Review

Combating *Fusarium* Infection Using *Bacillus*-Based Antimicrobials

Noor Khan 1, Maskit Maymon 1 and Ann M. Hirsch 1,2,*

1 Department of Molecular, Cell and Developmental Biology, University of California, Los Angeles, CA 90095, USA; noor.612@gmail.com (N.K.); maskit@ucla.edu (M.M.)
2 The Molecular Biology Institute, University of California, Los Angeles, CA 90095, USA
* Correspondence: ahirsch@ucla.edu; Tel.: +1-310-206-8673

Received: 14 October 2017; Accepted: 16 November 2017; Published: 22 November 2017

Abstract: Despite efforts to control toxigenic *Fusarium* species, wilt and head-blight infections are destructive and economically damaging diseases that have global effects. The utilization of biological control agents in disease management programs has provided an effective, safe, and sustainable means to control *Fusarium*-induced plant diseases. Among the most widely used microbes for biocontrol agents are members of the genus *Bacillus*. These species influence plant and fungal pathogen interactions by a number of mechanisms such as competing for essential nutrients, antagonizing pathogens by producing fungitoxic metabolites, or inducing systemic resistance in plants. The multivariate interactions among plant-biocontrol agent-pathogen are the subject of this study, in which we survey the advances made regarding the research on the *Bacillus*-*Fusarium* interaction and focus on the principles and mechanisms of action among plant-growth promoting *Bacillus* species. In particular, we highlight their use in limiting and controlling *Fusarium* spread and infestations of economically important crops. This knowledge will be useful to define strategies for exploiting this group of beneficial bacteria for use as inoculants by themselves or in combination with other microbes for enhanced crop protection.

Keywords: *Fusarium* sp.; *Bacillus* sp.; antagonism; antimicrobial peptide; biocontrol; plant protection

1. Introduction

Crop losses due to plant diseases pose a major threat to food security worldwide. The impact of losses ranges from a modest reduction of plant-growth measurements to more serious damage leading to plant death and reduced yield [1,2]. To prevent or control such pathogenic organisms and their infestations, many approaches have been undertaken, including the development of resistant varieties through plant breeding, the production of genetically modified resistant plants, and the use of chemical inputs such as fungicides. However, all have limitations. Development of resistant varieties requires time and moreover, resistance is not universal or permanent because the pathogen often evolves to overcome host plant resistance. Consequently, in the absence of effective and economically feasible alternatives, growers still rely heavily on easy-to-use conventional chemical pesticides and fungicides [3,4]. However, the utilization of these chemicals is strongly correlated with environmental contamination and disturbances in the natural balance of the soil microflora [4]. In addition, the presence of pesticide and fungicide residues on food may have adverse effects on human health, which has also raised significant concerns. Hence, with growing consumer awareness about low cost and sustainable agricultural methods, the need for effective biological control agents (BCA) is clear [5,6].

Among a variety of bacterial genera, species of *Bacillus*, *Pseudomonas*, and *Streptomyces* have been widely used as BCA [7,8]. However, plant-growth promoting (PGP) members of the genus *Bacillus* offer advantages over other microorganisms, owing to their ubiquity, ability to form endospores,
and tolerance to fluctuating pH, temperature, and osmotic conditions [9], as well as their lack of pathogenicity [10–12]. Bacillus spp. colonize and establish robust interactions with roots by forming biofilms [13]. They promote plant growth by increasing nutrient uptake through siderophores and organic acids involved in P-solubilization, producing phytohormones, acting as bacterial antagonists, or inducing plant resistance against pathogens, as well as lysing fungal mycelia via hydrolytic enzyme synthesis and secretion [14].

Soil-borne phytopathogens are serious constraints to plant growth and productivity [15]. Most soil-borne pathogens can survive in the soil for extended periods of time where they remain dormant until they find a suitable host [16]. Fusarium species are globally important pathogens of agricultural plants and livestock, and also humans [17]. By inducing necrosis, wilting, and producing mycotoxins, Fusarium fungi are responsible for massive economic losses of many staple cereal food crops worldwide. In this review, we will focus on two of the most devastating species, Fusarium oxysporum, which causes vascular wilt, root rot, and damping-off in many plants [18] and also F. graminearum, which causes head blight on barley and wheat and infects many other cereal grasses as well [19].

Our aim is to highlight the sustainable strategies available for the control of Fusarium using beneficial Bacillus species and the mechanisms whereby they achieve disease control. We analyze the recent literature on the utilization of Bacillus species and their products in reducing crop damage by Fusarium species.

2. F. oxysporum and Vascular Wilt

The genus Fusarium, a well-known soil-borne plant pathogen, consists of a large number of plant-associated fungal species that have serious damaging effects on infected plants, such as eliciting chlorosis, necrosis, premature leaf drop, browning of the vascular system, and wilting, all of which subsequently cause significant yield losses. Fusarium species demonstrate a high level of host specificity, and, based on the plant species and cultivars they infect, are classified into more than 120 formae speciales and races [20]. Included in the genus are wilt pathogens such as F. oxysporum, F. solani, F. graminearum, and F. verticillioides.

One of the most economically destructive Fusarium species is F. oxysporum Schlecht. emend. Synd. et Hans, which infects more than 150 different plant hosts [21], including tomato (Lycopersicon spp.; F. oxysporum f. sp. lycopersici), banana (Musa spp.; F. oxysporum f. sp. cubense), cabbage (Brassica spp.; F. oxysporum f. sp. conglutinans), cotton (Gossypium spp.; F. oxysporum f. sp. vasiinfectum), flax (Linum spp.; F. oxysporum f. sp. linii), watermelon (Citrullus spp.; F. oxysporum f. sp. niveum), muskmelon (Cucumis spp.; F. oxysporum f. sp. melonis), onion (Allium spp.; F. oxysporum f. sp. cepae), pea (Pisum spp.; F. oxysporum f. sp. pisi), gladiolus (Gladiolus spp.; F. oxysporum f. sp. gladioli), and tulip (Tulipa spp.; F. oxysporum f. sp. tulipae) [20,22]. De Sain and Rep [23] reported that F. oxysporum secretes small, cysteine-rich proteins that contribute to its virulence. Additionally, the presence and absence of individual pathogenicity-related Secreted In Xylem (SIX) genes and sequence variation within the SIX genes can be used to discriminate between different formae specialis and races of F. oxysporum [24].

Recent reports of the close association between a polyphagous beetle and a new, but yet undescribed Fusarium species, have elicited major concern because this new interaction has resulted in an increase in avocado dieback disease in Los Angeles and Orange Counties, California [25]. The presence of Fusarium-induced dieback in urban landscapes throughout southern California is a potential threat to both industry and natural environments not only because of possible spread to commercial avocado fields, but also to native trees [26]. Mendel et al. [27] described a similar infestation that caused significant damage to commercial avocado orchards in Israel in 2009.

