | [77]       |
| Banksii        | AA          | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                 | [77]       |
| Maia Oa        | AA          | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                 | [77]       |
| Musa Germplasm | Musa Genome | Race | Level of Tolerance or Resistance to Races | Institution and Location/Country Where Germplasm Was Screened | Known Use to Mitigate Fusarium Impact | References |
|---------------|-------------|------|------------------------------------------|--------------------------------------------------------------|---------------------------------------|------------|
| Zebrina       | AA          | TR4  | SS                                       | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Pa (Rayong)   | AA          | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Figue Rose    | AA          | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Khai (Kampengpeth) | AA | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Tani          | BB          | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Pisang Klutuk Wulung | BB | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Musa beccarii Callimusa | * | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Musa laterita Rhodochlamys | * | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Musa nacalayi separ. | * | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Khai Thong Ruang | AAA | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Kamaramasenge AB | TR4  | R    | (IFTR-GDAAS), Guangzhou, China            |                                                               | In breeding programs                  | [77]       |
| Rukumamb      | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Thap Maeo     | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Foconah       | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| Poingo        | AAB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77]       |
| FHIA-21       | AAAB        | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77,84]    |
| Blue Java     | ABB         | TR4  | R                                        | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77,107]   |
| Namwa Khom    | ABB         | TR4  | HR                                      | (IFTR-GDAAS), Guangzhou, China                               | In breeding programs                  | [77,101]   |
| FHIA-02       | AAAA        | TR4  | R                                        | DAFF, Australia                                              | In breeding programs                  | [72,84]    |
| SH-3362 ("Pita-16") | * | TR4  | R                                        | DAFF, Australia                                              | In breeding programs                  | [72]       |
| M. yunnanensis | * | TR4  | R                                        | South China Agricultural University                          | Wild germplasm                        | [75]       |
| M. basjoo     | *           | TR4  | R                                        | South China Agricultural University                          | Wild germplasm                        | [75]       |
| M. nagensium  | *           | TR4  | R                                        | South China Agricultural University                          | Wild germplasm                        | [75]       |
| Musa Germplasm | Musa Genome | Race | Level of Tolerance or Resistance to Races | Institution and Location/Country Where Germplasm Was Screened | Known Use to Mitigate Fusarium Impact | References |
|----------------|-------------|------|------------------------------------------|-------------------------------------------------------------|--------------------------------------|------------|
| M. ruiliensis  | *           | TR4  | R                                        | South China Agricultural University                         | Wild germplasm                       | [75]       |
| M. velutina    | *           | TR4  | R                                        | South China Agricultural University                         | Wild germplasm                       | [75]       |
| Nantianqing    | AAA         | TR4  | MR                                      | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| Dongjiao 1     | AAA         | TR4  | MR                                      | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| Kangku 1       | AAA         | TR4  | R                                       | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| G6-2           | AAA         | TR4  | R                                       | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| Yueke 1        | AAA         | TR4  | MR                                      | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| Nongke 1       | AAA         | TR4  | MR                                      | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| Kangku 5       | AAA         | TR4  | HR                                      | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| Nantianhuang   | AAA         | TR4  | MR                                      | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| BXM51          | AAA         | TR4  | MR                                      | Dongguan Banana Vegetable Institute, China                  | China                                | [51]       |
| Yueyoukang 1   | AAA         | TR4  | R                                       | South China Agricultural University                         | China                                | [113]      |
| Pisang Gajih Merah | AAA      | TR4  | SS                                      | University of Queensland, Australia                        | Australia                            | [72]       |
| GCTCV-218 Formosana | AAA | TR4  | R                                       | University of Queensland, Australia and Northern Mozambique | China, Taiwan, Philippines and Mozambique. | [5,72] |
| FHIA-01 (“Goldfinger”) | AAAB | Race 1/STR4 | R    | DAFF, Australia [84], FHIA, Honduras [93] | Africa, Australia, Honduras         | [84,93]   |
| Tuu Gia        | AA          | Race 1/TR4 | HR            | (IFTR-GDAAS), Guangzhou, China                       | In breeding programs                 | [77]       |
| Pisang Lilin   | AA          | Race 1/TR4 | R              | (IFTR-GDAAS), Guangzhou, China                       | In breeding programs                 | [77]       |
| Borneo         | AA          | Race 1/TR4 | R              | National Agricultural Research Laboratories (NARL) [31], (IFTR-GDAAS), Guangzhou, China [80] and Wageningen University and Research, Wageningen, Netherlands [102] | In breeding programs                 | [31,77,102] |
| Pisang Berlin  | AA          | Race 1/TR4 | R              | (IFTR-GDAAS), Guangzhou, China [77], Embrapa cassava and fruit growing, Brazil [78] | In breeding programs                 | [77,78]   |
| Zebrina GF     | *           | Race 1/TR4 | R              | University of Malaya, Kuala Lumpur, Malaysia [31], IFTR-GDAAS, Guangzhou, China [77] | In breeding programs                 | [31,77]   |
### Table 4. Cont.

| Germplasm          | Genome | Race | Level of Tolerance or Resistance to Races | Institution and Location/Country Where Germplasm Was Screened | Known Use to Mitigate Fusarium Impact | References |
|--------------------|--------|------|-------------------------------------------|----------------------------------------------------------------|--------------------------------------|------------|
| Pahang             | AA     | Race 1/STR4/TR4 | HR | University of Queensland, Australia [72], Yunnan Agricultural University, Kunming, China [74,114] and IFTR-GDAAS, Guangzhou, China [77] | In breeding programs | [72,74,77,114] |
| Calcutta-4         | AA     | Race 1/STR4/TR4 | HR | University of Queensland, Australia [66] and (IFTR-GDAAS), Guangzhou, China [72] | In breeding programs | [72,77] |
| Ma851              | AA     | STR4/TR4      | R  | University of Queensland, Australia | In breeding programs | [72] |
| Ma852              | AA     | STR4/TR4      | R  | University of Queensland, Australia | In breeding programs | [72] |
| Calcutta-4 IV9     | AA     | STR4/TR4      | R  | University of Queensland, Australia [66] and IFTR-GDAAS, Guangzhou, China [72] | In breeding programs | [72,77] |
| SH-3362            | AA     | STR4/TR4      | R  | University of Queensland, Australia | In breeding programs | [72] |
| SH-3142            | AA     | STR4/TR4      | R  | University of Queensland, Australia | In breeding programs | [72] |
| Madang Guadeloupe  | AA     | STR4/TR4      | R  | University of Queensland, Australia | In breeding programs of | [72] |
| FHIA-1 ("Gold Finger") | AAB | STR4/TR4      | R  | University of Queensland, Australia | Australia, Brazil, Mexico, Colombia, EUA | [72] |
| FHIA-25            | AAB    | STR4/TR4      | R  | University of Queensland, Australia [72], (IFTR-GDAAS), Guangzhou, China [77], Wageningen University and Research, Wageningen, Netherlands [102] | Africa, Latin America and Australia (Honduras, Colombia, Brazil, Jamaica, Mozambique) | [72,77,102] |
| GCTCV-119          | AAA    | STR4/TR4      | R  | University of Queensland, Australia and Northern Mozambique | China, Taiwan, The Philippines, Mozambique | [5,72] |
| Ma850              | AA     | ST4/TR4       | R  | University of Queensland, Australia | In breeding programs | [72] |
| Pisang Jari Buaya  | AA     | STR4/TR4      | R  | University of Queensland, Australia [72] and (IFTR-GDAAS), Guangzhou, China [77] | In breeding programs | [72,77] |
| FHIA-18            | AAB    | STR4/TR4      | R  | University of Queensland, Australia [72], IFTM Brazil [81], DAFF, Australia [84], Federal University of Santa Catarina, Brazil [111] | Africa, Latin America and Australia (Honduras, Colombia, Jamaica, Mozambique) | [72,81,84,111] |

R, SS, MS, S, and HS abbreviate resistant, slightly susceptible, moderately susceptible, susceptible, and highly susceptible. EAHBs = East African Highland Bananas; IFTR-GDAAS = Institute of Fruit Tree Research, Guangdong Academy of Agricultural Sciences; EMBRAPA = Brazilian agricultural research corporation; DAFF = Department of Agriculture, Fisheries and Forestry.
The resistance sources reported that are exclusively related to FOC TR4 included the diploid cultivars, Pahang, Calcutta-4, Zebrina, Pisang Lilin, Malaccensis, Jari Buaya, and Tuu Gia, all with a higher frequency, according to the word cloud (Figure 9A). Besides these, other cultivars have also been reported as resistant to FOC TR4 in field tests, such as the hybrids FHIA-01, FHIA-02, SH-3748, SH-3362, FHIA-25, SH-3142, and SH-3362 (Figure 9A). According to genome frequency data related to resistance sources, most genotypes reported as resistant to FOC TR4 are AA diploid genomes (45%), AAA triploid genomes (21%), and AAB triploid genomes (18%) (Figure 9B).
3.5. Gene Expression Analysis

Figure 10A shows the gene categories present in studies on gene analysis and expression. The highest frequency of articles found genes associated with pathogenesis and defense (57%) (Figure 10A). Other genes, studied at a lower frequency, are related to RNAs (12%), hormone biosynthesis (10%), kinases (9%), transcription factors (6%), genes related to autophagy (4%), and starch biosynthesis (2%). A summary of the main genes related to each category can be found in Table S1.

![Figure 10](image)

Figure 10. Gene expression studies of banana plants infected with *Fusarium oxysporum* f. sp. *cubense* in articles carried out in the last ten years. Categories of genes associated with the frequency of articles (a) and frequency of methods used for inoculation of plants to check gene expression (b).

Methods for host plant inoculation to analyze gene expression after FOC infection are not standardized among the analyzed articles (*n* = 27), with several methods adopted (Figure 10B). The highest frequency of articles related to the inoculation method with conidia suspension at a concentration of $1 \times 10^6$ spores mL$^{-1}$ (38%), followed by the inoculation method by mechanical damage to the roots and then immersion in suspension at a concentration of $1 \times 10^6$ mL$^{-1}$ spores (19%). Other methods that were present in a single article represented 15% cumulatively (Figure 10B). The method of mechanical root damage and immersion in suspension at a concentration of $5 \times 10^2$ spores mL$^{-1}$ represented 12% of the articles and the methods of mechanical root damage and immersion in suspension at a concentration of $5 \times 10^6$ spores mL$^{-1}$ and mechanical root damage and soil infestation with 50 g of colonized millet seeds represented 8% of the articles (Figure 10B). Therefore, we observed that the main differences were related to whether the roots were wounded and the spore concentration adopted in each case regarding the inoculation method.

