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Complete genome sequence of *Bacillus velezensis* QST713: A biocontrol agent that protects *Agaricus bisporus* crops against the green mould disease

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Abstract: *Bacillus subtilis* QST713 is extensively used as a biological control agent in agricultural fields including in the button mushroom culture, *Agaricus bisporus*. This last use exploits its inhibitory activity against microbial pathogens such as *Trichoderma aggressivum* f. *europaeum*, the main button mushroom green mould competitor. Here, we report the complete genome sequence of the QST713 biocontrol strain with a genome size of 4 233 757 bp, 4263 predicted genes and an average GC content of 45.9%. Based on phylogenomic analyses, the QST713 strain is finally designated as *Bacillus velezensis*. Genomic analyses revealed two clusters encoding potential new antimicrobials with NRPS and TransATPKS synthetase. *B. velezensis* QST713 genome also harbours several genes previously described as being involved in surface colonization and biofilm formation. This strain shows a strong ability to form in vitro spatially organized biofilm and to antagonize *T. aggressivum*. The availability of this genome sequence could bring new elements to understand the interactions with micro or/and macroorganisms in crops.

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Jouy-en-Josas, the 22th of February 2018

Dear Editor,

Please find attached the manuscript entitled “Complete genome sequence of *Bacillus velezensis* QST713: a biocontrol agent that protects *Agaricus bisporus* crops against the green mould disease.” to be submitted for publication in “*Journal of Biotechnology*”.

The main objective of this paper is to publish the complete genome sequence of the *Bacillus velezensis* QST713 strain, and to show its particularities compared to other species of the *Bacillus subtilis* species complex. This strain is hugely used as biological control agent in the world and for almost ten years in the field of the button mushroom *Agaricus bisporus* in France, but it is poorly documented. In this paper, we described the genome sequence of the QST713 strain and we show a strong capability to form biofilm and to produce two potential new antimicrobials compared to other *Bacillus* species. Furthermore, we show its ability to antagonize the pathogen of *A. bisporus* and to restore a great yield of *A. bisporus* through a biocontrol assay performed at the technical mushroom center in France. The publication of this genome sequence could permit a better understanding of the bioprotection mechanisms involved in interactions with macro- and microorganisms in agriculture. The biofilm mode of life and its specificities only start to be taken in consideration for the biotechnological use of beneficial organisms in agriculture. Invoking biofilm-associated mechanisms in the beneficial effects of biocontrol agents opens doors for sustainable biofilm applications as an alternative to chemical pollutants.

All authors agreed to submit this work and the manuscript has not been submitted to another journal. We believe that the reading of this paper should be of interest for readers of *Journal of Biotechnology*.

Best regards,

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Highlights

- ❖ *Bacillus velezensis* QST713 is hugely used as biocontrol agent in the world and strongly protects *Agaricus bisporus* crops against *Trichoderma aggressivum* f. *europaeum* in France.
- ❖ The complete genome of this commercial biofungicide was sequenced and described.
- ❖ It encodes at least 15 secondary metabolite gene clusters including two potential new antimicrobials.
- ❖ It forms robust and highly complex 3D structured biofilm.
- ❖ The availability of the genome data also provides information for further exploration and understanding of biocontrol mechanisms during interactions between microorganisms and micro-/macroorganisms in crops

1 **Complete genome sequence of *Bacillus velezensis* QST713: a biocontrol agent that**
2 **protects *Agaricus bisporus* crops against the green mould disease.**

3

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15

16

17 **Abstract**

18 *Bacillus subtilis* QST713 is extensively used as a biological control agent in agricultural fields
19 including in the button mushroom culture, *Agaricus bisporus*. This last use exploits its
20 inhibitory activity against microbial pathogens such as *Trichoderma aggressivum* f.
21 *europaeum*, the main button mushroom green mould competitor. Here, we report the complete
22 genome sequence of the QST713 biocontrol strain with a genome size of 4 233 757 bp, 4263
23 predicted genes and an average GC content of 45.9%. Based on phylogenomic analyses, the
24 QST713 strain is finally designated as *Bacillus velezensis*. Genomic analyses revealed two
25 clusters encoding potential new antimicrobials with NRPS and TransATPKS synthetase. *B.*

26 *velezensis* QST713 genome also harbours several genes previously described as being
27 involved in surface colonization and biofilm formation. This strain shows a strong ability to
28 form *in vitro* spatially organized biofilm and to antagonize *T. aggressivum*. The availability of
29 this genome sequence could bring new elements to understand the interactions with micro
30 or/and macroorganisms in crops.