Pathogenic F. oxysporum isolates infect their hosts through the roots. They invade the xylem vessels and eventually result in lethal wilting of the infected plant. Wilting results from the restriction of movement of water in the vascular bundles [28], but the pathogenesis and invasion of plants by F. oxysporum in part is brought about by the toxic metabolites produced by the fungus.
In addition to eliciting major crop diseases, *F. oxysporum* in clinical settings causes systemic fusariosis in immunocompromised individuals [29]. López-Berges et al. [30] studied the velvet protein complex-based regulation of beauvericin mycotoxin production in *F. oxysporum* f. sp. *lycopersici* strain 4287. Of the four major components of the complex, deletion of *velA*, *velB*, and to a minor extent *velC*, caused distortions in the shape and size of microconidia, whereas *velA* and *laeA* were shown to be required for full virulence of *F. oxysporum* on tomato plants and immunodepressed mice. These data confirmed the critical contribution of the velvet protein complex in the expression of the gene cluster for beauvericin, a mycotoxin that functions as a virulence determinant.

3. *F. graminearum*, Killer of Cereals

*Fusarium graminearum* (teleomorph *Gibberella zeae* (Schwein.) Petch), the causative agent of *Fusarium* head blight (FHB) and crown rot (CR) on cereal crops is responsible for substantial economic losses every year [31]. *Fusarium* head blight is worldwide one of the most devastating fungal diseases affecting major cereal crops including wheat, barley, and maize [32,33]. The pathogen poses a two-fold threat: first, infested cereals show significantly compromised seed quality and yield, and second, the scabby grain is often contaminated with mycotoxins, which could cause serious human and livestock health damage [34,35].

4. Major *Fusarium* Disease Determinants: Mycotoxins

*Fusarium* fungi are widespread in the cereal-growing areas of the world and produce a range of mycotoxins, whose distributions are also varied [36]. Mycotoxins are secondary chemical metabolites synthesized by a variety of fungi. Numerous mycotoxins produced by *Fusarium* species with the ability to cause diseases in plants and animals have been described [37].

Although fusaria are found in all cereal-growing regions, they exhibit significant geographical differences in their natural distribution, and so do their corresponding mycotoxins, the levels of which are influenced by a number of factors with environmental conditions, crop production, and storage methods being the major determinants [38]. Toxins produced by *F. oxysporum* include fusaric acid, beauvericin (BEA), moniliformin, naphthazarins, and sambutoxin [39]. Important mycotoxins produced by other *Fusarium* species that are hazardous to human and animal health include fumonisins, the trichothecenes (T2-toxin, nivalenol, and deoxynivalenol) and zearalenone [40]. Hernandes et al. [41] demonstrated that filtered *Fusarium oxysporum* extract induced an inflammatory reaction and programmed cell death in rat skin. Similarly, de Melo and Piccinin [42] reported the toxic activity of *F. oxysporum* where the fungal culture extracts provoked reactions that produced withering in cucumber cells and plantlets, leading to cell death.

Strains of the *F. graminearum* species complex (FGSC) cause head blight and spike disease, which is of significant economic importance. The reduced grain quality comes about from the accumulation of a diversity of *F. graminearum* mycotoxins. This pathogen typically produces one of the three potential trichothece profiles: (i) deoxynivalenol (DON) and 3-acetyldeoxynivalenol (the 3ADON chemotype); (ii) DON and 15-acetyldeoxynivalenol (the 15ADON chemotype); or (iii) nivalenol (NIV), its acetylated derivatives, and low levels of DON (the NIV chemotype) [43]. Deoxynivalenol (DON), also known as vomitoxin, is the most frequently detected trichothece and contaminant in grain samples. It causes multiple effects on eukaryotic cells with inhibition of protein synthesis being the primary one [44,45]. Maier et al. [46] reported that the mycotoxin DON was the major infection causing agent for *F. graminearum* disease in wheat spikes.

5. Management of *Fusarium* Wilt

*Fusarium* wilt has been a problem for many years and numerous strategies have been proposed to control this fungal pathogen [47]. However, attempts to control the disease have shown limited success, mainly due to the emergence of new pathogenic races [48]. The documented methods employed for controlling wilt infections are: cultural, biological, i.e., resistance development,
and chemical such as the use of fungicides [49] and/or natural products [50]. Control of *Fusarium* infections is usually accomplished by applying benomyl, prochloraz, carbendazim, fludioxonil, bromuconazole, or azoxystrobin [51]. Everts et al. [52] tested the efficacy of three soil-applied fungicides, prothioconazole, acibenzolar-S-methyl, and thiophanate-methyl, each of which reduced *Fusarium* wilt of field-grown watermelon. Nevertheless, the best control option for *Fusarium* wilt disease, when available, is using resistant cultivars. *Fusarium* wilts are difficult to manage without incorporating durably resistant cultivars. A number of other options that can help reduce the severity of the disease exist, but they are not always effective by themselves. They include: soil fumigation with 1,3-dichloropropene + chloropicrin [53], chloropicrin [54], methyl isothiocyanate [54,55], propylene oxide [56], and sodium azide [56]. Other strategies used are the avoidance of infected fields, cover cropping [57], crop rotation, and the use of other agro-chemicals.

The difficulties in controlling *Fusarium* wilt have stimulated renewed interest in biological control and the use of beneficial plant growth-promoting bacteria (PGPB) as a disease management alternative. For this purpose, plant root-colonizing, beneficial bacteria and fungi including species of *Pseudomonas* (*Pseudomonas fluorescens*, *P. putida*) [58], *Bacillus* (*Bacillus subtilis*, *B. polymyxa*, and *B. amyloliquefaciens*) [59], non-pathogenic *Fusarium* [60], and Actinobacteria [61] have been selected. However, *Bacillus* species are preferred not only for their ability to form stress-resistant endospores, but also for their safety in handling.

Another approach to improve the reliability and level of performance is to combine biocontrol agents in strain mixtures [62]. Lutz et al. [63] proposed using mixtures of antagonistic bacteria and fungi, and this approach has proven to be more effective than single strain treatments against a variety of plant diseases. Dunlap et al. [64] found that mixing biocontrol *Bacillus subtilis* OH 131.1 with *Cryptococcus flavescens* (telomorph: *Filobasidiella*) led to more effective control of *Fusarium* head blight infection in wheat under both greenhouse and field settings. A study by Zalila-Kolsi et al. [65] reported the use of a tripartite combination of *B. amyloliquefaciens*, *B. subtilis*, and *Paenibacillus polymyxa* that led to the highest protection rate of wheat against *F. graminearum*, when compared to the strains used individually. This result indicates that combining compatible BCAs could be a strategic approach in controlling plant diseases.