Table 5 is from the study by Wang et al. [115], which was modified, to show all the selected articles that evaluated the banana transcriptome infected by FOC TR4 and FOC R1. These studies observed the changes in expression of defense-related genes related to different enriched pathways, from gene annotation pathways, namely Gene Ontology (GO) annotation and the Kyoto encyclopedia of genes and genomes-based pathway analysis (KEGG-PATH). According to most transcriptome studies, the pathways activated after FOC infection were related to phenylpropanoid biosynthesis, sugar biosynthesis, cell wall modifications, flavonoid biosynthesis, and plant hormone signal transduction (Table 5). The main genes related to the above-mentioned pathways are listed in Table S1.
Table 5. Transcriptomic studies involving banana plants infected with *Fusarium oxysporum* f. sp. *cubense* in articles about the improvement of banana to *Fusarium* wilt, carried out in the last ten years *

| Article | Banana Variety | Plant Growth Stage | Race | Sampling (after Infection) | Pathways Enriched for Differentially Expressed Genes |
|---------|----------------|--------------------|------|---------------------------|------------------------------------------------------|
| Wang et al. [115] | Banana “Brazil” (susceptible) and “Formosana” (tolerant) | 4.5 months | FOC TR4 | 48 h | Flavonoid biosynthesis, flavone and flavonol biosynthesis, alpha-linolenic acid metabolism, starch and sucrose metabolism and phenylpropanoid biosynthesis. |
| Wang et al. [116] | Banana “Brazil” | 60 d | FOCTR4 | 0, 2, 4, 6 days | Phenylalanine metabolism, phenylpropanoid biosynthesis, drug metabolism—cytochrome P450, alpha-linolenic acid metabolism, amino sugar and nucleotide sugar metabolism. |
| Li et al. [37] | Banana “Brazil” | 50 d | FOC 1 and FOCTR4 | 3, 27, 51 h | PR proteins, phytoalexins and phenylpropanoid synthesis, cell wall modifications, biosynthesis via ethylene signaling. |
| Li et al. [117] | Banana “Brazil” and “Nongke N° 1” (resistant) | Plants with four or five leaves | FOCTR4 | 48, 96 h | Perception of PAMP by PRRs, hormone biosynthesis and signaling, transcription factors, cell wall modification, flavonoid biosynthesis, programmed cell death, PR proteins |
| Bai et al. [113] | Banana “Brazil” and “Yueyoukang 1” resistant | 8 weeks (plants with five leaves) | FOCTR4 | 0, 5, 1, 3, 5, 10 days | PR proteins, transcription factors, cell wall modification, phenylpropanoid biosynthesis, plant hormone signal transduction. |
| Zhang et al. [114] | *Musa acuminata* Pahang and Brazilian | FOCTR4 | at 14 days | PR proteins, transcription factors, cell wall modification, phenylpropanoid biosynthesis, plant hormone signal transduction. |
| Sun et al. [32] | *Musa acuminata* “Guijiao 9” and Williams | 6 months | FOCTR4 | At 6 days | Membrane-bound intracellular organelle, cell wall and cytoplasm, ions, transcription factor and oxidoreductase activity, plant-pathogen interaction, plant hormone signal transduction, phenylpropanoid biosynthesis and flavonoid biosynthesis. |
| Fei et al. [118] | Cavendish banana | 3 months | FOC 1 and FOCTR4 | At 28 days | Cell components, molecular function and biological process. |
| Cheng et al. [103] | *Musa acuminata cv. Tianbaojiao* | 11 weeks | FOCTR4 | 5, 10, 25 h | Auxin-activated signaling pathway, cellular response, auxin stimulation, phenylpropanoid catabolic process, lignin catabolic process, lignin metabolic process, via peroxisomes. |
| Song et al. [119] | Brazilian banana and señorita banana | In the five-leaf stage | FOC 1 and FOCTR4 | In the five-leaf stage | Cellular process, metabolic process and binding of organelles and nucleic acids or proteins, regulation of biological processes and transcription factors. |
| Li et al. [120] | Cavendish banana and Brazilian (BX) | 90 days | FOCTR4 | 27 h, 51 h | Secondary metabolite biosynthesis, plant-pathogen interaction, phenylpropanoid biosynthesis and phenylalanine metabolism, fatty acid metabolism, glycolipid and glycerophospholipid metabolism. |
| Niu et al. [121] | Yueyoukang 1 and Baxijiao | 2 weeks | FOCTR4 | 24 h | Cell wall biosynthesis and degradation, cell polysaccharide metabolic process, chitinase activity, pectinesterase activity and xyloglucan activity, fructose and mannose metabolism, sphingolipid metabolism, butanoate metabolism, porphyrin and chlorophyll metabolism, carotenoid and ribosome biosynthesis. |

* modified table by Wang et al. [115].
3.6. Studies on the Achievement and Evaluation of Hybrids and on Genetic Inheritance of *Musa* spp.

The studies related to crossbreeding to obtain resistant hybrids or those focused on evaluating the genetic inheritance in *Musa* spp., as well as the parental lineages used and their genealogies, are listed in Table 6. Ssali et al. [93] produced hybrids from crossbreeding the resistant diploid TMB2X8075 (originated from the cross between SH3362 (AA) and Calcutta 4 (AA)) and Sukali Ndizi (AAB), which is also resistant to FOC R1 and 4, to evaluate the inheritance of the resistance of *Musa* spp. to FOC R1 in three F2 populations. Concerning the progeny, the authors found that 115 were susceptible, and 48 were resistant. Similarly, in the study by Arinaitwe et al. [31], crossbreeding between Monyet (*Musa acuminata* ssp. Zebrina) and Kokopo (*Musa acuminata* ssp. Banksii) were performed to identify suitable banana germplasm to generate a segregating F1 population and to understand the mode of inheritance of resistance to FOC R1 (Table 6).

Table 6. Evaluation of hybrids and genetic inheritance studies in articles about the improvement of banana plants to fusarium wilt carried out in the last ten years.

| Hybrids | Parentage |
|---------|-----------|
| Article |           |
| Ssali et al. [93] | Diploid TMB2X8075 (“SH3362” (AA) × “Calcutta 4” (AA) × Sukali Ndizi (AAB)) |
| Arinaitwe et al. [31] | Monyet (*Musa acuminata* ssp. Zebrina) × Kokopo (*Musa acuminata* ssp. Banksii) |
| Ahmad et al. [108] | *Musa acuminata* ssp. Malaccensis (selfed) |
| Gonzalves et al. [33] | CNPMF0038 ((M53 × Madu) × (Malaccensis × Tjau Lagada)) |
| | CNPMF0496 ((M61 × Pisang Lilin) × (Terrinha × Calcutta 4)) |
| | CNPMF0513 ((M61 × Pisang Lilin) × (M53 × Kumburgh)) |
| | CNPMF0519 Self-fertilization (wild diploid Tambi) |
| | CNPMF0534 ((Calcutta 4 × Madang) × (Borneo × Guyod)) |
| | CNPMF0536 ((Calcutta 4 × Madang) × (Borneo × Guyod)) |
| | CNPMF0542 ((SH3263) × (M61 × Pisang Lilin) × (Malaccensis × Sinwobogi)) |
| | CNPMF0557 ((M61 × Pisang Lilin) × (Malaccensis × Tjau Lagada)) |
| | CNPMF0565 ((Calcutta 4 × Pahang) × (Borneo × Madang)) × Khae |
| | CNPMF0572 ((Khai × (Calcutta 4 × Madang)) × ((Calcutta 4 × Madang)) |
| | CNPMF0612 ((M53 × Madu) × Madu) × SH3263 |
| | CNPMF0731 ((Malaccensis × Madang) × (Tuugia × Calcutta 4)) |
| | CNPMF0767 (Malaccensis × Madang) × (Khai × (Calcutta 4 × Madang)) |
| | CNPMF0811 ((Khai × (Calcutta 4 × Madang)) × ((Calcutta 4 × Pahang) × (Borneo × Madang)) |
| | CNPMF0978 ((Calcutta 4 × Madang) × (Terrinha × Calcutta 4)) |
| | CNPMF0993 ((Borneo × Guyod) × (Tuugia × Calcutta 4)) × (Khai × (Calcutta 4 × Madang)) |
| | CNPMF0998 ((Borneo × Guyod) × (Borneo × Guyod) × SH3263) |
| | CNPMF1102 (Jari Buaya × (Calcutta 4 × Madang)) × (Borneo × Guyod) × (Tuugia × Calcutta 4)) |
| | CNPMF1105 ((Borneo × Guyod) × (Calcutta 4 × Heva)) × ((Calcutta 4 × Madang)) |
| | CNPMF1171 (Malaccensis × Madang) × (M53 × (Tuugia × Calcutta 4)) |
| | CNPMF1272 ((Borneo × Guyod) × (Calcutta 4 × Heva)) × (Tuugia × Calcutta 4)) |
| | CNPMF1286 (Calcutta 4 × Madang)) × (Terrinha × Calcutta 4)) |
The study by Ahmad et al. [108] is the first report of the genetic basis of resistance to FOC R1 in bananas using heterozygous wild banana *Musa acuminata* ssp. *malaccensis* (AA) to generate a mapping population and investigate the inheritance of resistance to FOC R1 and FOC TR4 through genetic mapping. This study demonstrated that resistance to FOC R1 is inherited as a single gene and that *M. acuminata* ssp. *malaccensis* is fertile and can be a potential parent to create resistance to *Fusarium* wilt.

Among the hybrids studied by Gonçalvez et al. [33], the improved diploids (CNPMF0038, CNPMF0513, CNPMF0767, and CNPMF1171) and the tetraploid hybrid BRS Princesa were considered moderately resistant (Table 6). All other hybrids evaluated in their study were considered resistant to *Fusarium* wilt caused by FOC R1. Gonçalvez et al. [33] mostly used improved male diploid parents, resulting from crossbreeding with diploids resistant to FOC R1 and FOC TR4, such as Calcutta 4 and M53.

### 3.7. Transgenesis

In the articles reporting the use of transgenesis (*n* = 14), the tool for genetic transformation was mediated by *Agrobacterium tumefaciens*, using embryogenic cell suspension culture. One exception is a method proposed by Subramaniam et al. [122], who, in addition to agroinoculation, developed a biolistics method. In this study, we used a table developed by Poon and Teo [123] as a model to show information about the works of this systematic review related to transgenesis (Table 7). In Table 7, we observed that most studies used the *Rasthali* cultivar (AAB) for genetic engineering.

### Table 6. Cont.

| Hybrids            | Parentage                                                                 |
|--------------------|---------------------------------------------------------------------------|
| CNPMF1323          | ((Malaccensis × Sinwobogi)) × ((Calcutta 4 × Heva))                        |
| CNPMF0241          | ((Pacovan × improved diploid))                                            |
| CNPMF0282          | ((Pacovan × improved diploid))                                            |
| CNPMF0351          | ((Prata Anã × improved diploid by FHIA))                                  |
| CNPMF0897          | ((Prata Anã)) × ((Malaccensis × Sinwobogi) × (Zebrina × Heva))            |
| CNPMF0898          | ((Prata Anã)) × ((Malaccensis × Sinwobogi) × (Calcutta 4 × Galeo))        |
| CNPMF0906          | ((Prata Santa Maria × improved diploid))                                  |
| CNPMF0908          | ((Silk × improved diploid))                                               |
| BRS Princesa       | ((Yangambi × M53))                                                       |
Among the genes used for transgenesis, there was a considerable frequency of studies using transgenes as the antiapoptosis gene (Ced9) from the nematode Caenorhabditis elegans (Table 7). Two genes derived from Musa acuminata ssp. malaccensis, one related to pathogenesis (MaPR-10) and the other a resistance analog (RGA2), were also successfully used in this case as cisgenes. Other cell death genes, MusaDAD1, MusaBAG1, and MusaBI1, from Musa acuminata were also efficient, particularly MusaBAG1. In addition to these, the RNA interference technology enables the silencing of vital genes of FOC when employing small interfering RNA (siRNA) and intron-containing hairpin RNA (ihpRNA) (Table 7).

