Abstract: Bacteria under the operational group Bacillus amyloliquefaciens (OGBa) are all Gram-positive, endospore-forming, and rod-shaped. Taxonomically, the OGBa belongs to the Bacillus subtilis species complex, family Bacillaceae, class Bacilli, and phylum Firmicutes. To date, the OGBa comprises four bacterial species: Bacillus amyloliquefaciens, Bacillus siamensis, Bacillus velezensis and Bacillus nakamurai. They are widely distributed in various niches including soil, plants, food, and water. A resurgence in genome mining has caused an increased focus on the biotechnological applications of bacterial species belonging to the OGBa. The members of OGBa are known as plant growth-promoting bacteria (PGPB) due to their abilities to fix nitrogen, solubilize phosphate, and produce siderophore and phytohormones, as well as antimicrobial compounds. Moreover, they are also reported to produce various enzymes including α-amylase, protease, lipase, cellulase, xylanase, pectinase, aminotransferase, barnase, peroxidase, and laccase. Antimicrobial compounds that able to inhibit the growth of pathogens including non-ribosomal peptides and polyketides are also produced by these bacteria. Within the OGBa, various B. velezensis strains are promising for use as probiotics for animals and fishes. Genome mining has revealed the potential applications of members of OGBa for removing organophosphorus (OPs) pesticides. Thus, this review focused on the applicability of members of OGBa as plant growth promoters, biocontrol agents, probiotics, bioremediation agents, as well as producers of commercial enzymes and antibiotics. Here, the bioformulations and commercial products available based on these bacteria are also highlighted. This review will better facilitate understandings of members of OGBa and their biotechnological applications.

Keywords: plant growth-promoting bacteria; biocontrol agent; enzymes; antimicrobial compounds; probiotics; bioremediation; Bacillus amyloliquefaciens; Bacillus velezensis; Bacillus siamensis; Bacillus nakamurai

1. Introduction

In 1943, a Japanese scientist, Juichiro Fukumoto, first isolated Bacillus amyloliquefaciens from the soil. The species is named after its unique character because it produced (faciens) a liquefying (lique) α-amylase (amylo) [1,2]. Later, B. amyloliquefaciens was combined with the closely related Bacillus subtilis and Bacillus licheniformis into the B. subtilis species complex, based on phylogenetic and phenetic evidence [3]. From the B. subtilis species complex, it can be further sub-grouped into the operational group Bacillus amyloliquefaciens (OGBa) that...
comprises four bacterial species; the soil-borne \textit{B. amyloliquefaciens}, the plant-associated \textit{Bacillus siamensis} and \textit{Bacillus velezensis}, and a black-pigment-producing strain \textit{Bacillus nakamurai} [4].

Previously, several bacterial species of the OG \textit{Ba}, namely \textit{B. amyloliquefaciens} subsp. \textit{plantarum}, \textit{Bacillus methylotrophicus} and \textit{Bacillus oryzicola}, were reclassified as strains of \textit{B. velezensis} [5]. Genome-based and gene-derived phylogenetic analyses revealed that \textit{B. velezensis} belongs to a conspecific group consisting of \textit{B. velezensis}, \textit{B. amyloliquefaciens} subsp. \textit{plantarum} FZB42 (reclassified as \textit{B. velezensis} FZB42) and \textit{B. methylotrophicus}. However, \textit{B. velezensis} is distinct from the closely related species of \textit{B. amyloliquefaciens} and \textit{B. siamensis} [4]. To date, a plethora of bacterial whole-genome sequences (WGS) from members of OG\textit{Ba} have been deposited into the National Center Biological Information (NCBI) database (Table S1). As confirmed taxonomically in 2019, 223 genomes belonged to \textit{B. velezensis}, 19 belonged to \textit{B. amyloliquefaciens}, 10 belonged to \textit{B. siamensis} and 2 belonged to \textit{B. nakamurai} [6].

The members of OG\textit{Ba} are found in various niches including soil, plants, food, animal faeces and aquatic environments [4]. Currently, genome mining has revealed their applicability as plant growth-promoters, biocontrol agents, probiotics, bioremediation agents as well as producers of commercial enzymes and antibiotics [7,8]. Therefore, knowledge of the biology of the OG\textit{Ba} is imperative to understanding the special qualities of the group. This review focused on the biotechnological applications of the bacterial strains belonging to the OG\textit{Ba}.

2. An Overview of the OG\textit{Ba}

2.1. Identification and Characterization

Bacterial species from the OG\textit{Ba} are all Gram-positive bacteria and motile by peritrichous flagella. They are endospore-forming bacteria from the \textit{B. subtilis} species complex. For many years, the speciation of OG\textit{Ba} within the \textit{B. subtilis} species complex has been uncertain, often leading to erroneous and variable results. They are difficult to distinguish using classical taxonomy parameters: morphological and physiological characteristics, cell wall compositions, 16S ribosomal RNA sequence, guanine–cytosine (G+C) content, fatty acid methyl esters (FAME) and DNA–DNA hybridization (DDH) [9]. Therefore, the taxonomic status of the bacterial species belonging to the OG\textit{Ba} is constantly causing confusion to researchers, especially for non-professional taxonomy researchers.

It is worth mentioning that some studies have used protein-coding genes in order to further ascertain the degree of relatedness of the OG\textit{Ba} within the \textit{B. subtilis} species complex [10,11]. The highly conserved DNA gyrase subunit B (\textit{gyrB}), signal transduction histidine kinase \textit{CheA} (\textit{cheA}) and RNA polymerase β-subunit (\textit{rpoB}) were used for the study of speciation within the \textit{B. subtilis} species complex before the advent of multilocus sequence analysis (MLSA) [11–13]. The taxonomical status of the members of OG\textit{Ba} has been solved by genome-based [4] and gene-derived [14] phylogeny analyses. The OG\textit{Ba} comprised four species: (i) \textit{B. amyloliquefaciens}; (ii) \textit{B. siamensis}; (iii) \textit{B. velezensis}; and (iv) \textit{B. nakamurai}, as confirmed by cladistic analysis (Figure 1; Table 1).
Figure 1. Neighbor-joining phylogenetic tree based on complete rpoB nucleotide sequences of bacterial species under the B. subtilis species complex. Evolutionary analyses were conducted using the MEGAX software [15]. The optimal tree with the sum of branch length = 0.66533958 is shown. The evolutionary distances were computed using the p-distance method. Bootstrap values, based on 1000 repetitions, are indicated at the branch points. The analysis involved 19 nucleotide sequences. There were 3534 positions in the final dataset. Bar, 0.02 substitutions per nucleotide position. Bacillus cereus ATTC 14579T was used as the outgroup.

Table 1. Characterizations of bacterial species under the operational group Bacillus amyloliquefaciens.

| Characterization     | B. amyloliquefaciens | B. siamensis | B. velezensis | B. nakamurai |
|----------------------|----------------------|--------------|---------------|--------------|
| Type Strain          | DSM 7T / ATCC 23350T / F1T | KCTC 13613T / PD-A10T / BCC 22614T | NRRL B-23189T / CR-502T / CECT 5686T / LMG 22478T | NRRL B-41091T / CCUG 68786T |
| Isolation Source     | Soil and industrial \(\alpha\)-amylase fermentations | Salted crab (poo-klam) in Thailand | Brackish water sample from the river Velez at Torredelmar in Ma’laga, southern Spain | Soil in Tierra del Fuego, Argentina |
| Size                 | 0.7–0.9 × 1.8–3.0 \(\mu\)m | 0.3–0.6 × \(1.5–3.5\) \(\mu\)m | 0.5 × \(1.5–3.5\) \(\mu\)m | 0.74–0.93 × \(1.39–2.04\) \(\mu\)m |
| Endospore            | Oval spores are central or paracentral in unswollen sporangia | Ellipsoidal spores are central or sub-terminal positions in swollen sporangia | Ellipsoidal spores are paracentral or sub-terminal positions in unswollen sporangia | Ellipsoidal spores are central in unswollen sporangia |
| G + C Content (mol %) | 44.6 | 41.4 | 46.1–46.4 | 43.8 |
| Growth Temperature   | Optimal growth temperature is 30–40 °C. No growth occurs below 15 °C or above 50 °C. | Optimal growth temperature is 37 °C. Growth occurs at 4 °C and 55 °C. | Grow within the temperature range of 15–45 °C | Grow within the temperature range of 17–50 °C, with an optimum of 37 °C |
| NaCl Resistance (w/v) | Growth occurs with 0–10% NaCl | Growth occurs with 0–14% NaCl | Growth occurs with 0–12% NaCl | Growth occurs with 0–9% NaCl |
| Substrate Utilization | Tyrosine | - | - | - |
| Fermentation (acid)  | Citrate | + | - | - |
|                      | Lactose | + | + | + |
|                      | Trehalose | + | - | + |
| Reference            | [1] | [16] | [17] | [18] |

Note: All the bacterial species are able to metabolize casein, gelatin, starch, fructose, cellobiose, glucose, glycerol, maltose, mannitol, raffinose, salicin and sucrose. Symbol: +, positive result; -, negative result.
2.2. Ecology, Isolation and Cultivation

The ability to produce endospores when facing harsh conditions allowed the members of the operational group to survive in various niches including soil, animal faeces, plants, food, bee products, drugs, air, and the aquatic environments (Table S1). Evidently, the members of OG\textsubscript{Ba} had been directly isolated from rare dormant volcanic soils \[19\], mango orchards \[20\] and animal faeces \[21,22\]. They had also been isolated from plant parts including fruits (such as lemons \[23\] and apples \[24\]), roots (such as Peruvian ground cherry \[25\] and peanut roots \[26\]) and leaves (such as lucerne \[27\] and camphor leaves \[28\]).