31 **Keywords** : *Bacillus velezensis*, Biofilm, Genome, Biocontrol, Secondary metabolites.

32

33

34 **1. Introduction**

35 *Bacillus spp.* are ubiquitous bacteria found in soils that are widely used as biocontrol
36 agents because of their ability to antagonize crops pathogens and the possibility to develop
37 stable spore-based commercial products (Borriss 2015). The described mechanisms associated
38 with their biocontrol effect include specific antagonism, spatial and nutritional competition,
39 antimicrobial production, stimulation of plant growth, and induction of plant resistance
40 (Pandin *et al.* 2017). Bacilli biocontrol agents are able to secrete a wide range of secondary
41 metabolites that can display antibacterial, antifungal, or both properties (Stein 2005; Ongena
42 & Jacques 2008; Chen *et al.* 2009; Zhao & Kuipers 2016). Another ability that should be
43 emphasized in the field of biocontrol is the formation of spatially organized biofilms, the most
44 prevalent microorganisms mode of life in environment that allow a better colonization and
45 persistence of microorganisms (Costerton *et al.* 1978, 1999; Morris *et al.* 2003; Epstein *et al.*
46 2011; Xu *et al.* 2014; Zeriouh *et al.* 2014; Abd el Daim *et al.* 2015; Pandin *et al.* 2017). For
47 almost ten years, *Bacillus velezensis* QST713 is used for the bioprotection of the button
48 mushroom cultures in France against *Trichoderma aggressivum* f. *europaeum*. This fungal
49 pathogen hinders the development of *Agaricus bisporus* by invading its culture substrate, the
50 compost (Mamoun *et al.* 2000; Samuels *et al.* 2002; Largeteau & Savoie 2010). However,

51 published reports on this specific strain are very scarce and its genome sequence is unknown
52 from databanks (Joshi and McSpadden Gardener 2006; Patel *et al.* 2011; Lahlali *et al.* 2013;
53 Cawoy *et al.* 2015; Punja *et al.* 2016). In this study, the genome sequence of the commercial
54 strain QST713 was determined, described and compared to other *Bacillus* strains.
55 Furthermore, phenotypic tests and biocontrol assay were carried out to emphasis abilities of
56 this biocontrol strain.

57

58 **2. Genomic structure and comparative genome analysis of *Bacillus velezensis* QST713** 59 **with *Bacillus* strains**

60 Genomic DNA was extracted from *B. velezensis* QST713 cultivated at 37°C in Luria-
61 Bertani medium (LB, Sigma, France) using the GenElute™ Bacterial Genomic DNA
62 extraction Kit (Sigma-Aldrich, St. Louis) and sequenced using Genome Sequencer Illumina
63 HiSeq2500 technology (GATC Biotech). Total of 6,364,797 high quality filtered paired-end
64 reads of length 126 bp were generated (Bokulich *et al.* 2013). SPAdes was used to assemble
65 the filtered reads (Bankevish *et al.* 2014). Tools are available at the Galaxy portal of the
66 MIGALE platform. The obtained contigs were ordered using Mauve genome alignment
67 software v2.1.3 (Darling *et al.* 2004), and assemblies were manually combined in one contig
68 with a total size of 4,23 Mb by identifying overlapping nucleotide sequences in reads and
69 mapping them against genomes of the closest *B. velezensis* strains CC09 (*accession n°:*
70 **NZ_CP015443**), CFSAN034339 (*accession n°:* **LYNB00000000**) and Bs006 (*accession n°:*
71 **NZ_LJAU00000000**). Genome annotation was accomplished using the NCBI Prokaryotic
72 Genomes Automatic Annotation Pipeline (PGAAP) (Angiuoli *et al.* 2008).