For developing a successful plant disease management program, examination of the sum total of interactions that occur between plant and pathogen, and the subsequent elimination of those interactions, or favoring those that tip the balance in favor of the plant is essential. Reduction of pathogen viability, i.e., population density, and/or functionality, and the ability to infect the host effectively are the keys to a successful antagonist. Fruitful management of *Fusarium* wilt diseases of vegetable crops needs to be multi-faceted and should include such strategies as breeding or introducing genes for host resistance, growth of cover crops that improve soil organic matter, enhancement of plant nutrition, and avoidance of diseased transplants.

6. Biocontrol Attributes of Various *Bacillus* Species

Beneficial bacteria (particularly those belonging to *Bacillus* and the closely related genus *Paenibacillus*) that reside in close association with plant roots are of particular interest for their antifungal and plant protective properties [66]. Some *Bacillus* spp. directly antagonize fungal pathogens by competing for niches and essential nutrients [67], or by producing fungitoxic compounds [68], and also by inducing systemic acquired resistance [69]. Siderophore production by bacteria is another attribute that promotes plant growth in two ways: (1) by supplying iron to plants; and (2) depriving the fungal pathogens of this essential nutrient. Heidarzadeh and Baghaee-Ravari [70] reported that a siderophore-producing *B. pumilis* strain was an effective BCA for *Fusarium* wilt of tomato. Production of extracellular enzymes by biocontrol bacteria that causes lysis of the phytopathogenic fungal cell wall is a well-documented phenomenon [71]. DasGupta et al. [72] performed scanning electron microscopic studies that demonstrated alteration and distortion in the hyphal cell walls of *F. oxysporum* f. sp. *ciceri* in response to chitinase and β-1,3-glucanase produced by *Paenibacillus lentimorbus* B30488.
In vitro studies showed that chitinase produced by *B. subtilis* caused lysis of the postharvest yam pathogen *F. oxysporum* [73]. This result was further validated by in vivo experiments where *B. subtilis* application inhibited the incidence of *F. oxysporum* by 83% in wound cavities of yam tubers. Moreover, Zhao et al. [74] found that *B. subtilis* strain SG6 exhibited strong antagonism against *F. graminearum* in dual culture plate assays and inhibited sporulation in the pathogen. These studies were further complemented by SEM and TEM analyses that revealed evidence of pathogen cell wall lysis by the biocontrol strain. Spectrometric analysis of the bacterial culture supernatant showed that the antimicrobial peptides (AMP), fengycin and surfactin, were present.

Recently, Veliz et al. [4] reviewed the literature on the importance of chitinases in pathogen control and the use of chitinolytic microorganisms as an effective solution in controlling fungal diseases. Gomaa [75] showed the efficacy of seed treatment of chitinase purified from *Bacillus thuringiensis* NM101-19 in controlling *Fusarium* infection in soybean. Studies report some other mechanisms employed for biocontrol. Yuan et al. [76] reported that *Bacillus amyloyticus* NNN-6 produces numerous volatile compounds (VOCs) that restrict growth and spore germination of *F. oxysporum* f. sp. *cubense*. *Bacillus fortis* IAGS162 earlier had been shown to induce systemic resistance in tomato plants against *Fusarium* wilt disease [77]. Additional findings by Akram et al. [78] identified phenyl acetic acid (PAA) produced by *B. fortis* IAGS162 as the major factor responsible for efficient bacterial colonization in the plant rhizosphere and the subsequent suppression of *Fusarium* wilt disease. Recently, *B. simplex*, an emerging PGPB, has been shown to inhibit the growth of three different *Fusarium* strains. This strain and a newly identified *B. subtilis* strain also promoted legume plant growth especially when coinnoculated with *Rhizobium* [79].

### 6.1. Bacillus Peptide Antibiotics

Several species of genus *Bacillus* are known to produce antibiotics, of which the peptide antibiotics form a dominant class. Based on their biosynthetic pathway, these metabolites can be grouped into two main categories, the ribosomally synthesized peptides (including bacteriocins) and small peptides synthesized enzymatically by non-ribosomal pathways [80].

Lanthipeptides (Class I) are a group of post-translationally modified peptides characterized by the presence of lanthionine (Lan) or methyllanthionine (MeLan) bridges. Currently, they are classified into four subclasses, but only gene clusters of two of the subclasses of lanthipeptides have been identified in *Bacillus* spp. strains [81,82]. On the basis of classification provided by Abriouel et al. [81], bacteriocins can be classified into post-translationally modified and non-modified peptides (Class II; also divided into subclasses) as summarized in Figure 1. Large peptides, such as the megacins (derived from *B. megaterium*), make up Class III.

![Figure 1. Classification of bacteriocins produced by *Bacillus* species (based on Abriouel et al. [81]).](image-url)

**Class I**

- Post-translationally modified peptides
  - Subclass I.1: Single-peptide, elongated bacteriocins (Subtilin, ericin S, ericin A)
  - Subclass I.2: Other single-peptide bacteriocins (Sublancin 168, mersacidin, pauibacillin)
  - Subclass I.3: Two-peptide bacteriocins (Balduascin, lichenacin)
  - Subclass I.4: Other post-translationally modified peptides (Subtilosin A)

**Class II**

- Nonmodified small, linear peptides
  - Subclass II.1: Peptidic-like peptides (Congulins, SRCAM 37, SRCAM 602, SRCAM 1580 Class Ia)
  - Subclass II.2: Thurmec-line peptides (Thurincin H, thurincin S, thurincin 17, baehmichcin F4, cerein MRX1)
  - Subclass II.3: Other linear peptides (Ceratin 7A, ceratin 7B, lichenin, thurincin 439)

**Class III**

- Large proteins
  - Megacin A-216, megacin A-19213
6.2. Non-Ribosomal Biosynthesized Peptides

The non-ribosomal synthesis of peptide antibiotics takes place through a multistep mechanism that includes the selection and condensation of amino acid residues such as cyclic lipopeptides (iturin group) and macrolactones (surfactins, fengycins, and plipastatins) [83]. Large multienzymes known as Non-Ribosomal Peptide Synthetases (NRPS), which are composed of modularly arranged catalytic domains [84], catalyze their biosynthesis. Structural representations of non-ribosomally synthesized peptide antibiotics are illustrated in Figure 2.