Moreover, traditional fermented foods including bibimbap \[29\], douchi \[30\] and doenjang \[31\] were reported as the sources of isolation of bacteria from this operational group. They also were isolated from bee products \[32–34\], heroin \[35\], and air \[36\]. In other related studies, bacteria of this operational group have been isolated from water \[37\], seawater \[38\] and sea sediment \[39\]. Chicken \[40\] and fish intestines \[41\] were also reported as the sources of origin for members of this operational group.

Generally, the members of OG\textsubscript{Ba} are cultivated routinely in Luria–Bertani (LB) medium at 30–37 °C aerobically \[11,16,17\]. Some members of OG\textsubscript{Ba} such as \textit{B. nakamurai} grew well on nutrient agar (NA), trypticase soy agar (TSA), Reasoner’s 2A agar (R2A) and tryptone glucose yeast extract agar (TGY) at 30 °C for two days \[18\]. Moreover, \textit{B. velezensis} and \textit{B. siamensis} were also reported to grow well on TSA at 37 °C and 32 °C, respectively \[16,17\].

2.3. Genome and Its Arrangement

In 2019, 254 bacterial strain genomes which had been deposited in the NCBI database were reported as belonging to the OG\textsubscript{Ba} \[6\]. Some of the examined strains were found to contain plasmids (Table S1). Most of the reported strains had only one plasmid, except for \textit{B. velezensis} 157, \textit{B. velezensis} DKU\textunderscore NT\textunderscore 04, and \textit{B. velezensis} NJAU\textunderscore Z9 (all contained two plasmids), and \textit{B. velezensis} LB002 (which contained three plasmids). Interestingly, some studies have focused on the functionality of the genes carried by the plasmid. For instance, the \textit{B. velezensis} S499 plasmid, pS499, was reported as containing a \textit{rap-phr} cassette. This cassette encoded for the regulator aspartate phosphatase (\textit{rap}) and the Rap regulatory peptide (\textit{phr}) with a role in governing protease secretion, growth and motility, biofilm formation and production of surfactin \[42\]. Meanwhile, \textit{B. amyloliquefaciens} LL3 plasmid, pMC1, has a 6.8 kbp plasmid that includes a \textit{rap} which is not homologous to the pS499 \[42\]. The hypothetical \textit{rap} and the origin of replication of the pMC1 plasmid were cloned into the pKSV7, vector which brought about the production of plasmid-cured strains. The plasmid-cured strains have increases in glutamate-independent poly-\gamma-glutamic acid production by 6% as compared to the \textit{B. amyloliquefaciens} LL3 \[43\].

Genome analysis allowed for further biological studies on the members of OG\textsubscript{Ba}. The genomic and metabolic features of the members of the group were similar; however, species-specific features including secondary metabolite biosynthesis-related and energy metabolism-related genes were also identified \[4,44\]. Secondary metabolism biosynthesis-related genes are enriched in \textit{B. velezensis}, whereas energy metabolism-related genes are enriched in \textit{B. amyloliquefaciens}. In the core-genome, \textit{B. velezensis} harbors more genes involved in the biosynthesis of antimicrobial compounds as well as genes involved in \textit{D\textsubscript{y}}-galacturonate and \textit{D\textsubscript{y}}-fructuronate metabolisms compared to \textit{B. amyloliquefaciens} and \textit{B. siamensis}. Moreover, a xanthine oxidase gene cluster that is involved in metabolizing xanthine and uric acid to glycine and oxalurate was found in the core-genome of all the members of the group. Pan-genome analysis revealed the abilities of members of OG\textsubscript{Ba} to metabolize diverse carbon sources aerobically or anaerobically. Their abilities to produce various metabolites such as lactate, ethanol, xylitol, diacetyl, acetoin, and 2,3-butanediol were also identified \[44\]. In addition, genome analysis suggested that the regions of genomic plasticity controlled the function and structure of the genome and governed the adaptations to different niches \[45\]. Genome analysis also enabled the prediction of uncharacterized gene clusters and assessed the capabilities of members of OG\textsubscript{Ba} to produce antimicrobial compounds \[6\].
3. The Importance and Applications of the OGBa

3.1. Plant Growth Promoters and Biocontrol Agents in Agriculture

In the agricultural sector, the biocontrol strategy has received great attention because it provides safe, environmentally friendly, long-lasting, and inexpensive alternatives [46]. The characterizations of the bacterial strains from the OGBa as biocontrol agents were determined based on their abilities to improve plant growth and health [47]. These abilities involve multiple mechanisms including direct (improve plant growth) and indirect (improve plant health) mechanisms (Figure 2). Direct mechanisms involve nitrogen fixation, phosphate solubilization, siderophore production and phytohormone production (e.g., indole-3-acetic acid (IAA) and enzymes such as 1-amyclocyclopropane-1-carboxylate (ACC) deaminase). It has been reported that the co-inoculation of B. velezensis S141 with Bradyrhizobium diazoefficiens USDA110 into soybean resulted in enhanced nodulation and nitrogen fixation efficiency by producing larger nodules [48]. In another related study, the members of OGBa were able to solubilize phosphate, and produce IAA, ACC deaminase and siderophores [49–51].

Meanwhile, the indirect mechanism is mainly due to their biocontrol activities attributed to the production of antimicrobial compounds in response to biotic stress [52]. The members of OGBa produced antimicrobial compounds such as hydrogen cyanide (HCN) and cyclic lipopeptides such as surfactin used to inhibit the growth of pathogenic microbes [53,54]. The interactions of biocontrol agents with plant roots enhance plant resistance against some competing microbes including pathogenic bacteria, fungi and viruses. This phenomenon is termed as induced systemic resistance (ISR) [6,55].

![Figure 2](image-url)

**Figure 2.** The biological control interactions. The illustration depicts the interactions between biocontrol agents, plant pathogens, and plants. The biocontrol agent colonized the plant root surface and produced antimicrobial compounds such as surfactin. In the plant rhizosphere, antibiosis and nutrient competition interaction suppressed the growth of pathogens. Due to the production of antimicrobial compounds and in the simultaneous presence of pathogens, the induced systemic resistance (ISR) is enhanced. Thus, this mediated the defense response of the plant towards pathogens and consequently improved plant growth and the defense mechanism against pathogens.

The members of OGBa were proven to provide advantages to the agricultural sector by contributing to plant pathogen disease suppression. In plant disease management, the members of OGBa acted as plant growth-promoting bacteria (PGPB) that aid in the devel-
opment of plants and reduce the proliferation of plant pathogens (Table 2). The secretion of antimicrobial compounds such as surfactin from PGPB was suggested to trigger the pathways of ISR which contributed to the suppressive effect of plant immunity [56,57]. Surfactin was determined to act as elicitors of plant immunity and enhance resistance towards further pathogenesis in plants [47]. In the lettuce rhizosphere, increased production of surfactin by *B. velezensis* FZB42 in the axenic system was suggested to contribute to the disease suppression towards *Rhizoctonia solani* infection [53]. Similarly, the treatment using *B. velezensis* FZB42 in tobacco plants was suggested improve ISR and enhance plant height and fresh weight, while lowering the disease severity rating of the tobacco mosaic virus (TMV) [58].

Table 2. Plant pathogen suppression by members of the operational group *Bacillus amyloliquefaciens* in various plant species.

| PGPB Strain | Disease and Pathogen | Plant Species | Reference |
|-------------|----------------------|---------------|-----------|
| *B. siamensis* KCTC 13613 | R. solani, Botrytis cinerea, Micrococcus luteus | Arabidopsis thaliana | [59] |
| *B. velezensis* B5 | Anthracnose disease | Zea mays, A. thaliana | [20] |
| *B. velezensis* B1-23 | Clavibacter michiganensis subsp. michiganensis | Solanum lycopersicum | [60] |
| *B. velezensis* BTS4 | Fusarium verticillioides | Z. mays | [61] |
| *B. velezensis* BTLK6A | Magnaporthe oryzae Triticum | Triticum aestivum | [62] |
| *B. velezensis* CCG11640 | Powdery mildew disease | T. aestivum | [28] |
| *B. velezensis* CCG11640 | Botryosphaeria dothidea | Carya cathayensis | [63] |
| *B. velezensis* CCG11640 | Verticillium dahliae, R. solani, Fusarium culmorum, Ralstonia solanacearum | Matricaria chamomilla | [64] |
| *B. velezensis* GB1 | Valsa mali | Malus domestica | [65] |
| *B. velezensis* GH1-13 | Fusarium fujikuroi, R. solani, Xanthomonas oryzae | Oryza sativa | [49] |
| *B. velezensis* GQJK49 | E. solani | Lycium barbarum L. | [66] |
| *B. velezensis* GYL4 | Anthracnose disease | Cucumis sativus L. cv. Cumnima | [67] |
| *B. velezensis* J-5 | B. cinerea | S. lycopersicum | [68] |
| *B. velezensis* JK | M. oryzae | O. sativa | [69] |
| *B. velezensis* L-1 | Botryosphaeria berengeriana | Pyrus communis | [70] |
| *B. velezensis* LM2303 | Fusarium graminearum | T. aestivum | [71] |
| *B. velezensis* M27 | Sclerotinia sclerotiorum | Lactuca sativa L. | [72] |
| *B. velezensis* NJAU-Z9 | Fusarium oxysporum f. sp. niveum, Ralstonia solanacearum | Capsicum annuum L. | [73] |
| *B. velezensis* NJN-6 | F. oxysporum f. sp. cubense | Musa sp. | [74] |
| *B. velezensis* OEE1 | F. solani | Olea europea L. | [75] |
| *B. velezensis* P42 | Bacterial wilt and early blight diseases | S. lycopersicum | [76] |
| *B. velezensis* PG12 | Apple ring rot disease | Malus domestica | [24] |
| *B. velezensis* TrigoCor1448 | Fusarium head blight disease | T. aestivum | [77] |
| *B. velezensis* UCMB5113 | Alternaria brassicae, B. cinerea, Leptosphaeria maculans, Verticillium longisporum | Brassica napus | [78] |
| *B. velezensis* XK-4-1 | Verticillium wilt disease | Gossypium sp. | [79] |
| *B. velezensis* ZF2 | Corynespora leaf spot diseases | C. sativus | [80] |
Bacterial species from the OGBa are used in bioformulations. For instance, the bacterial strain *B. velezensis* FZB42 had been established as a model strain for plant growth promotion and as a biocontrol agent [55]. In 2019, tomato seeds coated with gum arabic as adhesive along with liquid bioformulations containing *B. velezensis* FZB42 showed great inhibitory effects against *Fusarium solani* infections under in vitro conditions. Increments in germination percentage and germination rate as compared with the control were also reported [81].