73 The strain QST713 was known as *Bacillus subtilis* QST713 in previous studies (Patel *et al.*
74 2011; Lahlali *et al.* 2013). However, based on the comparative phylogenomic analysis of
75 *Bacillus* genomes (Table 1; Fig. 1), the QST713 strain initially designated as *Bacillus subtilis*

76 should be now reassigned as *Bacillus velezensis* species (formerly known as *Bacillus*
77 *amyloliquefaciens* subsp. *plantarum*, (Fan *et al.* 2017)). Indeed, digital DNA-DNA
78 Hybridization (dDDH), average nucleotide or amino acid identity (ANI/AAI) analyses
79 showed a higher similarity of the QST713 strain with *Bacillus velezensis* species than other
80 *Bacillus* species (Table 1). The genomic structure of the *B. velezensis* QST713 chromosome
81 of 4,233,757 bp length and a Blast comparison with *B. subtilis* and *B. velezensis* strain are
82 represented in Fig. 2. The genome sequence has a G+C content of 45,9% and 4263 predicted
83 genes, including 4056 coding sequences (CDS), 98 pseudo genes, 25 rRNA , 79 tRNA and 5
84 ncRNA genes. The classification of the QST713 genes into clusters of orthologous groups
85 (COG) assigned 2909 CDS in at least one COG group (71.7%) (Fig. S1). 1147 CDS were not
86 classified into COG. In those 1147 CDS, 602 were assigned to hypothetical proteins and 545
87 were conserved proteins, most are parts of prophage regions or involved in sporulation and
88 putative secondary metabolites synthesis. 21% of all assigned COG CDS was dedicated to the
89 transport and metabolism of amino acids, carbohydrates, lipids, inorganic ions, the defence
90 mechanisms and the biosynthesis, transport and catabolism of secondary metabolites. These
91 functions are essentials for a biocontrol agent in terms of nutritional/spatial competition and
92 antagonism against microorganisms to colonize and compete in various ecosystems.
93 PHASTER analysis of *B. velezensis* QST713 genome identified six prophage regions (Table
94 S1) depicted on the red ring in Fig. 2, which represent 8% of the entire genome. These regions
95 correspond to variable regions which can be visualized in Fig. 2 (rings 8 to 11) when
96 comparing the genome of *B. velezensis* QST713 with other *Bacillus* genomes, indicating a
97 strong genomic plasticity of the QST713 strain.

98

99 **3. Secondary metabolite clusters**

100 Through the antiSMASH genome analysis tool, fifteen clusters of secondary metabolites
101 have been identified in the genome of the QST713 strain (Table 2; Fig. 2), five encoding
102 NRPS (Non-Ribosomal Peptide Synthetase), two transATPKS (trans-Acyl Transferase
103 Polyketide Synthetase), three transATPKS-NRPS, two terpene, one lantipeptide, one T3PKS
104 and one otherKS. Nine clusters have been clearly identified as being involved in the synthesis
105 of surfactin, macrolactin, bacillaene, bacillomycin D, fengycin, difficidin, bacilysin, subtilin-
106 like/ericin and bacillibactin (siderophore). All have antimicrobial/antibacterial activities or are
107 implicated in antibiosis (Stein *et al.* 2002, 2005; Ongena *et al.* 2005; Ongena and Jacques
108 2008; Chen *et al.* 2009; Niazi *et al.* 2014). This analysis revealed that at least 12% of the
109 QST713 genome is allocated to the biosynthesis, regulation and transport of antimicrobials.
110 Secondary metabolites clusters have been compared to four *Bacillus* strains (FZB42, SQR9,
111 NCIB3610 and 168) (Table 2). For all fifteen clusters, genes have been verified, detailed and
112 compared to the reference strain *B. velezensis* FZB42, or when genes were absent from
113 FZB42 strain, to *B. velezensis* CC09 and *Bacillus subtilis* A13 (Table S2). The arrangement of
114 gene clusters in *B. velezensis* QST713 is very similar to those in FZB42 (98-99% nucleotide
115 identity) (Fig. 3; Table S2). *Bacillus velezensis* QST713 has three clusters that are not present
116 in all four *Bacillus* strains (Table 2; Fig. 3). The cluster ten responsible for the synthesis of
117 subtilin-like/ericin (Genbank accession number **AF233755.1**) and not present in FZB42, is
118 found in *Bacillus subtilis* A13 (unpublished genome) (Stein *et al.* 2002; 2005). We found two
119 clusters encoding potential novel metabolites and not yet described that are similar to gene
120 clusters in CC09 (Fig. 3; Table 2; Table S2). The cluster nine encoding TransATPKS-NRPS
121 shows 22% of gene similarity with rhizocticin, but the biosynthetic genes of the QST713
122 strain in this cluster do not correspond to rhizocticin biosynthetic genes from the MIBiG
123 database. In the same way, the cluster eleven encoding NRPS is also unknown from MIBiG

124 database (Fig. 3; Table 2; Table S2). In accordance with Cai *et al.* 2017 study, these two
125 clusters could encode two new metabolites specific to *B. velezensis* species.