![Figure 2. The structures of iturin, surfactin, and fengycin; all share a common structure consisting of a lipid tail linked to a short cyclic peptide. The derivatives of compounds in each group come from different amino acid components [85].](image)

In the context of biocontrol of wilt diseases, the three families of *Bacillus* lipopeptides, surfactins, iturins, and fengycins, have been extensively studied for their antagonistic activity [68]. Recently, Geissler et al. [86] established a high-performance thin-layer chromatography (HPTLC) method for the identification and simultaneous quantification of the cyclic lipopeptides surfactin, iturin A, and fengycin, in *Bacillus* culture samples. Sandrin et al. [87] reported strong antifungal activity of iturins and fengycins against fungal pathogens, whereas surfactins were not found to be very toxic by themselves. Nevertheless, they promoted the antagonistic potential of iturin A [88]. Surfactins have been suggested to assist in the formation of stable biofilms on host surfaces, thereby protecting the beneficial bacteria from antibiosis and competition exerted by other microorganisms [89]. Vitullo et al. [90] demonstrated the antifungal activity of purified surfactin from *B. amyloliquefaciens*, which suggested an important role of this molecule in the biocontrol of *F. oxysporum*. *Bacillus amyloliquefaciens* S76-3 isolated from diseased wheat spikes has strong antagonistic activity against *F. graminearum* [91]. Reverse-phase high performance liquid chromatography and electrospray ionization mass spectrometry analyses revealed that strain S76-3 produces three classes of cyclic lipopeptides, including iturin, plipastatin, and surfactin. However, only the iturins and plipastatin were responsible for biocontrol effectiveness.
Blacutt et al. [92] reported the presence of fengycin and surfactin lipopeptides in culture supernatants of *B. mojavensis* RRC101 that inhibited the growth of *F. verticillioides*. Microscopic analysis revealed hyphal distortions, vacuolization, and lysis of *F. verticillioides* on exposure to fengycin. Li et al. [93] reported that the encounter between *B. amyloliquefaciens* SQR9 and *F. oxysporum* resulted in an increased production of bacillomycin and fengycin, whereas when exposed to *Rhizoctonia solani* and *F. solani*, the production of surfactin increased in *B. amyloliquefaciens* SQR9, but fengycin production decreased. Zihahirwa Kulimushi et al. [94] observed much higher iturin and fengycin production in *B. subtilis* 98S on co-culturing it with *Pythium* and *Fusarium*, but a similar observation was not recorded in the presence of *Botrytis* [68]. Thus, it appears that activation of different suites of lipopeptides depends on the interacting fungal challenger and is likely to be strain-specific.

The presence of AMP biosynthetic genes has been linked to the antagonism of plant pathogens in several *Bacillus* strains, particularly the genes *ituC, bmyB, fenD* and *srfAB* [95]. The simultaneous production of different AMPs is important for an effective control of plant diseases and also is a key factor determining the broad range of antagonistic activity in *Bacillus* species. The dominance of these genes in *Bacillus* strains associated with plants strengthens the competitive role of surfactin, iturin, bacillomycin, fengycin and bacilysin in the improving the fitness of strains in fluctuating environmental conditions. The use of AMP gene markers may assist in the selection of putative BCA of plant pathogens [96].

Additional recent investigations have shed light on the fact that these lipopeptides can also influence the ecological fitness of the producing strain in terms of root colonization and their long-term persistence in the rhizosphere [94]. They also play a key role in the beneficial interaction of *Bacillus* species with plants by stimulating host defence mechanisms [97]. Choudhary and Johri [98] summarized various aspects of research on *Bacillus* plant growth-promoting rhizobacteria (PGPR) eliciting ISR, which leads to significant reductions in plant diseases coupled with enhancement in overall plant health.

Degradation of pathogen’s virulence factors by biocontrol bacteria is another promising strategy for controlling pathogen proliferation and subsequent disease infestations. For example, Guanhua et al. [99] studied the capability of *Bacillus licheniformis* CK1 on degrading zearalenone, thereby reducing its adverse effect on post-weaning female piglets.

7. Conclusions

During the past decades, chemical fungicides have been the main strategy to manage *Fusarium* infections. However, because of their non-targeted and negative effects on humans and the environment, beneficial bacteria are increasingly being tested as substitutes for the environmentally damaging chemicals. Beneficial strains of *Bacillus* rank high for their potential as BCA in part, not only for their PGPR traits, but also because they are spore-forming bacteria, which makes them easy to formulate and preserve as inoculants. With their ability to produce a range of metabolites that stimulate plant growth and reduce pathogen attack, either by suppressing fungal growth or inducing the plant immune system against pathogens, members of *Bacillus* and allied genera are preferred over other types of BCA. An overview of the multivariate influence of *Bacillus* on the interaction of pathogenic *Fusarium* and plant health is illustrated in Figure 3.

This literature survey highlights the need for a cost-effective, commercial *Bacillus*-based biofungicide that is effective against the major *Fusarium* species that cause disease. We have drawn attention to some of the key features of the biocontrol aspects of several *Bacillus* beneficial strains and have focused on the two major *Fusarium* pathogens. However, numerous *Bacillus* species that may be used as BCA and as biofertilizers are still being discovered and so far, remain untested. More research into the diversity of *Bacillus* strains and their mechanisms of biocontrol is needed to achieve an understanding of the interactions of these bacteria, particularly with other beneficial microbial inoculants.
Finally, consortia of microbial populations are more likely to harness more benefits in terms of reducing plant disease, improving crop growth, and maintaining environmental health through sustainable agriculture. More studies need to be pursued to test this hypothesis.

**Figure 3.** Schematic diagram illustrating the dynamic multifactorial interaction between *Bacillus* and *Fusarium* spp., and their relative impact on plant health.

**Acknowledgments:** This research was supported in part by a UCLA Faculty Award and a Shanbrom Family Foundation grant to A.M.H. We also thank Stefan J. Kirchanski for providing a high resolution version of Figure 3.

**Author Contributions:** N.K. conceptualized the study and wrote the manuscript. M.M. contributed intellectual advice and edited the manuscript. A.M.H. contributed intellectual advice, support, and helped in the writing of the manuscript.

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

**References**

1. Cao, Y.; Zhang, Z.; Ling, N.; Yuan, Y.; Zheng, X.; Shen, B.; Shen, Q. *Bacillus subtilis* SQR 9 can control *Fusarium* wilt in cucumber by colonizing plant roots. *Biol. Fertil. Soils* 2011, 47, 495–506. [CrossRef]
2. Mazzola, M.; Freilich, S. Prospects for biological soilborne disease control: Application of indigenous versus synthetic microbiomes. *Phytopathology* 2017, 107, 256–263. [CrossRef] [PubMed]
3. Haas, D.; Geneviève, D. Biological control of soil-borne pathogens by fluorescent pseudomonads. *Nat. Rev. Microbiol.* 2005, 3, 307–319. [CrossRef] [PubMed]
4. Veliz, E.A.; Martinez-Hidalgo, P.; Hirsch, A.M. Chitinase producing bacteria and their role in biocontrol. *AIMS Microbiol.* 2017, 3, 689–705. [CrossRef]
5. Seiber, J.N.; Coats, J.; Duke, S.O.; Gross, A.D. Biopesticides: State of the art and future opportunities. *J. Agric. Food Chem.* 2014, 62, 11613–11619. [CrossRef] [PubMed]
6. Bardin, M.; Ajouz, S.; Comby, M.; Lopez-Ferber, M.; Graillot, B.; Siegwart, M.; Nicot, P.C. Is the efficacy of biological control against plant diseases likely to be more durable than that of chemical pesticides? *Front. Plant Sci.* **2015**, *6*, 566. [CrossRef] [PubMed]