To date, there are a few bioformulations containing bacterial species from the OGBa available on the market (Table 3), such as SERENADE® (Bayer Crop Science, Germany) which contains *B. velezensis* QST 713 (previously *B. subtilis* QST 713) and Double Nickel 55™ (Certis Columbia, MD USA) which contains *B. velezensis* D747 (previously *B. amyloliquefaciens* D747) [55]. The application of SERENADE® together with Fracture fungicide (CEV, Portugal), which contains BLAD polypeptide, had shown notable success in controlling *Botrytis* blossom blight disease infection in blueberries [82]. Application of Double Nickel 55™ was found to be effective in controlling white mold in snap beans caused by *Sclerotinia sclerotiorum*. Double Nickel 55™, a biofungicide, was approved for organic vegetable production by the National Organic Program and Organic Materials Review Institute [83].

### Table 3. Some commercial products containing the members of the operational group *Bacillus amyloliquefaciens* available on the market.

| Bacterial Strain | Commercial Product | Company | Description |
|------------------|--------------------|---------|-------------|
| *B. velezensis* QST 713 (previously *B. subtilis* QST 713) | SERENADE Max | Bayer Crop Science, previously AgraQuest | EPA-registered biofungicide. Controls and suppresses fungal pathogens on foliage and in the soil |
| | SERENADE SOIL® | Bayer Crop Science, previously AgraQuest | EPA-registered biofungicide for food crops |
| | CEASE® | BioWorks, Inc., Victor, New York, U.S.A. | Aqueous suspension biofungicide for leafy and fruiting vegetables, herbs and spices, and ornamentals |
| *B. velezensis* FZB42 (previously *B. amyloliquefaciens* FZB42) | RhizoVital® 42 | ABiTEP GmbH, Berlin, Germany | Biofertilizer, plant-growth-promoting activity, provides protection against various soil-borne diseases |
| | FZB24® TB | ABiTEP GmbH, Berlin, Germany | Plant growth-promoting agent for plant strengthening |
| | Taegro® | Syngenta, Basel, previously Novozyme, Davis, California, and Earth Biosciences | EPA-registered biofungicide for use in North America |
| *B. velezensis* GB03 (previously *B. subtilis* GB03) | Kodiak™ | Bayer Crop Science, North Carolina, NC | EPA-registered biological seed treatment fungicide with demonstrable PGR activity. Efficient in cotton, beans, and vegetables |
| | Companion | Growth Products Ltd., White Plains, NY | EPA-registered biofungicide that prevents and controls plant diseases |
| *B. velezensis* D747 (previously *B. amyloliquefaciens* D747) | Double Nickel 55™ | Certis Columbia, MD, U.S.A. | EPA-registered biofungicide for control or suppression of fungal and bacterial plant diseases |
| | Amylo-X® | Certis Columbia, MD USA/Intrachem Bio Italia SpA | Biocontrol of *Botrytis* and other fungal diseases of grapes, strawberries, and vegetables, and bacterial diseases, such as fire blight in pome fruit and PSA in kiwi fruit |

Apart from the aforementioned uses, the members of OGBa have also been applied as biocontrol agents against parasitic nematodes and protist pathogens. In 2008, *B. velezensis* FZB42 was reported to reduce nematode eggs in roots, juvenile worms in soil and plant galls on tomato [84]. Genomic study revealed that the whole genome of *B. velezensis* FZB42 encoded a diverse spectrum of different antimicrobial compounds able to suppress harmful nematodes living within the plant rhizosphere [85]. In controlling the protist pathogen,
B. velezensis HB-26 (previously B. amyloliquefaciens HB-26) showed promising capability for controlling Plasmodiophora brassicae, a root-infecting protist that causes clubroot disease in brassica species. Many antimicrobial compounds showing specific activities against P. brassicae were found in the genome of B. velezensis HB-26 [86]. Overall, much more focus is still needed to fulfill the understanding of the molecular basis for the ability of members of OG Ba to inhibit nematodes and protists beyond in silico genomic studies. Understanding such attributes will help to shed light on the functionalities as well as the biological roles of antimicrobial compounds from OG Ba not only for improved plant growth but as biocontrol agents to minimize the proliferation of plant pathogens including viruses, bacteria, fungus, nematodes, and protists.

3.2. Source of Commercial Enzymes

Microbial enzymes such as α-amylase, protease, and lipase have been used in various biotechnological applications including textile applications, feed industry, food industry, and organic synthesis [87–89]. The U.S. Food and Drug Administration (FDA) in 1999 reported that enzymes such as α-amylase and protease originating from B. subtilis are Generally Recognized as Safe (GRAS) for use as direct food ingredients [90]. As members of the B. subtilis species complex, OG Ba bacteria are a potent bacterial group due to their abilities to produce various types of enzymes including α-amylase, protease, lipase, cellulase, xylanase, pectinase, aminotransferase, barnase, peroxidase, and laccase (Table 4).

| Bacterial Species | Enzymes | Reference |
|-------------------|---------|-----------|
| B. amyloliquefaciens KCP2 | α-amylase and protease | [91] |
| B. amyloliquefaciens NRRL 942 | α-amylase | [92] |
| B. siamensis JJC33M | α-amylase | [93] |
| B. velezensis 157 | α-amylase, cellulase, xylanase and pectinase | [94] |
| B. velezensis 275 | Cellulase, xylanase, peroxidase, and laccase | [95] |
| B. velezensis AP194 | Pectinase | [96] |
| B. velezensis AP214 | Pectinase | [96] |
| B. velezensis GZB | Laccase | [97] |
| B. velezensis JJ-D34 | α-amylase, protease and cellulase | [98] |
| B. velezensis Jxnuwx-1 | Protease | [99] |
| B. velezensis SB1216 | Barnase | [100] |
| B. velezensis SPZ1 | Lipase | [101] |
| B. velezensis SYBC H47 | Aminotransferase | [102] |
| B. velezensis ZL918 | α-amylase | [103] |

3.3. Antimicrobial Compounds Producer

The increment in the global antibiotic-resistant pathogens has led to the exploration of compounds with alternative therapeutic strategies [104]. The members of OG Ba were reported to produce antimicrobial compounds used in the suppression of pathogens [45]. The antimicrobial compounds produced by the member of OG Ba have been reviewed previously [8,105]. The members of OG Ba produced some important antimicrobial compounds (Figure 3), including non-ribosomal peptides (surfactin, fengycin, bacillomycin-D, bacilysin and bacillibactin) and polyketides (bacillaene, macrolactin and difficilein) [6,105].
Figure 3. Antimicrobial compounds produced by members of the operational group *Bacillus amyloliq- ufaciens*.

Non-ribosomal peptides produced by bacteria and fungi contain two or more moieties derived from amino acids [106]. The mode of action of non-ribosomal peptides involves the disruption to the cell membrane and inhibition on the transfer of peptidoglycan precursors to bactoprenol pyrophosphate [107]. In 2019, surfactins from *B. velezensis* 9D-6 were found to inhibit the in vitro growth of bacteria (*B. cereus*, *C. michiganensis*, *Pantoea agglomerans*, *Ralstonia solanacearum*, *Xanthomonas campestris* and *Xanthomonas euvesicatoria*) and fungi (*Alternaria solani*, *Cochliobolus carbo num*, *F. oxysporum*, *F. solani*, *Gibberella pulicaris*, *Gibberella zeae*, *Monilinia fructicola*, *Pyrenochaeta terrestris* and *R. solani*) pathogens [108]. In another related study, in silico genomic study of *B. siamensis* JFL15 had gene clusters involved in the biosynthesis of antimicrobial compounds. The LC–MS/MS analysis confirmed the presence of iturin A and bacillomycin F. Both compounds showed strong antifungal activities against *Magnap othe grisea*, *R. solani* and *Colletotrichum gloeosporioides*, as analyzed under in vitro conditions [109]. Moreover, the presence of fengycin, bacilysin, and bacillibactin had also been reported from *B. velezensis* OSY-S3 that showed inhibition activities against *Listeria innocua*, *Escherichia coli*, *Penicillium sp.*, *Cladosporium sp.* and *Staphylococcus aureus* [110].