126

127 **4. Biofilm phenotypes and swarming motility**

128 *B. velezensis* QST713 is provided with a large number of genes involved in the biofilm
129 formation process (Table 3). Indeed, it has two operons involved in the synthesis of
130 extracellular polysaccharides, *epsA-O* operon and *capABC* (*pgsABC*) operon. It also has the
131 *tasA-sipW-tapA* operon that codes for the TasA protein forming amyloid fibres (Table 3) (de
132 Jong *et al.* 2009; Romero *et al.* 2010). These genes are regulated by a large number of
133 regulatory genes such as *spo0A*, *remA*, *sinI/sinR*, *sigW*, *abrB* described in *B. subtilis* and also
134 present in *B. velezensis* QST713 (Winkelman *et al.* 2009; Vlamakis *et al.* 2013). Indeed, the
135 QST713 strain shows a complex macrocolony structure which is mucoid under a thick and
136 dry surface layer as compared to *B. subtilis* 168 which has flat and non-mucoid macrocolony
137 (Fig. 4). *B. velezensis* SQR9 also shows complex structure but without mucoid aspect.
138 However, *B. velezensis* FZB42 which also harbours these matrix genes shows a flat
139 macrocolony. We obtain the same results for pellicles experiment with a thick and solid
140 pellicle for QST713 strain compared to other strains (Fig. 4). The biofilm experiment shows,
141 like macrocolonies and pellicles experiments, more structured and denser cellular aggregates
142 for QST713 strain than for other strains capable of forming biofilms (Fig. 4). As observed by
143 Magno-Pérez-Bryan *et al.* 2015 and Norman *et al.* 2013, our results show that despite having
144 biofilm and regulatory genes, it may be possible that other regulatory pathways or epigenetics
145 event are involved in biofilm formation and related phenotype expressions.

146 Swarming motility is an essential skill to colonize environmental surfaces such as soils or
147 crops tissues (Fan *et al.* 2011; Mordini *et al.* 2013). *B. velezensis* QST713 has the *swr* genes
148 necessary for swarming motility but also the *fla-che* operon including *fla* genes that code for

149 flagellar components and are up-regulated by *swrA*, thus improving swarming motility
150 (Kearns *et al.* 2004; Ghelardi *et al.* 2012). All the strains tested except the negative swarming
151 control *B. subtilis* 168 showed a swarming motility characterized by the invasion of 9 cm
152 diameters of TSA 0.8% agar plates at 25°C in 24 hours (Fig. 4). Efficient swarming and
153 biofilm formation confer to biocontrol agents a better fitness to colonize substrata and to
154 outcompete pathogens.

155

156 **5. Biocontrol effect of *B. velezensis* QST713 against the green mould *T. aggressivum***

157 Biocontrol assay with *B. velezensis* QST713 in the mushroom field and antagonism tests
158 by measuring inhibition zones surrounding *Bacillus* strains were performed (Fig. 5).
159 Biocontrol assay was carried out from November 2017 to January 2018 at the technical
160 mushroom center (CTC, Distré, France). Results show a strong effect of the QST713 strain on
161 the yield of *A. bisporus* crops infected by *T. aggressivum*. When the culture compost is
162 contaminated by *T. aggressivum*, we observed a diminution of the yield of *A. bisporus* for
163 about 50% (Fig. 5A). However, when the compost contaminated is treated by the QST713
164 strain, the yield of *A. bisporus* returned to a value similar to the control yield (Fig. 5A).
165 Furthermore, antagonism test by *B. velezensis* QST713 shows a strong efficacy against the
166 green mould by a direct inhibition (inhibition zone: 4.7 ± 0.5 mm) of the growth of mycelium
167 and an inhibition of fungus sporulation (diminution of green colour) compared to *T.*
168 *aggressivum* alone (Fig. 5B(a),(b)). This second antagonism effect which is not located at the
169 direct interaction interface, could be due to a secretion of volatile organic compounds by the
170 QST713. This phenomenon has already been demonstrated on the inhibition of sporulation of
171 *Streptomyces scabies* (Meng *et al.* 2016).