Four antimicrobial peptides from the plant species Capsicum annuum, Petunia hybrida, Allium cepa, and Stellaria media and an antifungal activity gene from Trichoderma harzianum were also successfully used to obtain resistant transgenic banana plants (Table 7).

3.8. Induction of Resistance

Among the inducers, the biocontrol agents Bacillus subtilis, Trichoderma spp., and Penicillium citrinum were the most reported for exploring induction of systemic resistance (Table 8). Chemical induction agents were also reported, such as the plant hormones abscisic acid (ABA), methyl jasmonate (MeJA), and salicylic acid (SA), in addition to benzothiadiazole (BTH). Other studies explored induced systemic resistance with the FOC pathogen in different ways (Table 8).

**Table 7.** Genes used transgenics in studies on genetic improvement of banana to *Fusarium* wilt in the last ten years.

| Gene                                                                 | Sources                | Function                                | Banana Cultivar | References |
|---------------------------------------------------------------------|------------------------|-----------------------------------------|-----------------|------------|
| Ferredoxin (Atfd3) and ferredoxin-like protein (pflp)               | Capsicum annuum        | Antimicrobial peptide                   | cv. Pei Chiao (AAA) | [69]       |
| Petunia floral defenses                                            | Petunia hybrida        | Antimicrobial peptide                   | cv. Rasthali (AAB) | [124]      |
| (PhDef1 and PhDef2)                                                 |                        |                                         |                 |            |
| Onion—Ace-AMP1                                                     | Allium cepa            | Antimicrobial peptide                   | cv. Rasthali (AAB) | [88]       |
| Endochitinase (chit42)                                              | Trichoderma harzianum  | Antifungal activity                     | cv. Furenzhi (AA) | [125]      |
| Defensin (Sm-AMP-D1)                                                | Stellaria media        | Antimicrobial peptide                   | cv. Rasthali (AAB) | [126]      |
| Small interfering RNAs(siRNAs)/(ihpRNA)                           |                        | Silencing of vital fungal genes         | cv. Rasthali (AAB) | [83]       |
| (MusaDAD1, MusaBAG1 eMusaBI1)                                      | Musa acuminata ssp. malaccensis | Cell death is highly induced by FOC infection | cv. Rasthali (AAB) | [96]       |
| Cell death (Bcl-XL, Ced-9 e Bcl-23)                                 | Caenorhabditis elegans | Antiapoptosis                            | cv. Grand Naine | [89]       |
| Cell death (Ced9)                                                   | Caenorhabditis elegans | Antiapoptosis                            | cv. Sukali Ndizi (Musa ssp. AAB) | [100]      |
| Pathogenesis-reported (MaPR-10)                                     | Musa acuminata ssp. malaccensis | Pathogenesis (PR)                      | M. acuminata cv. Berangan | [73]       |
| (RGA2) and (Ced9)                                                   | Musa acuminata ssp. malaccensis /Caenorhabditis elegans | Resistance analog/antiapoptosis         | cv. Grand Naine | [127]      |
| Chitinases and 1.3-glucanase                                         | Oryza sativa           | Disease tolerance                       | cv. Rasthali (AAB) | [122]      |
| Synthesis of ergosterol (ERG6)                                      |                        | Silencing of vital fungal genes         | Cavendish       | [128]      |
| Small interfering RNAs–ihpRNA                                       |                        | Silencing of vital fungal genes         | cv. Rasthali (AAB) | [129]      |
Table 8. Resistance-inducing agents in banana plants reported in studies on improvement to *Fusarium* wilt in the last ten years.

| Inductor                      | Application                                      | References |
|-------------------------------|--------------------------------------------------|------------|
| *Bacillus subtilis*           | Inoculation of plants with suspension in a greenhouse | [130]      |
| *Trichoderma asperellum*      | Inoculation of plants with suspension in a greenhouse | [131]      |
| Abscisic acid (ABA), ethephon, methyl jasmonate (MeJA) and salicylic acid (SA) | Root treatment with inductor solutions | [132]      |
| *Penicillium citrinum*        | Inoculation of plants with suspension in a greenhouse | [88]       |
| *Bacillus subtilis*           | Treatment with in vitro fermented culture filtrate and inoculation of plants with suspension in a greenhouse | [90]       |
| Benzothiadiazole (BTH)        | Spraying leaves and roots                         | [133]      |
| Interaction with dead FOC pathogen | Inoculation of plants with suspension in a greenhouse | [134]      |
| Methyl jasmonate (MeJA)       | Exogenous solution treatment in soil and leaves   | [76]       |
| A strain of FOC 1 incompatible with inducing resistance against the tropical race 4 TR4 | Systemic resistance acquired by in vitro inoculation | [99]       |
| Isolates of *Trichoderma* spp. (*T. koningii*, *T. viride*, *T. harzianum*) | Biomass, liquid culture and culture filtrate | [135]      |

4. Discussion

4.1. Screening of the Studies

The studies analyzed were restricted to genetic improvement and in line with the questions proposed in the protocol formulated for this review. For this reason, articles on FOC genetic diversity, specific management strategies, and first reports of the disease were not considered in the analyses (Figure S1). Literature reviews were also excluded from the research to avoid bias since they could overestimate data, as many articles would be repeated.

Thus, the exclusion criteria used during the extraction stage of the article screening process revealed that many specific studies on FOC genetic diversity (*n* = 72) were generated in the last ten years, as well as many articles that escaped the proposed subject of this review (*n* = 47) and several literature reviews (*n* = 26) (Figure S1). Although these papers were excluded by the criteria, they revealed important aspects of the direction of research on *Fusarium* wilt in the last 10 years, considering the search string used.

The considerable amount of data on the genetic diversity of FOC generated in recent years was primarily in response to the need to understand the population structure of the pathogen in different locations and the evolutionary mechanisms of the fungus that culminate in the emergence of new races [48,136,137]. In fact, the potential for public investment in research that addresses the dissemination of the FOC TR4 can generate high returns and substantially delay the spread of this disease [138].

4.2. Locations of Knowledge Generation

A substantial amount of data on banana genetic improvement for resistance to *Fusarium* wilt was evaluated in this systematic review, the majority (50%) from China. This is a consequence of the number of projects to control *Fusarium* wilt in China, involving institutions, such as the Guangdong Academy of Agricultural Sciences (GDAAS), Chinese
Academy of Tropical Agricultural Sciences (CATAS), Fujian Agriculture and Forestry University, Hainan Academy of Agricultural Sciences, and Guangzhou Institute of Agricultural Sciences [139]. In addition, China is among the countries in Southwest Asia where banana plants were domesticated [140], in which bananas are one of the fruits with the oldest consumption record, and the country that ranks second among the top 10 banana producers worldwide [2].

Besides China, India (16.7%), Australia (10.4%), and Brazil (7.3%) have also contributed to the improvement in research on Musa spp. India is the largest banana producer globally, whereas Brazil ranks fourth among banana producers [2]. Furthermore, these countries host important research institutions, which work on banana improvement for the development of resistant hybrids from germplasm collections, such as the Brazilian collections of the National Research Center for Banana (NRCB) and EMBRAPA. Australia was the first country to report and describe Fusarium wilt and one of the first countries facing major problems with FOC TR4, which led to the end of the Cavendish banana industry in the Northern Territory in 2015 [35,141,142].

Overall, in recent years, a major stimulus for the growth in studies on Fusarium wilt has been the emergence of FOC TR4 as the most devastating threat to bananas worldwide. A clear demonstration of this is the estimate that 17% of the current banana cultivation area, with an annual production of 36 million tons worth approximately US $10 billion at current prices, could be lost over the next 20 years because of Fusarium wilt, which would necessitate investment in research aimed at improving the crop in this scenario [138,143].

4.3. Gene Expression Analysis

The genome of the diploid species Musa acuminata ssp. malaccensis, which is the ancestor of most banana triploid cultivars, has been sequenced [144]. In the present study, 50% of the articles used the banana genome as a tool for analysis. For this reason, the highest frequency of articles was related to in silico studies (45%), as part of gene expression analyses (30%) that mostly performed RT–qPCR and PCR analyses (34%), as well as bioinformatic analyses (23%).

Identifying genes related to host defense is one of the first steps to understand the underlying mechanism of resistance to diseases in plants [145]. Concerning FOC, knowledge of global gene expression patterns, influenced by infection of different races, has enhanced our understanding of host responses to infection. Moreover, the availability of banana transcriptomes was highly useful to improve the annotation of the banana genome and for biological research [37]. Based on the knowledge of the global patterns of gene expression influenced by infection of FOC R1 and FOC TR4, Li et al. [37] found a large number of simple nucleotide polymorphisms (SNPs) and short insertions and deletions (indels), which previously had not been annotated in the Musa genome. Other transcriptomic studies observed the regulated expression of defense genes, cell wall-modifying genes, and a phytoalexin, flavonoids, lignin biosynthesis genes and jasmonic acid and other plant hormones and transcription factors [37,113–117,146,147].

The lack of standardization pertaining to the inoculation methods for evaluating gene expression should be questioned to develop a universal method for plant host inoculation so that the results could be equated and compared. It should be noted that a striking difference between these methods is the generation of wounds in the roots before exposing them to a suspension with the fungus, which in fact does not reflect a similar situation in the field, except when there are interactions with other microorganisms in the soil, such as nematodes [107]. Therefore, we consider that the inoculation methods adopted in most studies should be reconsidered because they are primarily related to the mechanical opening of wounds made with sterile needles or crushing the roots. In addition, differences related to the concentration of spores in the infection process generated marked changes in the plant response to infection and in gene expression, especially when a high inoculation pressure is considered, such as at the concentration of $5 \times 10^6$ spores mL$^{-1}$ associated with wound generation. Consistent with this information, we know that F. oxysporum is
considered a hemibiotrophic pathogen because it begins its infection cycle as a biotroph and later changes to a necrotroph and as the gene expression changes that occur in the roots. Host responses may be prioritized to the perception of the pathogen, preventing the penetration of the root tissue during the biotrophic stage, which would not be possible to notice in previously injured tissue [46,148]. Therefore, we suggest that a standardized method should be adopted regarding the inoculation method of host plants to verify gene expression, aimed mainly to simulate situations in the system of banana cultivation, considering the mechanisms of dissemination of FOC that usually occur by movement and deposition of contaminated soil [30].