Polyketides are biopolymers of acetate and other short carboxylates that are biosynthesized by polyketide synthases, a natural metabolite produced by microorganisms and plants which possess various antifungal and antibacterial activities [111,112]. Since the discovery of polyketides (e.g., streptomycin in 1950), the exploration of new polyketides has assisted pharmaceutical companies in isolating new antibiotic-producing strains as the main sources of antibiotics [113]. Antibacterial polyketides including bacillaene, macrolactin and difficidin were reported from *B. velezensis* OSY-GA1 [109]. Moreover, *B. velezensis* YJ11-1-4 isolated from doenjang exhibited good antimicrobial activities against bacterial
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S. aureus AH159-1. These compounds inhibited (B. velezensis) probiotic potential was proven thought the Ames test (reported as non-mutagenic) and B. velezensis present in the genome of A. hydrophila rate after fed with auratus B. velezensis found to be upregulated by factor-immune-related genes in C. auratus administration of B. velezensis salmonicida activities against a broad range of bacterial fish pathogens (JW also manifested itself as a fish probiotic [123]. Strain JW showed antibacterial and glycosidases) that can improve feed digestion and prevent intestinal disorders are manifested itself as a probiotic [119]. Genes coding for hydrolases (peptidases, phytases the probiotic effects of B. velezensis H57 [27]. In another related study, B. velezensis FTC01 manifested itself as a probiotic [119]. Genomes for hydrolases (peptidases, phytases and glycosidases) that can improve feed digestion and prevent intestinal disorders are present in the genome of B. velezensis FTC01. Additionally, peptidylprolyl isomerase (prsA) gene (a gene that is involved in bacterial adhesion and signaling of biofilm formation in the host gut) was also found. Moreover, in silico genome analysis of B. velezensis FTC01 proved the presence of gene clusters involved in the synthesis of antimicrobial peptides. Similarly, gene clusters involved in the synthesis of antimicrobial peptides were also found in the genome of B. velezensis JT3-1, a probiotic strain isolated from faeces of the domestic yak [21]. The antimicrobial activity of B. velezensis JT3-1 was confirmed using an antimicrobial assay. Strain JT3-1 manifested strong antagonistic activities against various intestinal pathogenic flora including L. monocytogenes, S. aureus, E. coli, Salmonella typhimurium, Mannheimia haemolytica, Staphylococcus hominis, Clostridium perfringens and Mycoplasma bovis.

B. velezensis B-1895 (previously B. amylobiofaciens B-1895) has been commercially used as a probiotic in the fish industry, particularly for Alburnus leobergi [120,121]. Its probiotic potential was proven thought the Ames test (reported as non-mutagenic) and antimicrobial activities (against Streptococcus intermedius and Porphyromonas gingivalis). Moreover, the endospores of B. velezensis B-1895 were found tolerant to 0.3% (w/v) bile salts and survived incubation for 4 h in MRS broth at pH 2.0–3.0. Overall, the results suggested the potential of B. velezensis B-1895 as a fish probiotic [122]. In another related study, B. velezensis JW also manifested itself as a fish probiotic [123]. Strain JW showed antibacterial activities against a broad range of bacterial fish pathogens (Aeromonas hydrophila, Aeromonas salmonicida, Lactococcus garvieae, Streptococcus agalactiae and Vibrio parahemolyticus). Dietary administration of B. velezensis JW induced an immune response in Carassius auratus. The immune-related genes in C. auratus such as interferon gamma gene (IFN- γ), tumor necrosis factor-α (TNF-α), interleukin-1 (IL-1), interleukin-4 (IL-4) and interleukin-10 (IL-10) were found to be upregulated by B. velezensis JW-supplemented diets. It is noteworthy that C. auratus fed with B. velezensis JW-supplemented diets showed improvements in survival rate after A. hydrophila infection. This was supported genomically by the presence of antimicrobial gene clusters in the genome of B. velezensis JW [122]. Moreover, a potential probiotic effect of B. velezensis V4 on the growth performance of Oncorhynchus mykiss
had also been investigated [124]. Cell-free supernatant of *B. velezensis* V4 with anti-*A. salmonicida* was shown to contain antimicrobial compounds including iturin, macrolactin and difficidin. The mortality rate of *O. mykiss* was reduced by 27% and the weight gain ratio was increased by 71% through the 1% (v/w) addition of *B. velezensis* V4. Overall, the findings demonstrated that *B. velezensis* V4 was an effective probiotic in *O. mykiss*.

The commercialization of *B. amyloliquefaciens* as a probiotic in aquaculture is not as common compared to its agricultural applications (Table 3). Ecobiol® Soluble Plus, is one of the commercial probiotic products reported as containing *B. amyloliquefaciens* at a concentration of $10^9$ CFU/g, specifically formulated for applications in poultry and swine, as well as in aquaculture. There was research conducted on the commercial probiotic Ecobiol® Soluble to observe its positive effects on the biofloc culture of *Litopenaeus vannamei* and its benefits on water quality, growth performance and the immune system of shrimps. Three doses of probiotic ($9.48 \times 10^4$, $1.90 \times 10^5$ and $3.79 \times 10^5$ CFU/g) were applied to the culture water for 42 days. At the end of the trial, there was no significant improvement in the water quality. However, it showed notable changes in the immune system of the shrimp. As compared to the control treatment, there was an increase in the total protein concentration and granular hemocytes, and a decrease in the cell number with apoptosis in the hemolymph in all treatments. Therefore, other than being mixed with feed, *B. amyloliquefaciens* in the commercial probiotic Ecobiol® Soluble Plus could also be applied directly to the culture system; this research proved it provided better resistance to shrimps against the outbreak of pathogens in shrimp biofloc systems [125].

There is much ongoing research on the development and formulations of bacterial strains belonging to the OG*Ba* as potential probiotics for commercialization purposes in the aquaculture industry. Most of the studies have emphasized probiotic feed formulations, feeding trials on a small scale before moving to field trials. For instance, dietary inclusion of *B. amyloliquefaciens* at $10^6$ CFU/g fed to zebra fish improved the expression levels of metabolism-related genes, enzyme activities and oxidative stress-related genes in the fish liver as well as enhanced their immune resistance against pathogenic *A. hydrophila* and *S. agalactiae*. In addition, the strain of *B. amyloliquefaciens* used in this study was able to express recombinant xylanase, an important enzyme that aided in better feed digestibility and efficiency [126]. In another related study, the administration of *B. amyloliquefaciens* (1 × $10^6$ CFU/g), together with *Spirulina platensis* in formulated diet for tilapia, improved growth performance and feed utilization after a 60 day feeding trial. The mRNA level of the *TNF-α* gene and the transcription of *SOD* were considerably higher in tilapia fed with dietary *B. amyloliquefaciens* and *S. platensis* compared to the control group [127]. Moreover, *B. amyloliquefaciens* at a concentration of $10^6$ CFU/mL provided significant protection to juvenile blue swimming crabs, *Portunus pelagicus*, when challenged with *Vibrio harveyi* in in vivo trials [128]. Nevertheless, further studies are necessary, mainly on probiotic formulation along with larger field trials, to strengthen the outcomes in order to be able to commercialize bacterial strains belonging to the OG*Ba* for aquaculture use.

In vivo and field trials are critical in probiotic development. Occasionally, there were negative outcomes in in vivo studies which were carried out based upon the positive results acquired from the preliminary in vitro assays, which indicated the possibility of negative correlations between trials in vitro and in vivo. Hence, it is crucial to understand and to optimize various conditions in in vivo studies or field trials including the probiotic formulation which may affect the survival, colonization, proliferation, and interaction of the probiotic with the host in a certain environment [129].

### 3.5. Potential as Bioremediation Agents

The use of microorganisms as bioremediation agents has become a burgeoning trend [130]. To date, most research focused on the plant growth-promoting activity and antimicrobial compounds of OG*Ba* is as described above. Interestingly, in 2019, *B. amyloliquefaciens* YP6 was reported to exhibit both plant growth-promoting activity and broad-spectrum organophosphorus pesticide (OP) removal [131]. In silico genome analysis of *B.
amyloliquefaciens YP6 found it to contain a variety of promising genes, including phosphorus solubilizing and OP-degrading related genes (phoD, phoA, phrC, phoE, ycsE, bcrC and yoaK), indole-3-acetic acid synthesis related genes (amhX, cgeE and epsM), and siderophores synthesis related genes (entB, menF, entC and entA). The results hinted at the potential application of B. amyloliquefaciens YP6 in agricultural and environmental remediations. Overall, much more focus is still needed to understand the OP-degrading related genes beyond in silico genome analysis. Therefore, it is necessary to conduct further studies to determine the in vitro functional genomics and the OP-degrading enzyme activities of the members of OG Ba. Understanding such attributes will help to shed light on the applicability of the OG Ba in OPs degradation and in the bioremediation processes as a whole.

4. Concluding Remark and Future Perspectives

In conclusion, the progress of the research on the biotechnological applications of bacterial species that belong to OG Ba is remarkable. The bacteria are important not only industrially, but also environmentally. A plethora of studies have addressed the abilities of the members of OG Ba as plant growth-promoters, biocontrol agents, probiotics, bioremediation agents as well as producers of commercial enzymes and antibiotics. Moreover, the use of the bacteria in optimized bioformulations as well as the demonstration of the great success of the commercialized products give us hope towards more sustainable agricultural and aquacultural industries. Owing to the listed biotechnological applications and potentials, more research should be done focusing on the integration of system biology data derived from genomics, phenomics, proteomics, metabolomics and fluxomic analyses in order to expand our basic understanding on the versatility of the members of OG Ba. Enabling the prediction of cellular functions and metabolites produced by the members of this operational group could provide fundamental knowledge towards the enhancement of the applications of their potentials in biotechnology and bioprocessing for the benefit of all.

Supplementary Materials: The following are available online at https://www.mdpi.com/2076-2607/9/3/614/s1: Table S1. Bacterial strains from the operational group Bacillus amyloliquefaciens.