172

173 **6. Conclusion**

174 The phylogenetic analysis of the QST713 genome allows to reassign the strain QST713 as
175 a *Bacillus velezensis* strain. Its ability to form highly structured, thick and dense biofilms *in*
176 *vitro* and its ability to swarm on agar plates supposedly allow its efficient colonization and
177 persistence in crops. In addition, it is equipped with an antimicrobial battery enabling it to
178 fight with aggressors, including ericin as well as potentially one NRPS and one transATPKS-
179 NRPS not yet characterized and found only in few *B. velezensis*. All these features allow *B.*
180 *velezensis* QST713 to be highly competitive in the environment and makes it a particularly
181 efficient biocontrol agent.

182

183 **Nucleotide sequence accession numbers**

184 The complete genome sequence of *B. velezensis* QST713 has been deposited in NCBI under
185 the GenBank accession number **CP025079**.

186

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194

195 **References**

196 Abd El Daim, I., Häggblom, P., Karlsson, M., Stenström, E., Timmusk, S., 2015.
197 “*Paenibacillus polymyxa* A26 Sfp-Type PPTase inactivation limits bacterial antagonism

198 against *Fusarium graminearum* but not of *F. culmorum* in kernel assay.” *Frontiers in*
199 *Plant Science* 6: 368. doi:10.3389/fpls.2015.00368.

200 Alikhan, N.-F., Petty, N.K., Ben Zakour, N.L., Beatson, S.A., 2011. “BLAST Ring Image
201 Generator (BRIG): simple prokaryote genome comparisons.” *BMC Genomics* 12
202 (August): 402. doi:10.1186/1471-2164-12-402.

203 Angiuoli, S.V., Gussman, A., Klimke, W., Cochrane, G., Field, D., Garrity, G.M., Kodira,
204 C.D., Kyrpides, N., Madupu, R., Markowitz, V., Tatusova, T., Thomson, N., White, O.,
205 2008. « Toward an online repository of Standard Operating Procedures (SOPs) for (Meta)
206 genomic annotation ». *OMICS: a Journal of Integrative Biology* 12 (2):137- 41.
207 doi:10.1089/omi.2008.0017.

208 Arndt, D., Grant, J.R., Marcu, A., Sajed, T., Pon, A., Liang, Y., Wishart, D.S., 2016.
209 “PHASTER: a better, faster version of the PHAST phage search tool.” *Nucleic Acids*
210 *Research* 44 (W1): W16-21. doi:10.1093/nar/gkw387.

211 Bankevich, A., Nurk, S., Antipov, D., Gurevich, A.A., Dvorkin, M., Kulikov, A.S., Lesin,
212 V.M., Nikolenko, S.I., Pham, S., Prjibelski, A.D., Pyshkin, A.V., Sirotkin, A.V., Vyahhi,
213 N., Tesler, G., Alekseyev, M.A., Pevzner, P.A., 2012. “SPAdes: a new genome assembly
214 algorithm and its applications to single-cell sequencing.” *Journal of Computational*
215 *Biology: A Journal of Computational Molecular Cell Biology* 19 (5): 455–77.
216 doi:10.1089/cmb.2012.0021.

217 Blin, K., Medema, M.H., Kazempour, D., Fischbach, M.A., Breitling, R., Takano, E., Weber,
218 T., 2013. antiSMASH 2.0—a versatile platform for genome mining of secondary
219 metabolite producers. *Nucleic Acids Res.* 41, W204–W212. doi:10.1093/nar/gkt449.

220 Blom, J., Albaum, S.P., Doppmeier, D., Pühler, A., Vorhölter, F.-J., Zakrzewski, M.,
221 Goesmann, A., 2009. “EDGAR: a software framework for the comparative analysis of

222 prokaryotic genomes.” *BMC Bioinformatics* 10 (May): 154. doi:10.1186/1471-2105-10-
223 154.

224 Blom, J., Kreis, J., Spänig, S., Juhre, T., Bertelli, C., Ernst, C., Goesmann, A., 2016.
225 “EDGAR 2.0: an enhanced software platform for comparative gene content analyses.”
226 *Nucleic Acids Research* 44 (W1): W22-28. doi:10.1093/nar/gkw255.

227 Bokulich, N.A., Subramanian, S., Faith, J.J., Gevers, D., Gordon, J.I., Knight, R., Mills, D.A.,
228 Caporaso, J.G., 2013. Quality-filtering vastly improves diversity estimates from Illumina
229 amplicon sequencing. *Nat. Methods* 10, 57–59. doi:10.1038/nmeth.2276.