4.4. Studies on Resistance Sources

Although available edible banana cultivars originate from M. acuminata (genome A) and Musa balbisiana (genome B), genome B has been associated with the best vigor and tolerance to biotic and abiotic stresses and is, therefore, a target for Musa spp. improvement programs [149,150]. The AAA triploid genomes frequently occurred when considering all resistance sources related to both FOC R1 and FOC TR4 (Figure 8). In the studies with FOC TR4, the highest frequency of resistant genotypes were related to AA diploid genomes (Figure 9). This demonstrates that FOC TR4-related resistance sources are still mostly composed of wild diploids that have not yet been exploited for triploid cultivars, as in FOC R1, which already has a large panel of resistant cultivars available.

Thus, we have shown that some wild relatives of edible bananas, such as M. itinerans, Pahang, Calcutta 4, DH Pahang and Tuu Gia (Figure 9A), are valuable resources of resistance genes to FOC TR4 [77]. These data continue to be reaffirmed based on recent RNA-seq analyses that revealed aspects of the key responses of the relative resistance of wild banana to FOC TR4, where it could be seen that many differentially expressed genes were found in the resistant wild relative Musa acuminata ssp. Burmanicoides compared to the susceptible cultivar “Brazilian (AAA)” [147].

An example of banana resistant to FOC R1 and TR4 are the triploid banana referred to as East African Highland bananas (EAHB), which a recent study has revealed that Mchare and Matooke hybrids resistant to FOC R1 can replace susceptible cultivars in areas of production severely affected by the fungus and are important resources for the generation of resistant banana [112].

The genetic basis of resistance to FOC R1 in banana has been studied in three articles, of which Arinaitwe et al. [31] and Ahmad et al. [108] suggested that resistance to Fusarium wilt in Musa spp. is conditioned by a single dominant locus of resistance, contradicting Ssali et al. [93], who concluded that the gene was recessively inherited. However, the conclusions by Ahmad et al. [108] were based on genetic analyses that included mapping studies and not just segregation data based on phenotypic characters.

4.5. Main Methods and Tools Adopted

One of the most-used tools (12%), together with the symptomatological assessments to understand Musa × FOC interaction processes, is the genetic transformation of different FOC isolates with the GFP gene. This method allows researchers to follow the movements of the fungus within the tissues and compare the colonization path used by different FOC races [37,46,72,137,151]. A FOC STR4 strain, transformed with the GFP gene, was used to monitor the movement of the pathogen in two susceptible cultivars, Cavendish Williams (Musa AAA) and Lady Finger (Musa AAB) [46]. Those authors detected the presence of FOC on the roots, rhizome, and outer leaf sheaths of the pseudostem before the appearance of external symptoms. Another study using this method verified that, in some cases, the banana rhizome plays an important role as a barrier to the pathogen, preventing its migration to the rest of the plant [103].

The studies carried out in greenhouses corresponded to 13% of the articles, those in greenhouses and in the field to 5%, and those only in the field to 3%. The articles focused only on assessing Fusarium wilt symptoms are few since, overall, this type of
evaluation is complementary to several other analyses as a safe phenotypic confirmation of resistance. Most of the evaluation methods cited are related to the quantification of the severity of *Fusarium* wilt by visual categorization of the cross-sections based on the level of discoloration of the vascular tissue of the rhizome and the pseudostem of the root tissue, according to the scales mentioned in Table 2 [65–67,71,77,94].

The greatest difference found between the rating scales adopted for analysis and confirmation of banana resistance to FOC is related to the scoring grades for the disease’s severity. A universal scoring scale should be adopted, especially for comparison purposes between studies from different banana research centers, to avoid discrepant results, for example, when evaluating hybrids resulting from crossbreeding, plants obtained by transgenesis, resistance-induction, or other methods.

Although there are few studies with somaclonal variation (1%), this is a tool that presents promising results. The Cavendish somaclone GCTCV-218 for commercial cultivation under the name of Formosona, generated in 2004 by the Taiwan Banana Research Institute, is known to be tolerant to FOC TR4 and two other somaclonal variants of Cavendish called GCTCV-53 and GCTCV-119 [152]. In a recent study, tests with these Cavendish banana somaclones in northern Mozambique revealed that GCTCV-119 was more resistant to FOC TR4, but GCTCV-218 produced better bunches [5]. Another recent study obtained, through different combinations of plant regulators in a culture medium, two somaclones of the cultivar Prata-Aná, namely T2-1 and T2-2, which presented resistance to FOC race 1 in a greenhouse, characterizing an important result for the banana cultivation in Brazil since the pathogen FOC R1is present in most banana plantations and this cultivar is preferred by Brazilian consumers [153].

In the articles analyzed, transgenesis was the most-used method (14%), followed by resistance induction (10%), hybridization (4%), in vitro mutagenesis (4%), and somaclonal variation, clone selection, and somatic embryogenesis (1%). Although the transgenic method has a limitation related to the production of embryogenic cell suspensions, a time-consuming process, some protocols have facilitated their implementation [127,154]. Among the cited protocols, the most-used have been proposed by Ganapathi et al. [154], which included the establishment of embryogenic cell cultures from thin sections of the shoot tip of cultivated Rasthali (AAB) banana cultivar in vitro and by Khanna et al. [155], which proposed transformation mediated by *Agrobacterium tumefaciens* assisted by centrifugation (CAAT) from male flower embryogenic cells suspensions of the Cavendish (AAA) and Lady Finger (AAB) cultivars. A protocol established by Yip et al. [69] proposes the substitution of embryogenic cell suspensions for meristematic tissue, where they use multiple shoot clump (MSC) of Pei Chiao (AAA) and Gros Michel (AAA) bananas induced from shoots in the rhizome in MS medium; this could be another feasible option for banana cultivars where suspension cultures are difficult to establish. Another protocol was proposed by Subramaniam et al. [122] using the biobalistic gun method for the transformation of the ‘Rastali’ (AAB) banana cultivar. In addition, the availability of banana genes (cisgenes) and genes from other appropriate sources (transgenes) allowed the development and evaluation of transgenic plants (Table 6).

Conventional resistance improvement methods using hybridization between fertile diploids and crossbreeding with triploid or tetraploid cultivars are efficient. However, they have some limitations concerning the polyploid nature of the cultivars and the low female fertility, as well as the long life cycle leading to a long reproductive cycle [156,157]. Other challenges are related to the need for a large space, which results in high costs and limited knowledge about resistance genetics [31,158,159].

Transgenic methods permit the addition of a single gene or several genes to a highly desirable cultivar quickly [81,124–126]. Due to the sterility of these cultivars, the flow of transgenes and the crossing of modified genes between wild Musa species are unlikely; therefore, genetically modified (GM) bananas could be compatible with organic agriculture [159]. In addition, although no genome editing data associated with obtaining *Fusarium* wilt-resistant cultivars were identified in this study, the potential for using the
CRISPR/Cas9, a genome-editing tool for the development of disease-resistant banana varieties, also has been reported. The use of genome editing (GE) with the availability of a whole-genome sequence and its potential applications to develop disease-resistant bananas opens new areas of research [160–165]. Although there are no published data in banana breeding, another potential tool to be applied is resistance gene enrichment sequencing (RenSeq), a technology that enables the discovery and annotation of pathogen resistance gene families in plant genome sequences. The use of this high-throughput technique was well demonstrated in wheat (*Triticum estivum*) [164] and potato (*Solanum tuberosum*) [165].

These data encourage discussions on the current status of biosafety regulations and laws on the marketing of GM products that face some challenges because of the regulation of these products in several countries [162,163]. Furthermore, their outlook indicated that investments in GM banana plantations would bring few beneficiaries, given the assumption that countries with export-oriented banana production would not adopt GM varieties because of political and consumer concerns [138]. In this sense, it seems reasonable to invest more in improvements based on crossbreeding, considering that there are sources of resistance to *Fusarium* wilt caused by FOC R1 and FOC TR4, which enables the selection of resistant hybrids within the progeny generated.

Using an ex-ante quantitative risk index model, Staver et al. [138] showed that investments in different research areas assessed to address the threat and projected losses from FOC TR4 would provide positive returns and contribute to a reduction in poverty. Moreover, there would be superior returns in poverty reduction, especially in Africa, in the face of investments in the research areas related to the conventional improvement of cultivars resistant to *Fusarium* wilt, as well as in the research area related to improving exclusion and surveillance, as well as measures to eradicate or contain the disease, with 850,000 and 807,000 people lifted out of poverty in each case, respectively.

### 4.6. Perspectives

In this study, we found that several articles in the last 10 years have focused on a variety of analyses to improve our understanding and identification of genetic, molecular, biochemical, or structural mechanisms of banana resistance to FOC, based on a set of tools. Based on these articles, we also showed that there are sources of resistance to FOC R1 and FOC TR4 in banana germplasms and that the data generated in these studies are the basis for obtaining cultivars resistant to *Fusarium* wilt. Moreover, they can contribute significantly to the expansion of resistant cultivars, including those for export. Although there is not yet a banana cultivar resistant to FOC TR4 that can replace the cultivars of the Cavendish subgroup, from the resistance sources found in different studies, it would be possible to develop a “type” similar to the Cavendish cultivars resistant to FOC TR4 or other races.

Concerning the improvement methods, there is a growing incentive for new precise and efficient genetic technologies, and the use of the CRISPR/Cas9 genome editing tool will also contribute to obtaining banana cultivars with FOC resistance in a short span of time. Other tools, which explore acquired and induced systemic resistance, also emerged as important means to achieve resistance to the pathogen, supported by experiments on tissue culture. Meanwhile, conventional improvement seeks to overcome the challenges inherent to the plant species by offering seemingly more appropriate measures with a focus on family-based agriculture of banana production systems worldwide. Nevertheless, the debate concerning various improvement methods should not be focused on just one method since all of them contribute to improving the crop, and the existence of different scenarios of banana production should be considered for the use of each method.

Furthermore, it is important to emphasize that the results obtained in this study are linked to the keywords used in the search string. The use of different terms could lead to the inclusion and exclusion of other articles in the systematic review and, consequently, lead to other methods and conclusions.
5. Conclusions

Improvement programs of *Musa* spp. have sought to reinforce their methods through new technologies and accumulate knowledge on resistance to *Fusarium* wilt. The genome sequencing of Musa is a widely used data source for improving the identification and analysis of resistance-related genes. The production of transgenic bananas has been explored, leading to the need for social exposure regarding the acceptance of such products. Although the use of genome editing tools, such as CRISPR/Cas9, to obtain resistance to *Fusarium* wilt in banana plants has not been performed, it is a method with promising prospects. In this review, we highlighted sources of resistance to FOC (R1 and TR4) based on diploids resistant to *Fusarium* wilt, which is the starting point for genetic improvement.