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References

1. Priest, F.G.; Goodfellow, M.; Shute, L.A.; Berkeley, R.C.W. Bacillus amyloliquefaciens sp. nov., nom. rev. Int. J. Syst. Evol. Microbiol. 1987, 37, 69–71. [CrossRef]
2. Fukumoto, J. Studies on the production of bacterial amylase. 1. Isolation of bacteria secreting potent amylases and their distribution. Nippon. Nogeikagaku Kaishi 1943, 19, 487–503.
3. Berkeley, R.C.W.; Logan, N.A.; Shute, L.A.; Capey, A.G. Identification of Bacillus species. In Methods in Microbiology; Academic Press: London, UK, 1984; Volume 16, pp. 292–328.
4. Fan, B.; Blom, J.; Klenk, H.P.; Borriss, R. Bacillus amyloliquefaciens, Bacillus velezensis, and Bacillus siamensis form an “operational group B. amyloliquefaciens” within the B. subtilis species complex. Front. Microbiol. 2017, 8, 22. [CrossRef]
5. Dunlap, C.A.; Kim, S.J.; Kwon, S.W.; Rooney, A.P. *Bacillus velezensis* is not a later heterotypic synonym of *Bacillus amyloliquefaciens*; *Bacillus methylotrophicus*, *Bacillus amyloliquefaciens* subsp. plantarum and *Bacillus oryzicola* are later heterotypic synonyms of *Bacillus velezensis* based on phylogenetic. *Int. J. Syst. Evol. Microbiol.* **2016**, *66*, 1212–1217. [CrossRef] [PubMed]

6. Dunlap, C.A.; Bowman, M.J.; Rooney, A.P. Iturinic lipopeptide diversity in the *Bacillus subtilis* species group—Important antifungals for plant biocontrol applications. *Front. Microbiol.* **2019**, *10*, 1794. [CrossRef] [PubMed]

7. Ye, M.; Tang, X.; Yang, R.; Zhang, H.; Li, F.; Tao, F.; Li, F.; Wang, Z. Characteristics and application of a novel species of *Bacillus: Bacillus velezensis*. *ACS Chem. Biol.* **2018**, *13*, 500–505. [CrossRef] [PubMed]

8. Rabbee, M.F.; Sarafat Ali, M.; Choi, J.; Hwang, B.S.; Jeong, S.C.; Baek, K.H. *Bacillus velezensis*: A valuable member of bioactive molecules within plant microorganisms. *Molecules* **2019**, *24*, 1046. [CrossRef] [PubMed]

9. Auch, A.F.; von Jan, M.; Klenk, H.P.; Göker, M. Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. *Stand. Genomic Sci.* **2010**, *2*, 117–134. [CrossRef]

10. Connor, N.; Sikorski, J.; Rooney, A.P.; Kopac, S.; Koeppel, A.F.; Burger, A.; Cole, S.G.; Perry, E.B.; Krizanc, D.; Field, N.C.; et al. Ecology of speciation in the genus *Bacillus*. *Appl. Environ. Microbiol.* **2017**, *83*, 3149–3158. [CrossRef]

11. Borriss, R.; Chen, X.H.; Rueckert, C.; Blom, J.; Pukall, R.; Schumann, P.; Spröer, C.; et al. Relationship of *Bacillus amyloliquefaciens* subsp. amyloliquefaciens nov. and *Bacillus* based on complete genome sequence comparisons. *Int. J. Syst. Evol. Microbiol.* **2011**, *61*, 1786–1801. [CrossRef]

12. Chun, J.; Bae, K.S. Phylogenetic analysis of *Bacillus subtilis* and related taxa based on partial gyrA gene sequences. *Antonie Van Leeuwenhoek* **2000**, *78*, 123–127. [CrossRef]

13. Reva, O.N.; Dixelius, C.; Meijer, J.; Priest, F.G. Taxonomic characterization and plant colonizing abilities of some bacteria related to *Bacillus amyloliquefaciens* and *Bacillus subtilis*. *FEMS Microbiol. Ecol.* **2004**, *48*, 249–259. [CrossRef] [PubMed]

14. Ngalimat, M.S.; Sabri, S. Taxonomic note: Speciation within the operational group *Bacillus amyloliquefaciens* based on comparative phylogenies of housekeeping genes. *Asia-Pac. J. Mol. Biol. Biotechnol.* **2020**, *28*, 19–26. [CrossRef]

15. Kumar, S.; Stecher, G.; Li, M.; Knyaz, C.; Tamura, K. MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Mol. Biol. Evol.* **2018**, *35*, 1547–1549. [CrossRef] [PubMed]

16. Sumpavapol, P.; Tongyongk, L.; Tanasupawat, S.; Chokesajawatee, N.; Luxanani, P.; Visessanguan, W. *Bacillus siamensis* sp. nov., isolated from salted crab (poo-khem) in Thailand. *Int. J. Syst. Evol. Microbiol.* **2010**, *60*, 2364–2370. [CrossRef]

17. Ruiz-Garcia, C.; Bejar, V.; Martinez-Checa, F.; Quesada, E. *Bacillus velezensis* sp nov., a surfactant-producing bacterium isolated from the river velez in malaga, southern Spain. *Int. J. Syst. Evol. Microbiol.* **2005**, *55*, 191–195. [CrossRef]

18. Dunlap, C.A.; Saunders, L.P.; Schisler, D.A.; Leathers, T.D.; Naeem, N.; Cohen, F.M.; Rooney, A.P. *Bacillus nakamura* sp. nov., a black-pigment-producing strain. *Int. J. Syst. Evol. Microbiol.* **2016**, *66*, 2987–2991. [CrossRef]

19. Liu, B.; Ge, B.; Azhar, N.; Zhao, W.; Cui, H.; Zhang, K. Complete genome sequence of *Bacillus methylotrophicus* strain NKG-1, isolated from the changbai mountains, China. *Genome Announc.* **2018**, *6*, e01454-17. [CrossRef]

20. Balderas-Ruiz, K.A.; Bustos, P.; Santamaria, R.I.; González, V.; Cristiano-Fajardo, S.A.; Barrera-Ortiz, S.; Mezo-Villalobos, M.; Aranda-Ocampo, S.; Guevara-García, A.A.; Galindo, E.; et al. *Bacillus velezensis* 83 a bacterial strain from mango phyllosphere, useful for biological control and plant growth promotion. *AMB Express* **2020**, *10*, 163. [CrossRef]

21. Li, Y.; Li, X.; Jia, D.; Liu, J.; Wang, J.; Liu, A.; Liu, Z.; Guan, G.; Liu, G.; Luo, J.; et al. Complete genome sequence of *Bacillus velezensis* JT3-1, a microbial germicide isolated from yak feces. *bioRxiv* **2019**, 1, 555219. [CrossRef] [PubMed]

22. Nannan, C.; Gillis, A.; Caulier, S.; Mahillon, J. Complete genome sequence of *Bacillus velezensis* CN026 exhibiting antagonistic activity against Gram-negative foodborne pathogens. *Genome Announce*. **2018**, *6*, e01543-17. [CrossRef] [PubMed]

23. Zhang, Y.; Wang, Y.; Qin, Y.; Li, P. Complete genome sequence of *Bacillus velezensis* LPL-K103, an antifungal cyclic lipopeptide bacillomycin L producer from the surface of lemon. *3 Biotech* **2020**, *10*, 8. [CrossRef]

24. Zeng, Q.; Xie, J.; Li, Y.; Chen, X.; Wang, Q. Draft genome sequence of an endophytic biocontrol bacterium, *Bacillus velezensis* PG12, isolated from apple fruit. *Microbiol. Resour. Announc.* **2019**, *8*, e00468-19. [CrossRef] [PubMed]

25. Gamez, R.M.; Rodriguez, F.; Bernal, J.F.; Agarwala, R.; Landsman, D.; Mariño-Ramírez, L. Genome sequence of the banana plant growth-promoting rhizobacterium *Bacillus amyloliquefaciens* BS06. *Genome Announc.* **2015**, *3*, e01391-15. [CrossRef] [PubMed]

26. Chen, L.; Shi, H.; Heng, J.; Wang, D.; Bion, K. Antimicrobial, plant growth-promoting and genomic properties of the peanut endophyte *Bacillus velezensis* LDO2. *Microbiol. Res.* **2019**, *218*, 41–48. [CrossRef] [PubMed]

27. Schofield, B.J.; Skarshewski, A.; Lachner, N.; Ouwerverkerk, D.; Klieve, A.V.; Dart, P.; Hugenholtz, P. Near complete genome sequence of the animal feed probiotic, *Bacillus amyloliquefaciens* H57. *Stand. Genomic Sci.* **2016**, *11*, 60. [CrossRef] [PubMed]

28. Cai, X.; Kang, X.; Xi, H.; Liu, C.; Xue, Y. Complete genome sequence of the endophytic biocontrol strain *Bacillus velezensis* CC09. *Genome Announc.* **2016**, *4*, e01048-16. [CrossRef] [PubMed]

29. Geng, W.; Cao, M.; Song, C.; Zhang, W.; Jin, Y.; Du, Y.; et al. Complete genome sequence of *Bacillus amyloliquefaciens* LL3, which exhibits glutamic acid-independent production of poly-γ-glutamic acid. *J. Bacteriol.* **2011**, *193*, 3393–3394. [CrossRef] [PubMed]

30. Deng, Q.; Wang, R.; Sun, D.; Sun, L.; Wang, Y.; Pu, Y.; Fang, Z.; Xu, D.; Liu, Y.; Ye, R.; et al. Complete genome of *Bacillus velezensis* CMT-6 and comparative genome analysis reveals lipopeptide diversity. *Biochem. Genet.* **2020**, *58*, 1–15. [CrossRef] [PubMed]
31. Khalaf, E.M.; Raizada, M.N. Draft genome sequences of Bacillus and Paenibacillus species isolated from seeds of Citrullus lanatus (watermelon), Cucurbita moschata (butternut squash), and Cucurbita pepo L. var pepo L. (pumpkin). Microbiol. Resour. Announc. 2020, 9, e00727-20. [CrossRef] [PubMed]

32. Zhao, X.; Zhou, Z.; Han, Y.; Wang, Z.; Fan, J.; Xiao, H. Isolation and identification of antifungal peptides from Bacillus BH072, a novel bacterium isolated from honey. Microbiol. Res. 2013, 168, 598–606. [CrossRef]

33. Ngalimat, M.S.; Rahman, R.N.Z.R.A.; Yusof, M.T.; Syahir, A.; Sabri, S. Characterisation of bacteria isolated from the stingless bee, Heterotrigona itama, honey, bee bread and propolis. Peer 2019, 7, e7478. [CrossRef] [PubMed]