7. Ferreira, J.H.; Matthee, F.N.; Thomas, A.C. Biological control of *Eutypa lata* on grapevine by an antagonistic strain of *Bacillus subtilis*. *Phytopathology* **1991**, *81*, 283–287. [CrossRef]

8. Law, J.W.-F.; Ser, H.-L.; Khan, T.M.; Chuah, L.-H.; Pusparajah, P.; Chan, K.-G.; Goh, B.-H.; Lee, L.-H. The potential of *Streptomyces* as biocontrol agents against the rice blast fungus, *Magnaporthe oryzae* (*Pyricularia oryzae*). *Front. Microbiol.* **2017**, *8*, 3. [CrossRef] [PubMed]

9. Nicholson, W.L.; Munakata, N.; Horneck, G.; Melosh, H.J.; Setlow, P. Resistance of *Bacillus* endospores to extreme terrestrial and extraterrestrial environments. *Microbiol. Mol. Biol. Rev.* **2000**, *64*, 548–572. [CrossRef] [PubMed]

10. Angus, A.A.; Agapakis, C.M.; Fong, S.; Yerrapragada, S.; Estrada-de los Santos, P.; Yang, P.; Hirsch, A.M. Plant-associated symbiotic *Burkholderia* species lack hallmark strategies required in mammalian pathogenesis. *PLoS ONE* **2014**, *9*, e83779. [CrossRef] [PubMed]

11. Donato, V.; Ayala, F.R.; Cogliati, S.; Bauman, C.; Costa, J.B.; Lenini, C.; Grau, R. *Bacillus subtilis* biofilm extends *Caenorhabditis elegans* longevity through downregulation of the insulin-like signalling pathway. *Nat. Commun.* **2017**, *8*, 14332. [CrossRef] [PubMed]

12. Khan, N.; Arrabit, M.; Hirsch, A.M. Interactions of Plant Beneficial *Bacillus* spp. and *Caenorhabditis elegans*—A Tool to Evaluate Pathogenic Potential of Bioinoculants. 2017, manuscript in preparation.

13. Allard-Massicotte, R.; Tessier, L.; Lecuyer, F.; Lakshmanan, V.; Lucier, J.F.; Garneau, D.; Claudwell, L.; Vlamakis, H.; Bais, H.P.; Beauregard, P.B. *Bacillus subtilis* early colonization of *Arabidopsis thaliana* roots involve multiple chemotaxis receptors. *mBio* **2016**, *7*, e01664-16. [CrossRef] [PubMed]

14. Beneduzi, A.; Ambrosini, A.; Passaglia, L.M.P. Plant growth-promoting rhizobacteria (PGPR): Their potential as antagonists and biocontrol agents. *Genet. Mol. Biol.* **2012**, *35*, 1044–1051. [CrossRef] [PubMed]

15. Saraf, M.; Pandya, U.; Thakkar, A. Role of allelochemicals in plant growth promoting rhizobacteria for biocontrol of phytopathogens. *Microbiol. Res.* **2014**, *169*, 18–29. [CrossRef] [PubMed]

16. Shlevin, E.; Mahner, Y.; Katan, J. Effect of moisture on thermal inactivation of soilborne pathogens under structural solarization. *Phytopathology* **2004**, *94*, 132–137. [CrossRef] [PubMed]

17. Duan, C.; Qin, Z.; Yang, Z.; Li, W.; Sun, S.; Zou, Z.; Wang, X. Identification of pathogenic *Fusarium* spp. causing maize ear rot and potential mycotoxin production in China. *Toxins* **2016**, *8*, 186. [CrossRef] [PubMed]

18. Govern, R.J. Management of tomato diseases caused by *Fusarium oxysporum*. *Crop Protect.* **2015**, *73*, 78–92. [CrossRef]

19. Gu, Q.; Yang, Y.; Yuan, Q.; Shi, G.; Wu, L.; Lou, Z.; Huo, R.; Wu, H.; Borris, R.; Gao, X. Bacillomycin D produced by *Bacillus amyloliquefaciens* is involved in the antagonistic interaction with the plant-pathogenic fungus *Fusarium graminearum*. *Appl. Environ. Microbiol.* **2017**, *83*, e01075-17. [CrossRef] [PubMed]

20. Armstrong, G.M.; Armstrong, J.K. Formae specialis and races of *Fusarium oxysporum* causing wilt diseases. In *Fusarium: Diseases, Biology and Taxonomy*; Nelson, P.E., Toussoun, T.A., Eds.; Pennsylvania State University Press: University Park, PA, USA, 1981; pp. 391–399.

21. 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. *Infect. Genet. Evol.* **2011**, *11*, 533–542. [CrossRef] [PubMed]

22. MacHardy, W.E.; Beckman, C.H. Vascular wilt Fusaria: Infection and pathogenesis. In *Fusarium: Disease, Biology, and Taxonomy*; Nelson, P.E., Toussoun, T.A., Eds.; Pennsylvania State University Press: University Park, PA, USA, 1981; pp. 365–366.

23. De Sain, M.; Rep, M. The role of pathogen-secreted proteins in fungal vascular wilt diseases. *Int. J. Mol. Sci.* **2015**, *16*, 23970–23993. [CrossRef] [PubMed]

24. Chakrabarti, A.; Rep, M.; Wang, B.; Ashton, A.; Dodds, P.; Ellis, J. Variation in potential effector genes distinguishing Australian and non-Australian isolates of the cotton wilt pathogen *Fusarium oxysporum* f. sp. *vasinfectum*. *Plant Pathol.* **2011**, *60*, 232–243. [CrossRef]

25. Eskalen, A.; Gonzalez, A.; Wang, D.H.; Twizeyimana, M.; Mayorquin, M.; Lynch, S.C. First report of *Fusarium* sp. and its vector tea shot hole borer (*Euwallacea fornicatus*) causing *Fusarium* dieback on avocado in California. *Plant Dis.* **2012**, *96*, 1070. [CrossRef]
26. Eskalen, A.; Stouthamer, R.; Lynch, S.C.; Rugman-Jones, P.F.; Twizeyimana, M. Host range of Fusarium dieback and its ambrosia beetle (Coleoptera: Scolytinae) vector in southern California. *Plant Dis.* 2013, 97, 938–951. [CrossRef]

27. Mendel, Z.; Protosav, A.; Sharon, M.; Zveibil, A.; Ben Yahuda, S.; O'Donnell, K.; Rabaglia, R.; Wysocki, M.; Freeman, S. An Asian ambrosia beetle Euwallacea fornicatus and its novel symbiotic fungus Fusarium sp. pose a serious threat to Israeli avocado industry. *Phytoparasitica* 2012. [CrossRef]