Therefore, we confirm that genetic improvement is the best strategy for combating *Fusarium* wilt by expanding resistant cultivars to producers. From the data collected in our systematic review, we believe that future research efforts can be based on integrating the knowledge obtained thus far to obtain results with greater applicability and direct the next steps in research to produce banana species resistant to *Fusarium* wilt. We suggest that future studies address the following questions: How can we exploit germplasm sources resistant to FOC R1 and FOC TR4 in improvement programs? Could the standardization of protocols for plant inoculation facilitate the comparison of data regarding gene expression analysis? Should a universal scoring scale contemplating the disease’s external and internal symptoms be elaborated based on existing scales? Can existing molecular markers be used in a standard-assisted selection protocol for resistance to FOC R1 and FOC TR4?

In addition, strategies based on the integration of knowledge from different *Musa* spp. improvement research centers should be adopted for cooperative efforts so that different improvement programs can cooperate on a global scale. Considering that the current banana export scenario is based exclusively on a single group, strategies should be considered to ensure the agribusiness export’s sustainability, prioritizing the production of other cultivars resistant to FOC.

**Supplementary Materials:** The following are available online at https://www.mdpi.com/article/10.3390/jof7040249/s1, Figure S1. Frequency of articles by exclusion (E) and inclusion (I) criteria, used in the study extraction phase to composing a systematic review of the resistance of *Musa* spp. to *Fusarium* wilt; Table S1. Summarization of the main genes identified in the analysis of articles on the improvement of banana to *Fusarium* wilt carried out in the last ten years (additional to Figure 9B); Table S2. Origin and database of articles selected to compose a systematic review on the improvement of banana to *Fusarium* wilt.

**Author Contributions:** Conceptualization, A.d.J.R., F.H., E.P.A.; methodology, A.d.J.R.; J.M.d.S.S. and F.d.S.N.; software, A.d.J.R.; A.S.S.; validation, A.d.J.R., J.M.d.S.S., F.d.S.N., A.S.S., V.B.d.O.A., J.A.d.S.-S., C.F.F., F.H. and E.P.A.; formal analysis, A.d.J.R.; investigation, A.d.J.R., J.A.d.S.-S., F.H., E.P.A.; resources, E.P.A.; data curation, A.d.J.R., J.M.d.S.S. and F.d.S.N.; writing—original draft preparation, A.d.J.R., E.P.A.; writing—review and editing, A.d.J.R., J.A.d.S.-S., C.F.F., E.P.A.; visualization, A.d.J.R., J.M.d.S.S., F.d.S.N., A.S.S., V.B.d.O.A., J.A.d.S.-S., C.F.F., F.H. and E.P.A.; supervision, E.P.A.; project administration, E.P.A.; funding acquisition, E.P.A. All authors have read and agreed to the published version of the manuscript.

**Funding:** This research was funded by Embrapa, grant number 22.15.11.004.00.00 (Banana Breeding Project, Phase II) and Corporación Bananera Nacional (CORBANA) grant number 5153/Funarbe (Strategic alliance to develop Cavendish-type cultivars resistant to FOC TR4).

**Acknowledgments:** The authors thank the Graduate Program in Biotechnology (PPGBiotec) of the State University of Feira de Santana and CNPq for the research productivity grants to Amorim EP and Ferreira CF; Fapesb for providing Ph.D. scholarships to Rocha AJ, Soares JMS, and Nascimento FS; Professor Eduardo Mizubuti (Federal University of Viçosa) for the corrections and meaningful suggestions to improve this review; and the Corporación Bananera Nacional (Corbana) for financing the publication of this review and the strategic alliance with EMBRAPA to develop Cavendish-type cultivars resistant to FOC TR4, which began in 2020. We would like to acknowledge the financial
contribution of the CGIAR Research Program on Roots, Tubers and Bananas and the CGIAR Fund Donors for covering the open access fee of this publication.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. FAOSTAT. Available online: http://www.fao.org/faostat/en/#data/QC (accessed on 4 June 2020).
2. FAO. Available online: http://www.fao.org/fileadmin/templates/est/COMM_MARKETS_MONITORING/Bananas/Documents/Banana_Market_Review_Prelim_Results_2018.pdf. (accessed on 4 June 2020).
3. Adeniji, T.; Tenkuano, A.; Ezurike, J.; Ariyo, C.; Vroh-Bi, I. Value-adding post harvest processing of cooking bananas (Musa spp. AAB and ABB genome groups). Afr. J. Agric. Res. 2010, 9, 9135–9141.
4. Dotto, J.; Matemu, A.O.; Ndakidemi, P.A. Potential of cooking bananas in addressing food security in East Africa. Int. J. Biol. Sci. 2018, 13, 278–294.
5. Viljoen, A.; Mostert, D.; Chiconela, T.; Beukes, I.; Fraser, C.; Dwyer, J.; Amugoli, O.M. Occurrence and spread of the banana fungus Fusarium oxysporum f. sp. cubense TR4 in Mozambique. S. Afr. J. Sci. 2020, 116, 11–12. [CrossRef]
6. Dita, M.A.; Garming, H.; Van den Bergh, I.; Staver, C.; Lescot, T. Banana in Latin America and the Caribbean: Current state, challenges and perspectives. Acta Hortic. 2011, 986, 365–380. [CrossRef]
7. Lescot, T. Close-up Banana: Statistics. Fruityr 2011, 189, 59–62.
8. Gomes, E.W.F.; Willadino, L.; Martins, L.S.S.; Camara, T.R. The effects of salinity on five banana genotypes (Musa spp.). In Plant Nutrition; Horst, W.J., Schenk, M.K., Eds.; Springer: Dordrecht, The Netherlands, 2001; Volume 92, pp. 410–411. [CrossRef]
9. Willadino, L.; Camara, T.R.; Ribeiro, M.B.; Amaral, D.O.J.; Suassuna, F.; Silva, M.V.D. Mechanisms of tolerance to salinity in banana: Physiological, biochemical, and molecular aspects. Rev. Bras. de Frutic. 2017, 39, 1–8. [CrossRef]
10. Said, E.M.; Mahmoud, R.A.; Al-Akshar, R.; Safwat, G. Drought stress tolerance and enhancement of banana plantlets in vitro. Austin J. Biotechnol. Bioeng. 2015, 2, 1-10.
11. Marssaro, A.L.; Morais-Lino, L.S.; Cruz, J.L.; Ledo, C.A.S.; Santos-Serejo, J.A. Simulation of in vitro water deficit for selecting drought-tolerant banana genotypes. Pesqui. Agropecu. Bras. 2017, 52, 1301–1304. [CrossRef]
12. Nansamba, M.; Sibiya, J.; Tumuimbise, R.; Karamura, D.; Kubiriba, J.; Karamura, E. Breeding banana (Musa spp.) for drought tolerance: A review. Plant Breed. 2020, 139, 685–696. [CrossRef]
13. Xu, T.; Sikora, R.; Hauschild, R. Fusarium oxysporum endophytes induced systemic resistance against Radopholus similis on banana. Nematology 2006, 8, 847–852. [CrossRef]
14. Gaidashova, S.V.; Uwimpuhwe, B.; Karamura, E.B. Identification of banana variety systemic resistance to nematodes in Rwanda. Afr. Crop Sci. J. 2008, 16, 27–33. [CrossRef]
15. Tripathi, L.; Atkinson, H.; Roderick, H.; Kubiriba, J.; Tripathi, J.N. Genetically engineered bananas resistant to Xanthomonas wilt disease and nematodes. Food Energy Secur. 2017, 6, 37–47. [CrossRef]
16. Njau, N.; Mwangi, M.; Gathu, R.; Mbaka, J.; Muasya, R. Banana weevil (Cosmolites sordidus) reduces availability of corms for seedling production through macropropagation technology. J. Anim. Plant Sci. 2011, 12, 1537–1542.
17. Arinaite, I.K.; Hilman, E.; Sali, R.; Barekye, A.; Kubiriba, J.; Kagezi, G.; Talwana, H.; Ntinka, C.; Raga, P.E.; Tushemereirwe, W.K.; et al. Response of banana hybrids to the banana weevil (Cosmolites sordidus) in Uganda. Uganda J. Agric. Sci. 2014, 15, 73–85. [CrossRef]
18. Twesigye, C.K.; Sekekata, K.; Kiggundu, A.; Tushemereirwe, W.; Matovu, E.; Karamura, E. C. Dormage caused by banana weevils Cosmolites sordidus (German) collected from different banana growing regions in Uganda. Agric. Food Secur. 2018, 7, 1–8. [CrossRef]
19. Monteiro, J.D.; Santos, M.; Santos, J.R.P.; Carvalho, J.R.S.; Costa, D.D.C. Identification of plant parasitic nematodes in triploid and tetraploid bananas in Brazil. Rev. Caatinga 2020, 33, 865–877. [CrossRef]
20. Galvez, L.C.; Barbosa, C.F.C.; Koh, R.B.L.; Aquino, V.M. Loop-mediated isothermal amplification (LAMP) assays for the detection of abaca bunchy top virus and banana bunchy top virus in abaca. Crop. Prot. 2020, 131, 105101. [CrossRef]
21. Sairam, S.; Selvarajan, R.; Handanahalli, S.S.; Venkataraman, S.; Sairam, S.; Selvarajan, R.; Handanahalli, S.S.; Venkataraman, S. Towards understanding the structure of the capsid of Banana Bunchy Top Virus. BioRxiv 2020. [CrossRef]
22. Tripathi, L.; Tripathi, J.N.; Tushemereirwe, W.K. Strategies for resistance to bacterial wilt disease of bananas through genetic engineering. Afr. J. Biotechnol. 2004, 3, 688–692.
23. Nakato, V.; Mahuku, G.; Coutinho, T. Xanthomonas campestris pv. musacearum: A major constraint to banana, plantain and enset production in central and east Africa over the past decade. Mol. Plant Pathol. 2018, 19, 525–536. [CrossRef]
24. Geberewold, A.Z. Review on impact of banana bacterial wilt (Xanthomonas campestris pv. Musacearum) in East and Central Africa. Cogent Food Agric. 2019, 5, 1586075. [CrossRef]
25. Studholme, D.J.; Wicker, E.; Abrare, S.M.; Aspin, A.; Bogdanove, A.; Broders, K.; Dubrow, Z.; Grant, M.; Jones, J.B.; Karamura, G.; et al. Transfer of Xanthomonas campestris pv. araceae and X. campestris pv. musacearum to X. vasicola (Vauterin) as X. vasicola pv. araceae comb. nov. and X. vasicola pv. musacearum comb. nov. and description of X. vasicola pv. vasculum nov. Phytopathology 2020, 110, 1153–1160. [CrossRef] [PubMed]
26. Timm, S.E.; Pardo, H.L.; Coello, P.R.; Navarrete, C.T.; Villegas, N.O.; Ordóñez, S.E. Identification of differentially-expressed genes in response to Mycosphaerella fijiensis in the resistant Musa accession ‘Calcutta-4 using suppression subtractive hybridization. *PloS ONE* 2016, 11, 1–17. [CrossRef]