34. Zulkhairi Amin, F.A.; Sabri, S.; Ismail, M.; Chan, K.W.; Ismail, N.; Mohd Lila, M.A.; Zawawi, N. Probiotic properties of Bacillus strains isolated from stingless bee (Heterotrigona itama) honey collected across Malaysia. Int. J. Environ. Res. Public Health 2020, 17, 278. [CrossRef]

35. Kalinowski, J.; Ahrens, B.; Al-Dilaimi, A.; Winkler, A.; Schleenbecker, U.; Rückert, C.; Wölfel, R.; Grass, G. Isolation and whole genome analysis of endospore-forming bacteria from honey. Forensic Sci. Int. Genet. 2018, 32, 1–6. [CrossRef] [PubMed]

36. Lim, S.B.Y.; Junqueira, A.C.M.; Uchida, A.; Purbojati, R.W.; Houghton, J.N.I.; Ch

37. Guo, W.; Cui, P.; Chen, X. Complete genome of Bacillus sp. Pc3 isolated from the Antarctic seawater with antimicrobial activity. Mar. Genomics 2015, 20, 1–2. [CrossRef] [PubMed]

38. Agersø, Y.; Stuer-Lauridsen, B.; Bjerre, K.; Jensen, M.G.; Johansen, E.; Bennedsen, M.; Brockmann, E.; Nielsen, B. Antimicrobial susceptibility testing and tentative epidemiological cutoff values for five Bacillus species relevant for use as animal feed additives or for plant protection. Appl. Environmetal Microbiol. 2018, 84, e01108-18. [CrossRef]

39. Pan, H.Q.; Li, Q.L.; Hu, J.C. The complete genome sequence of Bacillus velezensis 9912D reveals its biocontrol mechanism as a novel commercial biological fungicide agent. J. Biotechnol. 2017, 247, 25–28. [CrossRef] [PubMed]

40. Guo, Y.; Zhou, J.; Tang, Y.; Ma; Q.; Zhang, J.; Ji, C.; Zhao, L. Characterization and genome analysis of a zearalenone-degrading Bacillus velezensis strain ANS801E. Curr. Microbiol. 2020, 77, 273–278. [CrossRef] [PubMed]

41. Wu, J.; Xu, G.; Jin, Y.; Sun, C.; Zhou, L.; Lin, G.; Xu, R.; Wei, L.; Fei, H.; Wang, D.; et al. Isolation and characterization of Bacillus sp. GFP-2, a novel Bacillus strain with antimicrobial activities, from whitespotted bamboo shark intestine. AMB Express 2018, 8, 84. [CrossRef]

42. Molinatto, G.; Franzil, L.; Steels, S.; Puopolo, G.; Pertot, I.; Ongena, M. Key impact of an uncommon plasmid on the Bacillus amyloliquefaciens subsp. plantarum S499 developmental traits and lipopeptide production. Front. Microbiol. 2017, 8, 17. [CrossRef]

43. Feng, J.; Gu, Y.; Wang, J.; Song, C.; Yang, C.; Xie, H.; Zhang, W.; Wang, S. Curing the plasmid pMC1 from the poly (γ-glutamic acid) producing Bacillus amyloliquefaciens LL3 strain using plasmid incompatibility. Appl. Biochem. Biotechnol. 2013, 171, 532–542. [CrossRef]

44. Chun, B.H.; Kim, K.H.; Jeong, S.E.; Jeon, C.O. Genomic and metabolic features of the Bacillus amyloliquefaciens group—B. amyloliquefaciens, B. velezensis, and B. siamensis—revealed by pan-genome analysis. Food Microbiol. 2019, 77, 146–157. [CrossRef]

45. Belbahri, L.; Chenari Bouket, A.; Rekik, I.; Alenezi, F.N.; Vallat, A.; Petrovova, E.; Oszako, T.; Cherrad, S.; Vacher, é; et al. Comparative genomics of Bacillus amyloliquefaciens strains reveals a core genome with traits for habitat adaptation and a secondary metabolites rich accessory genome. Front. Microbiol. 2017, 8, 1438. [CrossRef] [PubMed]

46. Kashyap, B.K.; Solanki, M.K.; Pednekar, A.D.; Prabha, S.; Kumar, P.; Kumari, B. Bacillus as plant growth promoting rhizobacteria (PGPR): A promising green agriculture technology. In Plant Health under Biotic Stress; Springer Nature Singapore Pte Ltd.: Singapore, 2019; pp. 219–236.

47. Chowdhury, S.P.; Hartmann, A.; Gao, X.; Borris, R. Biocontrol mechanism by root-associated Bacillus amyloliquefaciens FZB42—A Review. Front. Microbiol. 2015, 6, 780. [CrossRef]

48. Sibponkrung, S.; Kondo, T.; Tanaka, K.; Tittabutr, P.; Boonkerd, N.; Yoshida, K.I.; Teanmuang, N. Co-inoculation of Bacillus velezensis strain S141 and Bradyrhizobium strains promotes nodule growth and nitrogen fixation. Microorganisms 2020, 8, 678. [CrossRef] [PubMed]

49. Kim, S.Y.; Song, H.; Sang, M.K.; Weon, H.Y.; Song, J. The Complete genome sequence of Bacillus velezensis strain GH1-13 reveals agriculturally beneficial properties and a unique plasmid. J. Biotechnol. 2017, 259, 221–227. [CrossRef] [PubMed]

50. Lu, K.; Jin, Q.; Lin, Y.; Lu, W.; Li, S.; Zhou, C.; Jin, J.; Jiang, Q.; Ling, L.; Xiao, M. Cell-free fermentation broth of Bacillus velezensis strain S3-1 improves pak choi nutritional quality and changes the bacterial community structure of the rhizosphere soil. Front. Microbiol. 2020, 11, 2043. [CrossRef] [PubMed]

51. Wang, C.; Zhao, D.; Qi, G.; Mao, Z.; Hu, X.; Du, B.; Liu, K.; Ding, Y. Effects of Bacillus velezensis FKM10 for promoting the growth of Malus hupehensis rehd. and inhibiting Fusarium verticillioides. Front. Microbiol. 2020, 10, 2889. [CrossRef]

52. Kumar, A.; Kumar, R.; Kumari, M.; Goldar, S. Enhancement of plant growth by using PGPR for a sustainable agriculture: A review. Int. J. Curr. Microbiol. Appl. Sci. 2020, 9, 152–165. [CrossRef] [PubMed]

53. Chowdhury, S.P.; Uhl, J.; Grosch, R.; Alquéres, S.; Pittroff, S.; Dietel, K.; Schmitt-Kopplin, P.; Borris, R.; Hartmann, A. Cyclic lipopeptides of Bacillus amyloliquefaciens subsp. plantarum colonizing the lettuce rhizosphere enhance plant defense responses toward the bottom rot pathogen Rhizoctonia solani. Mol. Plant-Microbe Interact. 2015, 28, 984–995. [CrossRef] [PubMed]
54. Li, B.; Li, Q.; Xu, Z.; Zhang, N.; Shen, Q.; Zhang, R. Responses of beneficial Bacillus amyloliquefaciens SQR9 to different soilborne fungal pathogens through the alteration of antifungal compounds production. *Front. Microbiol.* 2014, 5, 636. [CrossRef] [PubMed]

55. Fan, B.; Wang, C.; Song, X.; Ding, X.; Wu, L.; Wu, H.; Gao, X.; Borriss, R. *Bacillus velezensis* FZB42 in 2018: The Gram-positive model strain for plant growth promotion and biocontrol. *Front. Microbiol.* 2018, 9, 2491. [CrossRef]

56. Doornbos, R.F.; van Loon, L.C.; Bakker, P.A. Impact of root exudates and plant defense signaling on bacterial communities in the rhizosphere. a review. *Agron. Sustain. Dev.* 2012, 32, 227–243. [CrossRef]

57. Erlacher, A.; Cardinale, M.; Grosch, R.; Grube, M.; Berg, G. The impact of the pathogen *Rhizoctonia solani* and its beneficial counterpart *Bacillus amyloliquefaciens* on the indigenous lettuce microbiome. *Front. Microbiol.* 2014, 5, 175. [CrossRef]

58. Wang, S.; Wu, H.; Qiao, J.; Ma, L.; Liu, J.; Xia, Y.; Gao, X. Molecular mechanism of plant growth promotion and induced systemic resistance to Tobacco Mosaic Virus by *Bacillus* spp. *J. Microbiol. Biotechnol.* 2009, 19, 1250–1258. [CrossRef]

59. Jeong, H.; Jeong, D.E.; Kim, S.H.; Song, G.C.; Park, S.Y.; Ryu, C.M.; Park, S.H.; Choi, S.K. Draft genome sequence of the plant growth-promoting bacterium *Bacillus siamensis* KCTC 13613T. *J. Bacteriol.* 2012, 194, 4148–4149. [CrossRef]

60. Laird, M.; Piccoli, D.; Weselowski, B.; McDowell, T.; Renaud, J.; MacDonald, J.; Yuan, Z.C. Surfactin-producing *Bacillus amyloliquefaciens* strain Co1-6, a plant growth-promoting rhizobacterium of *Bacillus velezensis* strain LM2303. [CrossRef] [PubMed]

61. Zhang, J.X.; Gu, Y.B.; Wu, H.; Qiao, J.; Ma, L.; Liu, J.; Xia, Y.; Gao, X.; Borriss, R. *Bacillus amyloliquefaciens* strain GQJK49, a plant growth-promoting rhizobacterium with antifungal activity. [CrossRef] [PubMed]