28. Yadeta, K.A.; Thomma, B.P. The xylem as battleground for plant hosts and vascular wilt pathogens. *Front. Plant Sci.* 2013, 4, 97. [CrossRef] [PubMed]

29. Fisher, M.C.; Henk, D.A.; Briggs, C.J.; Brownstein, J.S.; Madoff, L.C.; McCraw, S.L.; Gurr, S.J. Emerging fungal threats to animal, plant and ecosystem health. *Nature* 2012, 484, 186–194. [CrossRef] [PubMed]

30. López-Berges, M.S.; Hera, C.; Sulyok, M.; Schäfer, K.; Capilla, J.; Guarro, J.; Di Pietro, A. The velvet complex governs mycotoxin production and virulence of *Fusarium oxysporum* on plant and mammalian hosts. *Mol. Microbiol.* 2013, 87, 49–65. [CrossRef] [PubMed]

31. Kazan, K.; Gardiner, D.M. Transcriptomics of cereal-*Fusarium graminearum* interactions: What we have learned so far. *Mol. Plant Pathol.* 2017. [CrossRef] [PubMed]

32. Osborne, L.E.; Stein, J.M. Epidemiology of *Fusarium* head blight on small grain cereals. *Int. J. Food Microbiol.* 2007, 119, 103–108. [CrossRef] [PubMed]

33. Del Ponte, E.M.; Valent, B.; Bergstrom, G.C. A special issue on *Fusarium* toxins. *Toxins* 2014, 6, 228. [CrossRef] [PubMed]

34. Pestka, J.J.; Smolinski, A.T. Deoxynivalenol: Toxicology and potential effects on humans. *J. Toxicol. Environ. Health Part B Crit. Rev.* 2005, 8, 39–69. [CrossRef] [PubMed]

35. Dweba, C.C.; Figlan, S.; Shimelis, H.A.; Motaung, T.E.; Sydenham, S.; Mwadzingeni, L.; Tsilo, T.J. *Fusarium* head blight of wheat: Pathogenesis and control strategies. *Crop Prot.* 2017, 91, 114–122. [CrossRef]

36. Nesic, K.; Ivanovic, S.; Nesic, V. Fusarial toxins: Secondary metabolites of *Fusarium* fungi. *Rev. Environ. Contam. Toxicol.* 2014, 228, 1–143. [PubMed]

37. Antonissen, G.; Martel, A.; Pasmans, F.; Ducatelle, R.; Verbrugghe, E.; Vandenbroucke, V.; Li, S.; Haesebrouck, F.; Van Immerseel, F.; Croubels, S. The impact of *Fusarium* mycotoxins on human and animal host susceptibility to infectious diseases. *Toxins* 2014, 6, 430–452. [CrossRef] [PubMed]

38. Battilani, P.; Pietri, A.; Barbano, C.; Scandolara, A.; Bertuzzi, T.; Marocco, A. Logistic regression modeling of cropping systems to predict fumonisin contamination in maize. *J. Agric. Food Chem.* 2008, 56, 10433–10438. [CrossRef] [PubMed]

39. Bani, M.; Rispail, N.; Evidente, A.; Rubiales, D.; Cimmino, A. Identification of the main toxins isolated from *Fusarium oxysporum* f. sp. *pisi* Race 2 and their relation with isolates’ pathogenicity. *J. Agric. Food Chem.* 2014, 62, 2574–2580. [CrossRef] [PubMed]

40. Li, C.; Zuo, C.; Deng, G.; Kuang, R.; Yang, Q.; Hu, C.; Sheng, O.; Zhang, S.; Ma, L.; Wei, Y.; et al. Contamination of bananas with beauvericin and fusaric acid produced by *Fusarium oxysporum* f. sp. *cubense*. *PLoS ONE* 2013, 8, e70226. [CrossRef] [PubMed]

41. Hernandes, L.; Marango, A.V.; Salci, T.; Svidzinski, T.I.E. Toxic thermoresentant metabolites of *Fusarium oxysporum* are capable of inducing histopathological alterations in Wistar rats. *J. Venom. Anim. Toxins Incl. Trop. Dis.* 2012, 18, 144–149. [CrossRef]

42. De Melo, I.S.; Piccinin, E. Toxic metabolites from culture filtrate of *Fusarium oxysporum* and its effects on cucumber cells and plantlets. *Rev. Microbiol.* 1999, 30, 104–106. [CrossRef]

43. Dong, F.; Qiu, J.; Xu, J.; Yu, M.; Wang, S.; Sun, Y.; Zhang, G.; Shi, J. Effect of environmental factors on Fusarium population and associated trichothecenes in wheat grain grown in Jiangsu province, China. *Int. J. Food Microbiol.* 2016, 230, 58–63. [CrossRef] [PubMed]

44. Ok, H.E.; Choi, S.-W.; Chung, S.H.; Kang, Y.-W.; Kim, D.-S.; Chun, H.S. Natural occurrence of type-B trichothecene mycotoxins in Korean cereal-based products. *Food Addit. Contam. Part B Surv. Eill.* 2011, 4, 132–140. [CrossRef] [PubMed]