27. Arango Isaza, R.E.; Díaz-Trujillo, C.; Dhillon, B.; Aerts, A.; Carlier, J.; Crane, C.F.; Jong, T.V.; Vries, I.; Dietrich, R.; Farmer, A.D.; et al. Combating a global threat to a clonal crop: Banana black Sigatoka pathogen Pseudocercospora fijiensis (synonym Mycosphaerella fijiensis) genomes reveal clues for disease control. *Plos Genet.* 2016, 12, e1005876. [CrossRef]

28. Vázquez-Euán, R.; Chi-Manzano, B.; Hernández-Velázquez, I.; Tzec-Símá, M.; Islas-Flores, I.; Martínez-Bolaños, L.; Canto-Canché, B. Identification of new hosts of *pseudocercospora fijiensis* suggests innovative pest management programs for black sigatoka disease in banana plantations. *Agronomy* 2019, 9, 666. [CrossRef]

29. Nascimento, F.D.S.; Sousa, Y.M.; Rocha, A.D.J.; Ferreira, C.F.; Haddad, F.; Amorim, E.P. Sources of black Sigatoka resistance in wild banana diploids. *Rev. Bras. Frutic.* 2020, 42. [CrossRef]

30. Dita, M.; Barquero, M.; Heck, D.; Mizubuti, E.S.; Staver, C.P. Fusarium wilt of banana: Current knowledge on epidemiology and research needs toward sustainable disease management. *Front. Plant. Sci.* 2018, 9, 1468. [CrossRef]

31. Arinaitwe, I.K.; Teo, C.H.; Kayat, E.; Tumuhimbise, R.; Uwimana, B.; Kubiriba, J.; Swennen, R.; Harikrishna, J.A.; Othman, R.Y. Evaluation of banana germplasm and genetic analysis of an F1 population for resistance to *Fusarium oxysporum* f. sp. cubense race 1. *Euphytica* 2019, 215, 175. [CrossRef]

32. Sun, J.; Zhang, J.; Fang, H.; Peng, L.; Wei, S.; Li, C.; Lu, J. Comparative transcriptome analysis reveals resistance-related genes and pathways in *Musa acuminate* banana ‘Gujiao 9’ in response to Fusarium wilt. *Plant. Physiol. Biochem.* 2019, 141, 83–94. [CrossRef]

33. Gonçalves, Z.S.; Haddad, F.; Amorim, V.B.O.; Ferreira, C.F.; Oliveira, S.A.S.; Amorim, E.P. Agronomic characterization and identification of banana genotypes resistant to Fusarium wilt race 1. *Eur. J. Plant. Pathol.* 2019, 155, 1093–1103. [CrossRef]

34. Ploetz, R.C.; Kema, G.H.; Ma, L.J. Impact of diseases on export and smallholder production of banana. *Annu. Rev. Phytopathol.* 2015, 53, 269–288. [CrossRef]

35. Pegg, K.G.; Coates, L.M.; O’Neill, W.T.; Turner, D.W. The epidemiology of Fusarium wilt of banana. *Front. Plant. Sci.* 2019, 10, 1395. [CrossRef]

36. Ploetz, R.C. Fusarium wilt of banana. In *Handbook of Diseases of Banana, Abacá and Ense*; Jones, D., Ed.; CABI Publishing: Wallingford, UK, 2019; pp. 207–228.

37. Li, C.; Shao, J.; Fang, H.; Peng, L.; Wei, S.; Li, C.; Lu, J. Comparative transcriptome analysis reveals resistance-related genes and pathways in *Musa acuminate* banana ‘Gujiao 9’ in response to Fusarium wilt. *Plant. Physiol. Biochem.* 2019, 141, 83–94. [CrossRef]

38. Lopes, O.P.; Maia, V.M.; Xavier, A.A.; Costa, M.R.D.; Rodrigues, M.G.V. Diversidade genética, crescimento e produção de genótipos de bananeira ‘Prata-Anã’ em área com mal do panamá. *Rev. Bras. Frutic.* 2014, 36, 924–939. [CrossRef]

39. Stover, R.H. *Fusarial Wilt (Panama Disease) of Bananas and Other Musa Species*; Commonwealth Mycological Institute: Kew, UK, 1962; p. 117.

40. Ploetz, R.C. Fusarium wilt of banana is caused by several pathogens referred to as *Fusarium oxysporum* f. sp. cubense. *Phytopathology* 2006, 96, 653–656. [CrossRef]

41. Ploetz, R.; Freeman, S.; Konkol, J.; Al-Abed, A.; Naser, Z.; Shalan, K.; Israeli, Y. Tropical race 4 of Panama disease in the Middle East. *Phytoparasitica* 2015, 43, 283–293. [CrossRef]

42. García-Bastidas, F.A.; Quintero-Vargas, J.C.; Ayala-Vasquez, M.; Schermer, T.; Seidl, M.F.; Santos-Paiva, M.; Noguera, A.M.; Aguiler-LaGalvez, C.; Wittenberg, A.; Hofsteder, R.; et al. First report of Fusarium wilt Tropical Race 4 infecting Cavendish bananas caused by *Fusarium odoratissimum* f. sp. cubense. *Plant. Dis.* 2020, 104, 994. [CrossRef]

43. FAO. Available online: http://www.fao.org/3/ca6911en/CA6911EN_TR4EN.pdf (accessed on 4 June 2020).

44. Thangavelu, R.; Edwin Raj, E.; Loganathan, M.; Pushpakanth, P.; Uma, S. Draft genome of *Fusarium oxysporum* f. sp. *cubense* strain Tropical Race-4 infecting Cavendish (AAA) group of banana in India. *Plant. Dis.* 2020, 105, 481–483. [CrossRef]

45. Gang, G.; Bizun, W.; WeiHong, M.; XiaoFen, L.; XiaoLin, Y.; Chaohua, Z.; JianHong, M.; Huicai, Z. Biocontrol of Fusarium wilt of banana: Key influence factors and strategies. *Afr. J. Microbiol. Res.* 2013, 7, 4835–4843. [CrossRef]

46. Warman, N.M.; Aitken, E.A. The movement of *Fusarium oxysporum* f. sp. *cubense* (sub-tropical race 4) in susceptible cultivars of banana. *Front. Plant. Sci.* 2018, 9, 1748. [CrossRef]

47. Mostert, D.; Molina, A.B.; Daniells, J.; Fourie, G.; Hermanto, C.; Chao, C.P.; Fabregat, E.; Sinohin, V.G.S.; Masdek, N.; Thangavelu, R.A.; et al. The distribution and host range of the banana Fusarium wilt fungus, *Fusarium oxysporum* f. sp. *cubense*, in Asia. *PLoS ONE* 2017, 12, e0181630. [CrossRef]

48. Costa, S.N.; Bragança, C.A.D.; Ribeiro, L.R.; Amorim, E.P.; Oliveira, S.A.S.; Dita, M.A.; Laranjeira, F.F.; Haddad, F. Genetic structure of *Fusarium oxysporum* f. sp. *cubense* in different regions from Brazil. *Plant. Pathol.* 2015, 64, 137–146. [CrossRef]

49. Fourie, G.; Steenkamp, E.T.; Ploetz, R.C.; Gordon, T.R.; Viljoen, A. Current status of the taxonomic position of *Fusarium oxysporum formae specialis cubense* within the *Fusarium oxysporum* complex. *Infec. Genet. Evol.* 2011, 11, 533–542. [CrossRef][PubMed]

50. Amorim, E.P.; Amorim, V.B.O.; Silva, M.S.; Haddad, F.; Ferreira, C.F.; Santos-Serejo, J.A. Developing hybrid banana varieties with improved properties. In *Achieving Sustainable Cultivation of Bananas: Germplasm and Genetic Improvement*; Kema, G.H.J., Drenth, A., Eds.; Burleigh Dodds Science Publishing: Cambridge, UK, 2021; Volume 2, pp. 1–17, ISBN 978 1 78767 344 0.
76. Sun, D.; Lu, X.; Hu, Y.; Li, W.; Hong, K.; Mo, Y.; Xie, J. Methyl jasmonate induced defense responses increase resistance to *Fusarium oxysporum* f. sp. *cubense* race 4 in banana. *Sci. Hortic.* 2013, 164, 484–491. [CrossRef]

77. Zuo, C.; Deng, G.; Li, B.; Huo, H.; Li, C.; Hu, C.; Kuang, R.; Yang, Q.; Dong, T.; Sheng, O.; et al. Germplasm screening of *Musa* spp. for resistance to *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (Foc TR4). *Eur. J. Plant. Pathol.* 2018, 151, 723–734. [CrossRef]

78. Ribeiro, L.R.; Oliveira, S.A.S.D.; Amorim, E.P.; Serejo, J.A.S.; Haddad, F. Sources of resistance to *Fusarium oxysporum* f. sp. *cubense* in banana germplasm. *Rev. Bras. Frutic.* 2018, 40, 1–8. [CrossRef]

79. Mohamed, A.A.; Mak, C.; Liew, K.W.; Ho, Y.W. Early evaluation of banana plants at nursery stage for Fusarium wilt tolerance. In *Fusarium Wilt Management: Towards Sustainable Cultivation, Proceedings of the International Workshop Banana Fusarium Wilt Diseases,* Genting Highlands Resort, Malaysia, 18–20 October 1999; Molina, A., Mak, C., Liew, K.W., Ho, Y.W., Masdek, N.K., Liew, K.W., Eds.; Biosversity International: Rome, Italy, 2001.

80. Wei, Y.; Hu, W.; Wang, Q.; Zeng, H.; Li, X.; Yan, Y.; Reiter, R.J.; He, C.; Shi, H. Identification, transcriptional and functional analysis of heat-shock protein 90s in banana (*Musa acuminata* L.) highlight their novel role in melatonin-mediated plant response to Fusarium wilt. *J. Pineal Res.* 2016, 62, e12367. [CrossRef]

81. Garcez, M.; Martins, J.A.S.; Rodrigues, E.R. Evaluation of different banana genotypes for resistance to panama disease. *Biosci. J.* 2016, 32, 431–435. [CrossRef]

82. Rodriguez, M.A.D.; Ribeiro, L.; Amarop, E.P.; Cordeiro, Z.J.M.; Silva, S.O. *Metodologia Para a Caracterização de Genótipos de Bananeira Quanto à Resistência ao Mal-do-Panamá em Casa de Vegetação;* Embrapa Mandioca e Fruticultura. Comunicado Técnico, 150; Embrapa Mandioca e Almas, Brazil, 2011; 5p.

83. Ghag, S.B.; Shekhawat, U.K.; Ganapathi, T.R. Host-induced post-transcriptional hairpin RNA-mediated gene silencing of vital fungal genes confers efficient resistance against Fusarium wilt in banana. *Plant. Biotechnol. J.* 2014, 12, 541–553. [CrossRef]

84. Smith, M.K.; Langdon, P.W.; Pegg, K.G.; Daniells, J.W. Growth, yield and Fusarium wilt resistance of six FHIA tetraploid bananas (*Musa* spp.) grown in the Australian sub-tropics. *Sci. Hortic.* 2014, 170, 176–181. [CrossRef]

85. Jones, D.R. *The Improvement and Testing of Musa: A Global Partnership. International Network for the Improvement of Banana and Plantain;* International Network for the Improvement of Banana and Plantain (INIBAP): Montpellier, France, 1994; p. 303.