62. Jing, R.; Li, N.; Wang, W.; Liu, Y. An endophytic strain JK of genus *Bacillus* isolated from the seeds of super hybrid rice (*Oryza sativa* L., Shenliangyou 5814) has antagonistic activity against rice blast pathogen. *Microbiol. Biotechnol.* 2018, 5942–5944. [CrossRef] [PubMed]

63. Jia, Z.; Jin, W.; Huang, Y.; Song, S. Complete genome sequence of *Bacillus subtilis* J-5, a potential biocontrol agent. *Genome Announc.* 2017, 5, e00922-17. [CrossRef] [PubMed]

64. Jia, Z.; Jin, W.; Huang, Y.; Song, S. Complete genome sequence of *Bacillus velezensis* GQJK49, a plant growth-promoting rhizobacterium with antifungal activity. *Genome Announc.* 2017, 5, e00275-17. [CrossRef] [PubMed]

65. Jin, R.; Li, N.; Wang, W.; Liu, Y. An endophytic strain JK of genus *Bacillus* isolated from the seeds of super hybrid rice (*Oryza sativa* L., Shenliangyou 5814) has antagonistic activity against rice blast pathogen. *Microb. Pathog.* 2020, 147, 104422. [CrossRef] [PubMed]

66. Sun, P.; Cui, J.; Jia, X.; Wang, W. Complete genome sequence of *Bacillus velezensis* L-1, which has antagonistic activity against pear diseases. *Genome Announc.* 2017, 5, e01271-17. [CrossRef]

67. Chen, L.; Heng, J.; Qin, S.; Bian, K. A Comprehensive understanding of the biocontrol potential of *Bacillus velezensis* LM2303 against *Fusarium* head blight. *PloS ONE* 2018, 13, e0198560. [CrossRef]

68. Lee, S.Y.; Kim, B.Y.; Ahn, J.H.; Song, J.; Seol, Y.J.; Kim, W.G.; Weon, H.Y. Draft genome sequence of the biocontrol bacterium *Bacillus amyloliquefaciens* strain M27. *J. Bacteriol.* 2012, 194, 6934–6935. [CrossRef]

69. Zhang, Y.; Gao, X.; Wang, S.; Zhu, C.; Li, R.; Shen, Q. Application of *Bacillus velezensis* NJAU-Z9 enhanced plant growth associated with efficient rhizospheric colonization monitored by QPCR with primers designed from the whole genome sequence. *Curr. Microbiol.* 2018, 75, 1574–1583. [CrossRef]

70. Yuan, J.; Raza, W.; Shen, Q.; Huang, Q. Antifungal activity of *Bacillus amyloliquefaciens* NIN-6 volatile compounds against *Fusarium oxysporum f. sp. cubense*. *Appl. Environ. Microbiol.* 2012, 78, 5942–5944. [CrossRef]
78. Niazi, A.; Manzoor, S.; Asari, S.; Beijai, S.; Meijer, J.; Bongcam-Rudloff, E. Genome analysis of Bacillus amyloliquefaciens subsp. plantarum UCMB5113: A rhizobacterium that improves plant growth and stress management. PLoS ONE 2014, 9, e104651. [CrossRef] [PubMed]

79. Sun, Z.; Hsiang, T.; Zhou, Y.; Zhou, J. Draft genome sequence of Bacillus amyloliquefaciens XK-4-1, a plant growth-promoting endophyte with antifungal activity. Genome Announc. 2015, 3, e01306-15. [CrossRef] [PubMed]

80. Xu, S.; Xie, X.; Zhao, Y.; Shi, Y.; Chai, A.; Li, L.; Li, B. Whole-genome analysis of Bacillus velezensis ZF2, a biocontrol agent that protects Cucumis sativus against corynespora leaf spot diseases. 3 Biotech 2020, 10, 186. [CrossRef] [PubMed]

81. De Curtis, F.; Ianiri, G.; Raiola, A.; Ritieni, A.; Succi, M.; Tremonte, P.; Castoria, R. Integration of biological and chemical control of brown rot of stone fruits to reduce disease incidence on fruits and minimize fungicide residues in juice. Crop Prot. 2019, 119, 158–165. [CrossRef]

82. Burkett-Cadena, M.; Kokalis-Burelle, N.; Lawrence, K.S.; Van Santen, E.; Kloepper, J.W. Suppressiveness of root-knot nematodes mediated by rhizobacteria. Biol. Control 2008, 47, 55–59. [CrossRef]

83. Chen, X.H.; Koomouts, A.; Scholz, R.; Eisenreich, A.; Schneider, K.; Heinemeyer, I.; Morgenstern, B.; Voss, B.; Hess, W.R.; Reva, O.; et al. Comparative analysis of the complete genome sequence of the plant-growth–promoting bacterium Bacillus amyloliquefaciens FZB42. Nat. Biotechnol. 2007, 25, 1007–1014. [CrossRef] [PubMed]

84. Liu, X.Y.; Min, Y.; Wang, K.M.; Wan, Z.Y.; Zhang, Z.G.; Cao, C.X.; Zhou, R.H.; Jiang, A.B.; Liu, C.J.; Zhang, G.Y.; et al. Draft genome sequence of Bacillus amyloliquefaciens FD62. Genomics Data 2018, 20, 1–5. [CrossRef]

85. Devaraj, K.; Aathika, S.; Periyasamy, K.; Periyaraman, P.M.; Palaniyandi, S.; Subramanian, S. Production of thermostable multiple enzymes from Bacillus subtilis KUB29. Nat. Prod. Res. 2019, 33, 1674–1677. [CrossRef]

86. Kalawong, R.; Wakayama, M.; Anantalahbchais, S.; Wongsawad, C.; Sangwijit, K. Comparison and characterization of purified cellulase and xylanase from Bacillus amyloliquefaciens CX1 and Bacillus subtilis B4. Chiang Mai J. Sci. 2018, 45, 92–105.

87. Farhat-Khemakhem, A.; Blibech, M.; Boukhris, I.; Makni, M.; Chouayekh, H. Assessment of the potential of the multi-enzyme producer Bacillus subtilis US573 as alternative feed additive. J. Sci. Food Agric. 2018, 98, 1208–1215. [CrossRef]

88. Sewalt, V.; Shanahan, D.; Gregg, L.; La Marta, J.; Carrillo, R. The Generally Recognized as Safe (GRAS) process for industrial microbial enzymes. Ind. Biotechnol. 2016, 12, 295–302. [CrossRef]

89. Prajapati, V.S.; Ray, S.; Narayanan, J.; Joshi, C.C.; Patel, K.C.; Trivedi, U.B.; Patel, R.M. Draft genome sequence of a thermostable, alkaliophilic α-amylase and protease producing Bacillus amyloliquefaciens strain KCP2. 3 Biotech 2017, 7, 372. [CrossRef]

90. Meier, M.J.; Dodge, A.; Beaudette, L.A. Draft genome sequence of the industrially significant bacterium Bacillus amyloliquefaciens NRRL 942. Matthew. Microbiol. Resour. Announc. 2018, 7, e01374-18.

91. Montor-Antonio, J.J.; Sachman-Ruiz, B.; Lozano, L.; del Moral, S. Draft genome sequence of Bacillus amyloliquefaciens JCC33M, isolated from sugarcane soils in the papaloapan region, Mexico. Genome Announc. 2015, 3, e01519-14. [CrossRef] [PubMed]

92. Chen, L.; Gu, W.; Xu, H-Y.; Yang, G.L.; Shan, X.F.; Chen, G.; Wang, C.F.; Qian, A.D. Complete genome sequence of Bacillus velezensis 157 isolated from Eucommia ulmoides with pathogenic bacteria inhibiting and lignocellulolytic enzymes production by SSF. 3 Biotech 2018, 8, 114. [CrossRef] [PubMed]

93. Gong, G.; Kim, S.; Lee, S.M.; Woo, H.M.; Park, T.H.; Um, Y. Complete genome sequence of Bacillus sp. 275, producing extracellular cellulolytic, xylanolytic and ligninolytic enzymes. J. Biotechnol. 2017, 254, 59–62. [CrossRef]

94. Hassan, M. The Role of Pectin Utilization in Root Colonization and Plant Growth-Promotion by Bacillus amyloliquefaciens subsp. plantarum (Bap). Master’s Thesis, Auburn University, Auburn, ME, USA, 2016.

95. Das, R.; Liang, Z.; Li, G.; Mai, B.; An, T. Genome sequence of a spore-laccose forming, BPA-degrading Bacillus sp. GZB isolated from an electronic-waste recycling site reveals insights into BPA degradation pathways. Arch. Microbiol. 2019, 201, 623–638. [CrossRef] [PubMed]

96. Jung, J.Y.; Chun, B.H.; Moon, J.Y.; Yeo, S.H.; Jeon, C.O. Complete genome sequence of Bacillus methylotrophicus JJ-D34 isolated from deonjjang, a korean traditional fermented soybean paste. J. Biotechnol. 2016, 219, 36–37. [CrossRef] [PubMed]

97. Yang, H.; Yang, L.; Li, X.; Li, H.; Tu, Z.; Wang, X. Genome sequencing, purification, and biochemical characterization of a strongly fibrinolytic enzyme from Bacillus amyloliquefaciens Jxnuwx-1 isolated from chinese traditional douchi. J. Gen. Appl. Microbiol. 2019, in Press. [CrossRef] [PubMed]

98. Marasini, D.; Cornell, C.R.; Oyewole, O.; Sheaff, R.J.; Fakhr, M.K. The whole-genome sequence of Bacillus velezensis strain SB1216 isolated from the great salt plains of Oklahoma reveals the presence of a novel extracellular RNase with antitumor activity. Genome Announc. 2017, 5, e01343-17. [CrossRef]

99. Song, P.; Xu, X.; Jiang, L.; Zhang, R.; Wang, J.; Xu, Q.; Li, S. Genome sequence of Bacillus subtilis SPZ1, an evolved strain for higher uptake rate of tributyrin. Genome Announc. 2013, 1, e00511-13. [CrossRef]