45. Tian, Y.; Tan, Y.; Liu, N.; Liao, Y.; Sun, C.; Wang, S.; Wu, A. Functional agents to biologically control deoxynivalenol contamination in cereal grains. *Front. Microbiol.* 2016, 7, 395. [CrossRef] [PubMed]
46. Maier, F.J.; Miedaner, T.; Salomon, S.; Hadeler, B.; Felk, A.; Lemmens, M.; Schäfer, W. The involvement of trichothecenes in fusarioses of wheat, barley, and maize evaluated by gene disruption of the trichothecene synthase gene in three field isolates of different chemotype and aggressiveness. *Mol. Plant Pathol.* 2006, 7, 449–461. [CrossRef] [PubMed]
47. Seo, Y.; Kim, Y.H. Potential reasons for prevalence of *Fusarium* wilt in Oriental Melon in Korea. *Plant Pathol. J.* 2017, 33, 249–263. [PubMed]
48. Silva, J.C.; Bettiol, W. Potential of non-pathogenic *Fusarium oxysporum* isolates for control of *Fusarium* wilt of tomato. *Fitopatologia Brasileira* 2005, 30, 409–412. [CrossRef]
49. Compant, S.; Duffy, B.; Nowak, J.; Clément, C.; Barka, E.A. Use of plant growth promoting bacteria for biocontrol of plant diseases: Principles, mechanisms of action, and future prospects. *Appl. Environ. Microbiol.* 2005, 7, 4951–4959. [CrossRef] [PubMed]
50. Ma, Y.-T.; Fan, H.-F.; Gao, Y.-Q.; Li, H.; Zhang, A.-L.; Gao, J.-M. Natural products as sources of new fungicides (I): Synthesis and antifungal activity of acetophenone derivatives against phytopathogenic fungi. *Chem. Biol. Drug Res.* 2013, 81, 545–552. [CrossRef] [PubMed]
51. Uesugi, Y. Fungicide Classes: Chemistry, Uses and Mode of Action. In *Fungicidal Activity: Chemical and Biological Approaches to Plant Protection*; Hutson, D., Miyamoto, J., Eds.; John Wiley & Sons, Ltd.: New York, NY, USA, 1998; pp. 23–56.
52. Everts, K.L.; Himmelstein, J.C. *Fusarium* wilt of watermelon: Towards sustainable management of a re-emerging plant disease. *Crop Prot.* 2015, 73, 93–99. [CrossRef]
53. Minuto, A.; Gullino, M.L.; Lamberti, F.; D’Addabbo, T.; Tesardi, E.; Garibaldi, A. Application of an emulsifiable mixture of 1,3-dichloropropene and chloropirin against root knot nematodes and soilborne fungi for greenhouse tomatoes in Italy. *Crop Prot.* 2006, 25, 1244–1252. [CrossRef]
54. Gilreath, J.P.; Santos, B.M. Efficacy of 1,3-dichloropropene plus chloropicrin in combination with herbicides for control of a re-emerging plant disease. *Crop Prot.* 2006, 25, 690–695. [CrossRef]
55. Drinkwater, L.E.; Letourneau, D.K.; Workneh, F.; van Bruggen, A.H.C.; Shennan, C. Fundamental differences between conventional and organic tomato agroecosystems in California. *Ecol. Appl.* 1995, 5, 1098–1112. [CrossRef]
56. Santos, B.M.; Gilreath, J.P.; Motis, T.N.; Noling, J.W.; Jones, J.P.; Norton, J.A. Comparing methyl bromide alternatives for soilborne disease, nematode and weed management in fresh market tomato. *Crop Prot.* 2006, 25, 690–695. [CrossRef]
57. Heydari, A.; Pessarakli, M. A review on biological control of fungal plant pathogens using microbial antagonists. *J. Biol. Sci.* 2010, 10, 273–290. [CrossRef]
58. Arguelles-Arias, A.; Ongena, M.; Halimi, B.; Lara, Y.; Brans, A.; Joris, B.; Fickers, P. *Bacillus amyloliquefaciens* GA1 as a source of potent antibiotics and other secondary metabolites for biocontrol of plant pathogens. *Microb. Cell Fact.* 2009, 8, 63. [CrossRef] [PubMed]
59. Fravel, D.; Olivain, C.; Alabouvette, C. *Fusarium oxysporum* and its biocontrol. *New Phytol.* 2003, 157, 493–502. [CrossRef]
60. Bakker, M.G.; Glover, J.D.; Maib, J.G.; Kinkela, L.L. Plant community effects on the diversity and pathogen suppressive activity of soil streptomycetes. *Appl. Soil Ecol.* 2010, 46, 35–42. [CrossRef]
61. Pierson, E.A.; Weller, D.M. Use of mixtures of fluorescent pseudomonads to suppress take-all and improve the growth of wheat. *Phytopathology* 1994, 84, 940–947. [CrossRef]
62. Lutz, M.P.; Wenger, S.; Maurhofer, M.; Défago, G.; Duffy, B. Signaling between bacterial and fungal biocontrol agents in a strain mixture. *FEMS Microbiol. Ecol.* 2004, 48, 447–455. [CrossRef] [PubMed]
63. Dunlap, C.A.; Schisler, D.A.; Bowman, M.J.; Rooney, A.P. Genomic analysis of *Bacillus subtilis* OH 131.1 and co-culturing with *Cryptococcus flavescentis* for control of *Fusarium* head blight. *Plant Gene* 2015, 2, 1–9. [CrossRef]
64. Zalila-Kolsi, I.; Mahmoud, A.B.; Ali, H.; Sellami, S.; Nasfi, Z.; Tounsi, S.; Jamoussi, K. Antagonist effects of *Bacillus* spp. strains against *Fusarium graminearum* for protection of durum wheat (*Triticum turgidum* L. sub sp. durum). *Microbiol. Res.* 2016, 192, 148–158. [CrossRef] [PubMed]
66. Khan, N.; Mishra, A.; Nautiyal, C.S. *Paenibacillus lentimorbus* B-30488ª controls early blight disease in tomato by inducing host resistance associated gene expression and inhibiting *Alternaria solani*. *Biol. Control*. 2012, 62, 65–74. [CrossRef]

67. Whipps, J.M. Microbial interactions and biocontrol in the rhizosphere. *J. Exp. Bot.* 2001, 511, 487–511. [CrossRef]

68. Cawoy, H.; Debois, D.; Franzl, L.; De Pauw, E.; Thonart, P.; Ongena, M. Lipopeptides as main ingredients for inhibition of fungal phytopathogens by *Bacillus subtilis/amyloliquefaciens*. *Microb. Biotechnol.* 2015, 8, 281–295. [CrossRef] [PubMed]

69. Radhakrishnan, R.; Hashem, A.; Abd Allah, E.F. *Bacillus*: A biological tool for crop improvement through bio-molecular changes in adverse environments. *Front. Physiol.* 2017, 8, 667. [CrossRef] [PubMed]

70. Heidarzadeh, N.; Baghaee-Ravari, S. Application of *Bacillus* as a potential biocontrol agent of *Fusarium* wilt of tomato. *Arch. Phytopathol. Plant Protect.* 2015, 48, 13–16. [CrossRef]

71. Swiontek, B.M.; Jankiewicz, U.; Burkowska, A.; Walczak, M. Chitinolytic microorganisms and their possible application in environmental protection. *Curr. Microbiol.* 2014, 68, 71–81. [CrossRef] [PubMed]

72. DasGupta, S.M.; Khan, N.; Nautiyal, C.S. Biologic control ability of plant growth-promoting *Paenibacillus lentimorbus* NRRL B-30488 isolated from milk. *Curr. Microbiol.* 2006, 53, 502–505. [CrossRef] [PubMed]

73. Swain, R.C.; Ray, R.C.; Nautiyal, C.S. Biocontrol efficacy of *Bacillus subtilis* strains isolated from cow dung against postharvest yam (*Dioscorea rotundata* L.) pathogens. *Curr. Microbiol.* 2008, 57, 407–411. [CrossRef] [PubMed]

74. Zhao, Y.; Selvaraj, J.N.; Xing, F.; Zhou, L.; Wang, Y.; Song, H.; Tan, X.; Sun, L.; Sangare, L.; Folly, Y.M.E.; et al. Antagonistic action of *Bacillus subtilis* strain SG6 on *Fusarium graminearum*. *PLoS ONE* 2014, 9, e92486. [CrossRef] [PubMed]

75. Gomaa, E.Z. Chitinase production by *Bacillus thuringiensis* and *Bacillus licheniformis*: Their potential in antifungal biocontrol. *J. Microbiol.* 2012, 50, 103–111. [CrossRef] [PubMed]

76. Yuan, J.; Raza, W.; Shen, Q.; Huang, Q. Antifungal activity of *Bacillus amyloliquefaciens* NJN-6 volatile compounds against *Fusarium oxysporum* f. sp. *cubense*. *Appl. Environ. Microbiol.* 2012, 78, 5942–5944. [CrossRef] [PubMed]

77. Akram, W.; Anjum, T.; Ali, B.; Ahmad, A. Screening of native *Bacillus* strains to induce systemic resistance in tomato plants against *Fusarium* wilt in split root system and its field applications. *Int. J. Agric. Biol.* 2013, 15, 1289–1294.