86. Mohandas, S.; Sowmya, H.D.; Saxena, A.K.; Meenakshi, S.; Rani, R.T.; Mahmood, R. Transgenic banana cv. *Rasthali* (AAB, Silk gp) harboring Ace-AMP1 gene imparts enhanced resistance to *Fusarium oxysporum* f. sp. *cubense* race 1. *Sci. Hortic.* 2013, 164, 392–399. [CrossRef]

87. Nasir, N.; Pittaway, P.A.; Pegg, K.G.; Lisle, A.T. A foliar rating system for comparing the resistance of banana cultivar grown as tissue cultured plantlets in the laboratory to Fusarium wilt. *Plant. Pathol.* 2003, 52, 521–526. [CrossRef]

88. Ting, A.S.Y.; Mah, S.W.; Tee, C.S. Evaluating the feasibility of induced host resistance by endophytic isolate *Penicillium citrinum* BTF08 as a control mechanism for Fusarium wilt in banana plantlets. *Biol. Control.* 2012, 61, 155–159. [CrossRef]

89. Paul, J.Y.; Becker, D.K.; Dickman, M.B.; Harding, R.M.; Khanna, H.K.; Dale, J.L. Apoptosis-related genes confer resistance to Fusarium wilt in transgenic ‘Lady Finger’ bananas. *Afr. J. Microbiol. Res.* 2011, 5, 709–713. [CrossRef]

90. Wu, Y.; Yi, G.; Peng, X.; Huang, B.; Liu, E.; Zhang, J. Systemic acquired resistance in Cavendish banana induced by infection with an incompatible strain of *Fusarium oxysporum* f. sp. *cubense.* *J. Plant. Physiol.* 2013, 170, 1039–1046. [CrossRef]

91. Ploetz, R.C.; Vazquez, A.; Haynes, J.L. Response of new banana accessions in South Florida to Panama disease. *J. Crop. Prot.* 1999, 18, 445–449. [CrossRef]

92. Tan, Y.L.; Yi, G.J.; Peng, X.X. Rapid screening of *Musa* species for resistance to Fusarium wilt in an in vitro bioassay. *Eur. J. Plant. Pathol.* 2010, 128, 409–415. [CrossRef]

93. Aslam, R.; Siddiqui, A.; Iqbal, M.; Iqbal, M. Inheritance of resistance to *Fusarium oxysporum* f. sp. *cubense* race 1 in bananas. *Euphytica* 2013, 194, 425–430. [CrossRef]

94. Smith, L.J.; Smith, M.K.; Tee, D.; O’Keefe, D.; Galea, V.J. Development of a small-plant bioassay to assess banana grown from tissue culture for consistent infection by *Fusarium oxysporum* f. sp. *cubense.* *Australas. Plant. Path.* 2008, 37, 171–179. [CrossRef]

95. Li, W.; Ge, X.; Wu, W.; Wang, W.; Hu, Y.; Mo, Y.; Sun, D.; Shi, S.; Xie, J. Identification of defense-related genes in banana roots infected by *Fusarium oxysporum* f. sp. *cubense* tropical race 4. *Euphytica* 2015, 205, 837–849. [CrossRef]

96. Ghag, S.B.; Shekhawat, U.K.S.; Ganapathi, T.R. Characterization of Fusarium wilt resistant somaclonal variants of banana cv. *Rasthali* by cDNA-RAPD. *Mol. Biol. Rep.* 2014, 41, 7929–7935. [CrossRef] [PubMed]

97. Mohamed, A.A.; Mak, C.; Liew, K.W.; Ho, Y.W. Evaluation of banana plants at nursery stage for Fusarium wilt tolerance. In *Fusarium Wilt Management: Towards Sustainable Cultivation, Proceedings of the International Workshop Banana Fusarium Wilt Diseases,* Genting Highlands Resort, Malaysia, 18–20 October 1999; Molina, A., Mak, C., Liew, K.W., Ho, Y.W., Masdek, N.K., Liew, K.W., Eds.; Biosversity International: Rome, Italy, 2001.

98. Ghag, S.B.; Shekhawat, U.K.S.; Ganapathi, T.R. Native cell-death genes as candidates for developing wilt resistance in transgenic bananas. *Aob Plants* 2015, 83, 837–849. [CrossRef]

99. Wang, Y.; Yi, G.; Peng, X.; Huang, B.; Liu, E.; Zhang, J. Systemic acquired resistance in Cavendish banana induced by infection with an incompatible strain of *Fusarium oxysporum* f. sp. *cubense.* *J. Plant. Physiol.* 2013, 170, 1039–1046. [CrossRef]

100. Magambo, B.; Harjeet, K.; Arinaitwe, G.; Tendo, S.; Arinaitwe, I.K.; Kubiriba, J.; Tushemereirwe, W.; Dale, J. Inhibition of cell death as an approach for development of transgenic resistance against Fusarium wilt disease. *Afr. J. Biotechnol.* 2016, 15, 786–797. [CrossRef]
101. Smith, M.K.; Daniells, J.W.; Peasley, D.; O’Neill, W.; Samuelian, S.; Wright, C.; Drenth, A. Field evaluation of six Gros Michel banana accessions (Musa spp., AAA group) for agronomic performance, resistance to Fusarium wilt race 1 and yellow Sigatoka. J. Crop. Prot. 2018, 113, 84–89. [CrossRef]

102. Garcia-Bastidas, F.A.; Van der Veen, A.; Nakasato-Tagami, G.; Meijer, H.J.; Arango-Isaza, R.E.; Kema, G.H. An improved phenotyping protocol for banana disease in banana. Front. Plant. Sci. 2019, 10, 1006. [CrossRef]

103. Cheng, C.; Liu, F.; Sun, X.; Tian, N.; Mensah, R.A.; Li, D.; Lai, Z. Identification of Fusarium oxysporum f. sp. cubense tropical race 4 (Foc TR4) responsive miRNAs in banana root. Sci. Rep. 2019, 9, 1–16. [CrossRef]

104. Buregyeya, H.; Tumuhimbise, R.; Matovu, M.; Tumwesigye, K.S.; Kubiriba, J.; Nowankunda, K.; Tushemereirwe, W.K.; Karamura, D.; Karamura, E.; Kityo, R.M.; et al. Fuscumoxysporum f. sp. cubense Race 1 resistance and quality traits variations in apple banana germplasm. J. Plant. Breed. Crop. Sci. 2020, 12, 16–24. [CrossRef]

105. Sunisha, C.; Sowmya, H.D.; Usharani, T.R.; Umesha, M.; Gopalkrishna, H.R.; Saxena, A. Deployment of Stacked Antimicrobial Genes in Banana for Stable Tolerance Against Fusarium oxysporum f. sp. cubense Through Genetic Transformation. Mol. Biotechnol. 2020, 62, 8–17. [CrossRef]

106. Ahmad, F.; Martawi, N.M.; Poerba, Y.S.; Jong, H.; Schouten, H.; Kema, G.H. Genetic mapping of Fusarium wilt resistance in a wild banana Musa acuminata sp. malaccensis accession. Appl. Genet. 2020, 133, 3409–3418. [CrossRef]

107. Silva, P.R.O.; de Jesus, O.N.; Bragança, C.A.D.; Haddad, F.; Amorim, E.P.; Ferreira, C.F. Development of a thematic collection of Musa spp accessions using SCAR markers for preventive breeding against Fusarium oxysporum f. sp cubense tropical race 4. Genet. Mol. Res. 2016, 15, 15017765. [CrossRef]

108. Wang, W.; Hu, Y.; Sun, D.; Staehelin, C.; Xin, D.; Xie, J. Identification and evaluation of two diagnostic markers linked to Fusarium wilt resistance (race 4) in banana (Musa spp.). Mol. Bio. Rep. 2012, 39, 451–459. [CrossRef]

109. Cunha, C.M.; Hinz, R.H.; Pereira, A.; Tacceno, F.A.; Paulino, E.C.; Stadnik, M.J.A. SCAR Marker for identifying susceptibility to Fusarium oxysporum f. sp. cubense in banana. Sci. Hortic. 2015, 191, 108–112. [CrossRef]

110. Ahmed, F.; Martawi, N.M.; Poerba, Y.S.; Jong, H.; Schouten, H.; Kema, G.H. Genetic mapping of Fusarium wilt resistance in a wild banana Musa acuminata sp. malaccensis accession. Appl. Genet. 2020, 133, 3409–3418. [CrossRef]

111. Ni, Y.; Hu, B.; Li, X.; Chen, H.; Šamaj, J.; Xu, C. Comparative digital gene expression analysis of tissue-cultured plantlets of highly resistant and susceptible banana cultivars in response to Fusarium oxysporum. Int. J. Mol. Sci. 2018, 19, 350. [CrossRef]

112. Subramaniam, S.; Mahmod, M.; Meon, S.; Ratham, X. Genetic engineering for tolerance to Fusarium wilt race 1 in Musa sapientum cv. Rastali (ABB) using biolistic gun transformation system. Tree For. Sci. Biotechnol. 2010, 4, 65–75.

113. Poon, N.K.; Teo, C.H. Fusarium Wilt Disease of Banana: Current Development of Fusarium Resistant Banana. J. Microbiol. Biotechnol. 2019, 4, 000134. [CrossRef]
124. Ghag, S.B.; Shekhawat, U.K.S.; Ganapathi, T.R. Petunia floral defensins with unique prodomains as novel candidates for development of Fusarium wilt resistance in transgenic banana plants. PloS ONE 2012, 7, e93557. [CrossRef]

125. Hu, C.H.; Wei, Y.R.; Huang, Y.H.; Yi, G.J. An efficient protocol for the production of chi42 transgenic Furenzhi banana (Musa spp. AA group) resistant to Fusarium oxysporum. In Vitro Cell. Dev. Biol. Plant 2013, 49, 584–592. [CrossRef]

126. Ghag, S.B.; Shekhawat, U.K.S.; Ganapathi, T.R. Transgenic banana plants expressing a Stellaria media defensin gene (Sm-AMP-D1) demonstrate improved resistance to Fusarium oxysporum. Plant. Cell Tissue Organ. Cult. 2014, 119, 247–253. [CrossRef]

127. Dale, J.; James, A.; Paul, J.Y.; Khanna, H.; Smith, M.; Peraza-Echeverria, S.; Garcia-Bastidas, F.; Kema, G.; Waterhouse, P.; Mengersen, K.; et al. Transgenic Cavendish bananas with resistance to Fusarium wilt tropical race 4. Nat. Commun. 2017, 8, 1–8. [CrossRef]

128. Dou, T.; Shao, X.; Hu, C.; Liu, S.; Sheng, O.; Bi, F.; Deng, G.; Ding, L.; Li, C.; Dong, T.; et al. Host-induced gene silencing of Foc TR 4 ERG 6/11 genes exhibits superior defense response to Fusarium wilt of banana. Plant. Biotechnol. J. 2020, 18, 11–13. [CrossRef]

129. Ghag, S.B.; Shekhawat, U.K.; Hadapad, A.B.; Ganapathi, T.R. Stacking of host-induced gene silencing mediated resistance to banana bunchy top virus and fusarium wilt disease in transgenic banana plants. Curr. Trends Biotechnol. Pharm. 2015, 9, 212–221.