230 Borriss, R., 2015. “*Bacillus*, a plant-beneficial bacterium.” In *Principles of Plant-Microbe*
231 *Interactions: Microbes for Sustainable Agriculture*, edited by Ben Lugtenberg, 379–91.
232 Cham: Springer International Publishing. doi:10.1007/978-3-319-08575-3_40.

233 Cai, X.-C., Liu, C.-H., Wang, B.-T., Xue, Y.-R., 2017. “Genomic and metabolic traits endow
234 *Bacillus velezensis* CC09 with a potential biocontrol agent in control of wheat powdery
235 mildew disease.” *Microbiological Research* 196 (March): 89–94.
236 doi:10.1016/j.micres.2016.12.007.

237 Cawoy, H., Debois, D., Franzil, L., De Pauw, E., Thonart, P., Ongena, M., 2015.
238 « Lipopeptides as main ingredients for inhibition of fungal phytopathogens by *Bacillus*
239 *subtilis/amyloliquefaciens* ». *Microbial Biotechnology* 8 (2):281- 95. doi:10.1111/1751-
240 7915.12238.

241 Chen, X.H., Koumoutsis, A., Scholz, R., Schneider, K., Vater, J., Süssmuth, R., Piel, J.,
242 Borriss, R., 2009. “Genome analysis of *Bacillus amyloliquefaciens* FZB42 reveals its
243 potential for biocontrol of plant pathogens.” *Journal of Biotechnology, Functional*
244 *Genome Research on Bacteria Relevant for Agriculture, Environment and Biotechnology*
245 *Functional Genome Research*, 140 (1–2): 27–37. doi:10.1016/j.jbiotec.2008.10.011.

246 Costerton, J.W., Geesey, G.G., Cheng, K.J., 1978. “How bacteria stick.” *Scientific American*
247 238 (1): 86–95. doi: 10.1038/scientificamerican0178-86.

248 Costerton, J.W., Stewart, P.S., Greenberg, E.P., 1999. “Bacterial biofilms: a common cause of
249 persistent infections.” *Science* 284 (5418): 1318–22. doi:10.1126/science.284.5418.1318.

250 Darling, A.C.E., Mau, B., Blattner, F.R., Perna, N.T., 2004. “Mauve: multiple alignment of
251 conserved genomic sequence with rearrangements.” *Genome Research* 14 (7): 1394–
252 1403. doi:10.1101/gr.2289704.

253 Edgar, R.C., 2004a. « MUSCLE: multiple sequence alignment with high accuracy and high
254 throughput ». *Nucleic Acids Research* 32 (5):1792- 97. doi:10.1093/nar/gkh340.

255 Edgar, R.C., 2004b. « MUSCLE: a multiple sequence alignment method with reduced time
256 and space complexity ». *BMC Bioinformatics* 5 (aout):113. doi:10.1186/1471-2105-5-
257 113.

258 Epstein, A.K., Pokroy, B., Seminara, A., Aizenberg, J., 2011. “Bacterial biofilm shows
259 persistent resistance to liquid wetting and gas penetration.” *Proceedings of the National*
260 *Academy of Sciences* 108 (3): 995–1000. doi:10.1073/pnas.1011033108.

261 Fan, B., Chen, X.H., Budiharjo, A., Bleiss, W., Vater, J., Borriss, R., 2011. “Efficient
262 colonization of plant roots by the plant growth promoting bacterium *Bacillus*
263 *amyloliquefaciens* FZB42, Engineered to Express Green Fluorescent Protein.” *Journal of*
264 *Biotechnology* 151 (4): 303–11. doi:10.1016/j.jbiotec.2010.12.022.

265 Fan, B., Blom, J., Klenk, H.-P., Borriss, R., 2017. “*Bacillus amyloliquefaciens*, *Bacillus*
266 *velezensis*, and *Bacillus siamensis* form an ‘operational group *B. amyloliquefaciens*’
267 within the *B. subtilis* species complex.” *Frontiers in Microbiology* 8.
268 doi:10.3389/fmicb.2017.00022.