78. Akram, W.; Anjum, T.; Ali, B. Phenylicetic acid is ISR determinant produced by *Bacillus fortis* IAGS162, which involves extensive re-modulation in metabolomics of tomato to protect against *Fusarium* wilt. *Front. Plant Sci.* 2016, 7, 498. [CrossRef] [PubMed]

79. Schwartz, A.; Ortiz, I.; Maymon, M.; Herbold, C.; Fujiwshige, N.; Vijanderan, J.; Villesla, W.; Hanamoto, K.; Diener, A.; Sanders, E.; et al. *Bacillus simplex*—A little known PGPB with anti-fungal activity-alters pea legume root architecture and nodule morphology when coinoculated with *Rhizobium leguminosarum* bv. *viciae*. *Agronomy* 2013, 3, 595–620. [CrossRef]

80. Michiko, M.N.; Zubler, P. Molecular biology of antibiotic production in *Bacillus*. *Crit. Rev. Biotechnol.* 1990, 10, 223–240.

81. Abriouel, H.; Franz, C.; El Bakali, N.; Gálvez, A. Diversity and applications of *Bacillus* bacteriocins. *FEMS Microbiol. Rev.* 2011, 35, 201–232. [CrossRef] [PubMed]

82. Barbosa, J.; Caetano, T.; Mendo, S. Class I and Class II lanthipeptides produced by *Bacillus* spp. *J. Nat. Prod.* 2015, 78, 2850–2866. [CrossRef] [PubMed]

83. Inès, M.; Dhouha, G. Lipopeptide surfactants: Production, recovery and pore forming capacity. *Peptides* 2015, 71, 100–112. [CrossRef] [PubMed]

84. Stein, T. *Bacillus subtilis* antibiotics: Structures, syntheses and specific functions. *Mol. Microbiol.* 2005, 56, 845–857. [CrossRef] [PubMed]

85. Hamley, I.W. Lipopeptides: From self-assembly to bioactivity. *Chem. Commun.* 2015, 51, 8574–8583. [CrossRef] [PubMed]
86. Geissler, M.; Oellig, C.; Moss, K.; Schwack, W.; Henkel, M.; Hausmann, R. High-performance thin-layer chromatography (HPTLC) for the simultaneous quantification of the cyclic lipopeptides surfactin, iturin A and fengycin in culture samples of Bacillus species. J. Chromatogr. B 2017, 1044–1045, 214–224. [CrossRef] [PubMed]

87. Sandrin, C.; Peypoux, F.; Michel, G. Coproduction of surfactin and iturin A, lipopeptides with surfactant and antifungal properties, by Bacillus subtilis. Biotechnol. Appl. Biochem. 1990, 12, 370–375. [PubMed]

88. Maget-Dana, R.; Thimon, L.; Peypoux, F.; Ptak, M. Surfactin/iturin A interactions may explain the synergistic effect of surfactin on the biological properties of iturin A. Biochimie 1992, 74, 1047–1051. [CrossRef]

89. Raaijmakers, J.M.; Bruijn, I.D.; Nybroe, O.; Ongena, M. Natural functions of lipopeptides from Bacillus and Pseudomonas: More than surfactants and antibiotics. FEMS Microbiol. Rev. 2010, 34, 1037–1062. [CrossRef]

90. Vitullo, D.; Di Pietro, A.; Romano, A.; Lanzotti, V.; Lima, G. Role of new bacterial surfactins in the antifungal interaction between Bacillus amyloliquefaciens and Fusarium oxysporum. Plant Pathol. 2012, 61, 689–699. [CrossRef]

91. Gong, A.D.; Li, H.P.; Yuan, Q.S.; Song, X.S.; Yao, W.; He, W.J.; Zhang, J.B.; Liao, Y.C. Antagonistic Mechanism of iturin A and piklupastatin A from Bacillus amyloliquefaciens S76-3 from wheat spikes against Fusarium graminearum. PLoS ONE 2015, 10, e0116871. [CrossRef] [PubMed]

92. Blacutt, A.A.; Mitchell, T.R.; Bacon, C.W.; Gold, S.E. Bacillus mojavensis RRC101 lipopeptides provoke physiological and metabolic changes during antagonism against Fusarium verticillioides. MPMI 2016, 29, 713–723. [CrossRef] [PubMed]

93. Li, B.; Li, Q.; Xu, Z.; Zhang, N.; Shen, Q.; Zhang, R. Responses of beneficial Bacillus amyloliquefaciens SQR9 to different soil borne fungal pathogens through the alteration of antifungal compounds production. Front. Microbiol. 2014, 5, 636. [CrossRef] [PubMed]

94. Zihalirwa Kulimushi, P.; Argüelles Arias, A.; Franzil, L.; Steels, S.; Ongena, M. Stimulation of fengycin-type antifungal lipopeptides in Bacillus amyloliquefaciens in the presence of the maize fungal pathogen Rhizomucor variabilis. Front. Microbiol. 2017, 8, 850. [CrossRef] [PubMed]

95. González-Sánchez, M.A.; Pérez-Jimenez, R.M.; Pliego, C.; Ramos, C.; de Vicente, A.; Cazorla, F.M. Biocontrol bacteria selected by a direct plant protection strategy against avocado white root rot show antagonism as a prevalent trait. J. Appl. Microbiol. 2010, 109, 65–78. [PubMed]

96. Joshi, R.; McSpadden-Gardener, B.B. Identification and characterization of novel genetic markers associated with biological control activities in Bacillus subtilis. Phytopathology 2006, 96, 145–154. [CrossRef] [PubMed]

97. Ongena, M.; Jacques, P. Bacillus lipopeptides: Versatile weapons for plant disease biocontrol. Trends Microbiol. 2008, 16, 115–125. [CrossRef] [PubMed]

98. Choudhary, D.K.; Johri, B.N. Interactions of Bacillus spp. and plants—With special reference to induced systemic resistance (ISR). Microbiol. Res. 2009, 164, 493–513. [CrossRef] [PubMed]

99. Guanhua, F.; Junfei, M.; Lihong, W.; Xin, Y.; Jeruei, L.; Zhao, X. Effect of degradation of zearalenone-contaminated feed by Bacillus licheniformis CK1 on post weaning female piglets. Toxins 2016, 8, 300.