100. Zhou, L.; Ren, R.; Meng, D.; Tian, Q.; Guan, Z.; Cai, Y.; Liao, X. Comparison of aminotransferases of three Bacillus strains Bacillus altitudinis W3, Bacillus velezensis SYBC H47, and Bacillus amyloliquefaciens YP6 via genome analysis and bioinformatics. J. Appl. Genet. 2019, 60, 427–430. [CrossRef]
103. Wu, L.; Li, X.; Ma, L.; Blom, J.; Wu, H.; Gu, Q.; Borriess, R.; Gao, X. The “pseudo-pathogenic” effect of plant growth-promoting bacilli on starchy plant storage organs is due to their α-amylase activity which is stimulating endogenous opportunistic pathogens. *Appl. Microbiol. Biotechnol.* **2020**, *104*, 2701–2714. [CrossRef]

104. Clatworthy, A.E.; Pierson, E.; Hung, D.T. Targeting virulence: A new paradigm for antimicrobial therapy. *Nat. Chem. Biol.* **2007**, *3*, 541–548. [CrossRef]

105. Fazle Rabbee, M.; Baek, K.H. Antimicrobial activities of lipopeptides and polyketides of *Bacillus velezensis* for agricultural applications. *Molecules* **2020**, *25*, 4973. [CrossRef]

106. Perlman, D.; Bodanszey, M. Biosynthesis of peptide antibiotics. *Annu. Rev. Microbiol.* **1971**, *40*, 449–464. [CrossRef]

107. Hancock, R.E.; Chapple, D.S. Peptide antibiotics. *Antimicrob. Agents Chemother.* **1999**, *43*, 1317–1323. [CrossRef] [PubMed]

108. Grady, E.N.; MacDonald, J.; Ho, M.T.; Wesełowski, B.; McDowell, T.; Solomon, O.; Renaud, J.; Yuan, Z.C. Characterization and complete genome analysis of the surfactin-producing, plant-protecting bacterium *Bacillus velezensis* 9D-6. * BMC Microbiol.* **2019**, *19*, 5. [CrossRef] [PubMed]

109. Abdelhamid, A.G.; Hussein, W.E.; Gerst, M.M.; Yousef, A.E. Draft genome sequence of *Bacillus velezensis* OSY-GA1, which encodes multiple antimicrobial metabolites and expresses antimicrobial activity against foodborne pathogens. *Microbiol. Resour. Announc.* **2019**, *8*, e01725-18. [CrossRef] [PubMed]

110. Huffman, J.; Gerber, R.; Du, L. Recent advancements in the biosynthetic mechanisms for polyketide-derived mycotoxins. *Biopolymers* **2010**, *93*, 764–776. [CrossRef] [PubMed]

111. Weissman, K.J. Introduction to polyketide biosynthesis. *Methods Enzymol.* **2009**, *459*, 3–16. [PubMed]

112. Gomes, E.S.; Schuch, V.; Lemos, E.G.D.M. Biotechnology of polyketides: New breath of life for the novel antibiotic genetic pathways discovery through metagenomics. *Brazilian J. Microbiol.* **2013**, *44*, 1007–1034. [CrossRef] [PubMed]

113. Zheng, C.J.; Lee, S.; Lee, C.H.; Kim, W.G. Macrolactins O–R, glycosylated 24-membered lactones from *Streptomyces avermitilis*. *Appl. Microbiol. Biotechnol.* **2017**, *91*, 541–548. [CrossRef] [PubMed]

114. Lee, H.J.; Chun, B.H.; Jeon, H.H.; Kim, Y.B.; Lee, S.H. Complete genome sequence of *Bacillus amyloliquefaciens* JFL15. *PLoS ONE* **2018**, *13*, e0202893. [CrossRef]

115. Pereira, J.Q.; Ritter, A.C.; Cibulski, S.; Brandelli, A. Functional genome annotation depicts probiotic properties of *Bacillus amyloliquefaciens* SRCM 100731 as probiotic resource for companion animal. *Microbiol. Soc. Korea* **2018**, *54*, 384–397.

116. Kechagia, M.; Basoulis, D.; Konstantopoulou, S.; Dimitriadi, D.; Gyftopoulou, K.; Skarmoutsou, N.; Fakiri, E.M. Health benefits of *Bacillus amyloliquefaciens* on the growth performance, intestinal histomorphology, and immune response of Nile tilapia (*Oreochromis niloticus*). *Fish Shellfish Immunol.* **2017**, *65*, 1632–1635. [CrossRef] [PubMed]

117. Brown, S.; Dart, P. Testing Hay Treated with Mould-Inhibiting, Biocontrol Inoculum; Rural Industries Research and Development Corporation: Canberra, Australia, 2005.

118. Pereira, J.Q.; Ritter, A.C.; Cibulski, S.; Brandelli, A. Functional genome annotation depicts probiotic properties of *Bacillus velezensis* FCT01. *Gene* **2019**, *713*, 143971. [CrossRef] [PubMed]

119. Golovko, G.; Zipelt, L.; Karpenko, G.; Chistyakov, V.; Saizykina, M.; Kolenko, M. Method for Growth of Young Azov-Chernomorskaya Royal Fish in Ponds. RU Patent No. 2,376,755, 23 July 2008.

120. AlGburi, A.; Volski, A.; Cugini, C.; Walsh, E.M.; Chistyakov, V.A.; Mazanko, M.S.; Bren, A.B.; Dicks, L.M.T.; Chikindas, M.L. Complete genome analysis of the surfactin-producing, plant-protecting bacterium *Bacillus velezensis* JFL15. *J. Nat. Prod.* **2013**, *76*, 1632–1635. [CrossRef] [PubMed]

121. Kechagia, M.; Basoulis, D.; Konstantopoulou, S.; Dimitriadi, D.; Gyftopoulou, K.; Skarmoutsou, N.; Fakiri, E.M. Health benefits of *Bacillus amyloliquefaciens* on the growth performance, intestinal histomorphology, and immune response of Nile tilapia (*Oreochromis niloticus*). *Fish Shellfish Immunol.* **2017**, *65*, 1632–1635. [CrossRef] [PubMed]

122. AlGburi, A.; Volski, A.; Cugini, C.; Walsh, E.M.; Chistyakov, V.A.; Mazanko, M.S.; Bren, A.B.; Dicks, L.M.T.; Chikindas, M.L. Safety properties and probiotic potential of *Bacillus subtilis* KATMIRA1933 and *Bacillus amyloliquefaciens* B-1895. *Adv. Microbiol.* **2016**, *6*, 432–452. [CrossRef]

123. Yi, Y.; Zhang, Z.; Zhao, F.; Liu, H.; Yu, L.; Zha, J.; Wang, G. Probiotic potential of *Bacillus velezensis* JW: Antimicrobial activity against fish pathogenic bacteria and immune enhancement effects on *Carassius auratus*. *Fish Shellfish Immunol.* **2018**, *78*, 322–330. [CrossRef]

124. Gao, X.Y.; Liu, Y.; Miao, L.L.; Li, E.W.; Sun, G.X.; Liu, Y.; Liu, Z.P. Characterization and mechanism of anti- *Aeromonas salmonicida* activity of a marine probiotic strain, *Bacillus velezensis* V4. *Appl. Microbiol. Biotechnol.* **2017**, *101*, 3759–3768. [CrossRef] [PubMed]

125. Llario, F.; Romano, L.A.; Rodilla, M.; Sebastiá-Frasquet, M.T.; Poersch, L.H. Application of *Bacillus amyloliquefaciens* as probiotic for *Litorina nasuta* (Boone, 1931) cultivated in a biofloc system. *Iran. J. Fish. Sci.* **2020**, *19*, 904–920.

126. Lin, Y.S.; Saputra, F.; Chen, Y.C.; Hu, S.Y. Dietary administration of *Bacillus amyloliquefaciens* R8 reduces hepatic oxidative stress and enhances nutrient metabolism and immunity against *Aeromonas hydrophila* and *Streptococcus agalaciae* in zebrafish (*Danio rerio*). *Fish Shellfish Immunol.* **2019**, *86*, 410–419. [CrossRef]

127. Al-Deriny, S.H.; Dawood, M.A.; Abou Zaid, A.A.; Wael, F.; Paray, B.A.; Van Doan, H.; Mohamed, R.A. The synergistic effects of *Spirulina platensis* and *Bacillus amyloliquefaciens* on the growth performance, intestinal histomorphology, and immune response of *Nile tilapia* (*Oreochromis niloticus*). *Aquacult. Repor.* **2020**, *17*, 100390. [CrossRef]

128. Chauhan, A.; Singh, R. Probiotics in aquaculture: A promising emerging alternative approach. *Symbiosis* **2019**, *77*, 99–113. [CrossRef]
129. Azrin, N.A.R.; Yuzine, E.; Ina-Salwany, M.Y.; Karim, M. The Efficacy of Potential Probiotic Bacillus amyloliquefaciens Strain L11 in Protecting Artemia Nauplii and Blue Crab Juveniles against Vibrio harveyi Infection. *J. Pure Appl. Microbiol.* **2019**, *13*, 923–931.

130. Abatenh, E.; Gizaw, B.; Tsegaye, Z.; Wassie, M. The role of microorganisms in bioremediation—a review. *Open J. Environ. Biol.* **2017**, *1*, 38–46. [CrossRef]

131. Meng, D.; Zhai, L.X.; Tian, Q.P.; Guan, Z.B.; Cai, Y.J.; Liao, X.R. Complete genome sequence of *Bacillus amyloliquefaciens* YP6, a plant growth rhizobacterium efficiently degrading a wide range of organophosphorus pesticides. *J. Integr. Agric.* **2019**, *18*, 2668–2672. [CrossRef]