130. Zhang, L.; Liu, L.; Cheng, P.; Shen, H.; Rong, B.; Liu, W.; Yu, G. Identification and validation of reference genes for RT-qPCR analysis in banana (Musa spp.) under Fusarium wilt resistance induction conditions. J. Phytopathol. 2017, 165, 746–754. [CrossRef]

131. Chandrasekaran, M.; Raman, C.; Karthikeyan, K.; Paramasivan, M. Functional Annotation of Hypothetical Proteins Derived from Suppressive Subtraction Hybridization (SSH) Analysis Shows NPrI (Non-Pathogenesis Related)-Like Activity. Agronomy 2019, 9, 57. [CrossRef]

132. Wang, Z.; Jia, C.; Li, J.; Huang, S.; Xu, B.; Jin, Z. Activation of salicylic acid metabolism and signal transduction can enhance resistance to Fusarium wilt in banana (Musa acuminata L. AAA group, cv. Cavendish). Funct. Integr. Genomics 2015, 15, 47–62. [CrossRef]

133. Cheng, Z.; Yu, X.; Li, S.; Wu, Q. Genome-wide transcriptome analysis and identification of benzo[1,2-b:4,3-b']diazole-induced genes and pathways potentially associated with defense response in banana. BMC Genom. 2018, 19, 1–19. [CrossRef]

134. Thakker, J.N.; Patel, S.; Dhandhukia, P.C. Induction of defense-related enzymes in banana plants: Effect of live and dead pathogenic strain of Fusarium oxysporum f. sp. cubense. Isrn Biotechnol. 2013, 1–6. [CrossRef]

135. Nasir, N.; Dharma, A.; Habazar, T. The Chitinase Activity in Banana Seedling that Induce by Trichoderma spp as Resistance Responce to Fusarium Oxysporum f. sp. cubenese. Int. J. Adv. Sci. Eng. Inf. Technol. 2016, 6, 356–360. [CrossRef]

136. Magdama, F.; Monserrat-Maggi, L.; Serrano, L.; Onofre, J.G.; Jimenez-Gasco, M.D.M. Genetic Diversity of Fusarium oxysporum f. sp. cubenese, the Fusarium Wilt Pathogen of Banana, in Ecuador. Plants 2020, 9, 1133. [CrossRef]

137. Guo, L.; Han, L.; Yang, L.; Zeng, H.; Fan, D.; Zhu, Y.; Feng, Y.; Wang, G.; Peng, C.; Jiang, X.; et al. Genome and Transcriptome Analysis of the Fungal Pathogen Fusarium oxysporum f. sp. cubenese Causing Banana Vascular Wilt Disease. PLoS ONE 2015, 10, e0117621. [CrossRef]

138. Staver, C.; Pemsl, D.E.; Scheerer, L.; Vicente, L.P.; Dita, M. Ex ante assessment of returns on research investments to address the impact of Fusarium wilt tropical race 4 on global banana production. Front. Plant. Sci. 2020, 11. [CrossRef]

139. Limbing, X.; Hu, Y.; Bingzhi, H.; Yuerong, W. Banana research and production in China. In Advancing Banana and Plantain R&D in Asia and the Pacific; Molina, A.B., Xu, L.B., Roa, V.N., Van den Berghand, I., Borromeo, K.H., Eds.; International Network for the Improvement of Banana and Plantain (INIBAP): Brussels, Belgium, 2004; Volume 13, p. 51.

140. Simmonds, N.W. Evolution of Bananas Longman: London, UK, 1962; pp. 5–25.

141. Bancroft, J. Report of the board appointed to enquire into the cause of disease affecting livestock and plants. Votes Proc. 1876, 3, 1011–1038.

142. O'Neill, W.T.; Henderson, J.; Pattemore, J.A.; O'Dwyer, C.; Perry, S.; Beasley, D.R.; Tan, Y.P.; Smyth, A.L.; Goosem, C.H.; Thomson, K.M.; et al. Detection of Fusarium oxysporum f. sp. plantani Race 4 ERG 6/11 genes exhibits superior resistance to Fusarium wilt of banana. J. Phytopathol. 2016, 164, 213–217. [CrossRef]

143. Raman, A.S.; White, K.I.; Ranganathan, R. Origins of allostery and evolvability in proteins: A case study. Nature 2014, 488, 213–217. [CrossRef]

144. Raman, A.S.; White, K.I.; Ranganathan, R. Origins of allostery and evolvability in proteins: A case study. Cell 2016, 166, 468–480. [CrossRef]

145. Dong, H.; Ye, Y.; Guo, Y.; Li, H. Comparison trancriptome analysis revealed resistance differences of Cavendish bananas to Fusarium oxysporum f. sp. cubenese race1 and race 4. BMC Genom. 2020, 21, 122. [CrossRef]

146. Li, W.M.; Dita, M.; Rouard, M.; Wu, R.; Rous, N.; Xie, J.H.; Ge, X.J. Deep RNA-seq analysis reveals key responding aspects of wild banana relative resistance to Fusarium oxysporum f. sp. cubenese tropical race 4. Funct. Integr. Genom. 2020, 20, 551–562. [CrossRef]

147. Chen, Y.C.; Wong, C.L.; Muzzi, F.; Vlaardingerbroek, I.; Kidd, B.N.; Schenk, P.M. Root defense analysis against Fusarium oxysporum reveals new regulators to confer resistance. Sci. Rep. 2014, 2014, 5584. [CrossRef]

148. Wang, Z.; Miao, H.; Liu, J.; Xu, B.; Yao, X.; Xu, C.; Zhang, J. Musa balbisiana genome reveals subgenome evolution and functional divergence. Nat. Plants 2019, 5, 810–821. [CrossRef]

149. Davey, M.W.; Gudimella, R.; Harikrishna, J.A.; Sin, L.W.; Khalid, N.; Keulemans, J. A draft Musa balbisiana genome sequence for molecular genetics in polyploid, inter-and intra-specific Musa hybrids. BMC Genom. 2013, 14, 683. [CrossRef] [PubMed]
151. Wei, Y.; Liu, W.; Hu, W.; Liu, G.; Wu, C.; Liu, W.; Zeng, H.; He, Z.; Shi, H. Genome-wide analysis of autophagy-related genes in banana highlights MaATG8s in cell death and autophagy in immune response to Fusarium wilt. *Plant. Cell Rep.* 2017, 36, 1237–1250. [CrossRef]

152. Hwang, S.C.; Ko, W.H. Cavendish banana cultivars resistant to Fusarium wilt acquired through somaclonal variation in Taiwan. *Plant. Dis.* 2004, 88, 580–588. [CrossRef] [PubMed]

153. Ferreira, M.D.S.; Moura, É.R.D.; Lino, L.S.M.; Amorim, E.P.; Santos-Serejo, J.A.D.; Haddad, F. Selection of somaclonal variants of the cultivar 'Prata-Anã' for resistance to *Fusarium oxysporum* f. sp. cubense race 1. *Rev. Bras. Frutic.* 2020, 42. [CrossRef]

154. Ganapathi, T.R.; Higgs, N.S.; Balint-Kurti, P.J.; Arntzen, C.J.; May, G.D.; Van Eck, J.M. Agrobacterium-mediated transformation of embryogenic cell suspensions of the banana cultivar Rasthali (AAB). *Plant. Cell Rep.* 2001, 20, 157–162. [CrossRef]

155. Khanna, H.; Becker, D.; Kleidon, J.; Dale, J.L. Centrifugation assisted Agrobacterium tumefaciens-mediated transformation (CAAT) of embryogenic cell suspensions of banana (*Musa* spp. Cavendish AAA and Lady finger AAB). *Mol. Breed.* 2004, 14, 239–252. [CrossRef] [PubMed]

156. Damodaran, T.; Kumar, N.; Kavino, M. Breeding and evaluation of *Musa* hybrids resistant to *Fusarium oxysporum* f. sp. cubense race 1. *Fruits* 2009, 64, 3–12. [CrossRef]

157. Brown, A.; Tumuhimbise, R.; Amah, D.; Uwimana, B.; Nyine, M.; Mduma, H.; Talengerwa, D.; Karamura, D.; Kuriba, J.; Swennen, R. The genetic improvement of bananas and plantains (*Musa* spp.). In *Genetic Improvement of Tropical Crops*; Caligari, P.D.S., Ed.; Springer: Cham, Switzerland, 2017; pp. 219–240.

158. Nyine, M.; Uwimana, B.; Blavet, N.; Hřibová, E.; Vanrespaillé, H.; Batte, M.; Akech, V.; Brown, A.; Lorenzen, J.; Swennen, R.; et al. Genomic prediction in a multiploid crop: Genotype by environment interaction and allele dosage effects on predictive ability in banana. *Plant. Genome* 2018, 11. [CrossRef]

159. Dale, J.; Paul, J.Y.; Dugdale, B.; Harding, R. Modifying bananas: From transgenics to organics? *Sustainability* 2017, 9, 333. [CrossRef]

160. Ntui, V.O.; Tripathi, J.N.; Tripathi, L. Robust CRISPR/Cas9 mediated genome editing tool for banana and plantain (*Musa* spp.). *Curr. Plant. Biol.* 2019, 21, 100128. [CrossRef]

161. Tripathi, L.; Ntui, V.O.; Tripathi, J.N. Application of genetic modification and genome editing for developing climate-smart banana. *Food Energy Secur.* 2019, 8, e00168. [CrossRef]

162. Tripathi, J.N.; Ntui, V.O.; Ron, M.; Muiruri, S.K.; Britt, A.; Tripathi, L. CRISPR/Cas9 editing of endogenous banana streak virus in the B genome of *Musa* spp. overcomes a major challenge in banana breeding. *Commun. Biol.* 2020, 2, 1–11. [CrossRef]

163. Tripathi, L.; Ntui, V.O.; Tripathi, J.N. CRISPR/Cas9-based genome editing of banana for disease resistance. *Curr. Opin. Plant Biol.* 2020, 56, 118–126. [CrossRef]

164. Arora, S.; Steuernagel, B.; Gaurav, K.; Chandramohan, S.; Long, Y.; Matny, O.; Johnson, R.; Enk, J.; Periyannan, S.; Singh, N.; et al. Resistance gene cloning from a wild crop relative by sequence capture and association genetics. *Nat. Biotechnol.* 2019, 37, 139–143. [CrossRef]

165. Jupe, F.; Witek, K.; Verweij, W.; Sliwka, J.; Pritchard, L.; Etherington, G.J.; Maclean, D.; Cock, P.J.; Leggett, R.M.; Bryan, G.J.; et al. Resistance gene enrichment sequencing (RemSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. *Plant. J.* 2013, 76, 530–544. [CrossRef]