269 Ghelardi, E., Salvetti, S., Ceragioli, M., Gueye, S.A., Celandroni, F., Senesi, S., 2012.
270 “Contribution of surfactin and SwrA to flagellin expression, swimming, and surface

271 motility in *Bacillus subtilis*.” *Applied and Environmental Microbiology* 78 (18): 6540–44.
272 doi:10.1128/AEM.01341-12.

273 Goris, J., Konstantinidis, K.T., Klappenbach, J.A., Coenye, T., Vandamme, P., Tiedje, J.M.,
274 2007. DNA–DNA hybridization values and their relationship to whole-genome sequence
275 similarities. *Int. J. Syst. Evol. Microbiol.* 57, 81–91. <https://doi.org/10.1099/ijs.0.64483-0>.

276 Gouy, M., Guindon, S., Gascuel, O., 2010. “SeaView version 4: a multiplatform graphical
277 user interface for sequence alignment and phylogenetic tree building.” *Molecular Biology*
278 *and Evolution* 27 (2): 221–24. doi:10.1093/molbev/msp259.

279 de Jong, W., Wösten, H.A.B., Dijkhuizen, L., Claessen, D., 2009. “Attachment of
280 *Streptomyces coelicolor* is mediated by amyloid fimbriae that are anchored to the cell
281 surface via cellulose.” *Molecular Microbiology* 73 (6): 1128–40. doi:10.1111/j.1365-
282 2958.2009.06838.x.

283 Jones, C.J., Wozniak, D.J., 2017. « Congo red stain identifies matrix overproduction and is an
284 indirect measurement for c-Di-GMP in many species of bacteria ». In C-Di-GMP
285 Signaling, 147- 156. *Methods in Molecular Biology*. Humana Press, New York, NY.
286 doi:10.1007/978-1-4939-7240-1_12.

287 Joshi, R., McSpadden Gardener, B.B., 2006. « Identification and characterization of novel
288 genetic markers associated with biological control activities in *Bacillus subtilis* ».
289 *Phytopathology* 96 (2):145- 54. doi:10.1094/PHYTO-96-0145.

290 Kearns, D.B., Chu, F., Rudner, R., Losick, R., 2004. “Genes governing swarming in *Bacillus*
291 *subtilis* and evidence for a phase variation mechanism controlling surface motility.”
292 *Molecular Microbiology* 52 (2): 357–69. doi:10.1111/j.1365-2958.2004.03996.x.

293 Lahlali, R., Peng, G., Gossen, B.D., McGregor, L., Yu, F.Q., Hynes, R.K., Hwang, S.F.,
294 McDonald, M.R., Boyetchko, S.M., 2013. “Evidence that the biofungicide serenade

295 (*Bacillus subtilis*) suppresses clubroot on canola via antibiosis and induced host
296 resistance.” *Phytopathology* 103 (3): 245–54. doi:10.1094/PHYTO-06-12-0123-R.

297 Largeteau, M.L., Savoie, J.-M., 2010. “Microbially Induced Diseases of *Agaricus Bisporus*:
298 biochemical mechanisms and impact on commercial mushroom production.” *Applied*
299 *Microbiology and Biotechnology* 86 (1): 63–73. doi:10.1007/s00253-010-2445-2.

300 Magno-Pérez-Bryan, M.C., Martinez-Garcia, P.M., Hierrezuelo, J., Rodriguez-Palenzuela, P.,
301 Arrebola, E., Ramos, C., de Vicente, A., Perez-Garcia, A., Romero, D.F., 2015.
302 “Comparative genomics within the *Bacillus* genus reveal the singularities of two robust
303 *Bacillus amyloliquefaciens* biocontrol strains.” *Molecular Plant-Microbe Interactions*:
304 *MPMI*, June. doi:10.1094/MPMI-02-15-0023-R.

305 Mamoun, M.L., Iapicco, R., Savoie, J.M., Olivier, J.M., 2000. “Green mould disease in
306 France: *Trichoderma harzianum* Th2 and other species causing damages on mushroom
307 farms.” *In Sci. Cultiv. of Edible Fungi. Edited by L. Van Griensven. Balkema,*
308 *Rotterdam. 625–632.*

309 Medema, M.H., Blin, K., Cimermancic, P., de Jager, V., Zakrzewski, P., Fischbach, M.A.,
310 Weber, T., Takano, E., Breitling, R., 2011. antiSMASH: rapid identification, annotation
311 and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal
312 genome sequences. *Nucleic Acids Res.* 39, W339–W346. doi:10.1093/nar/gkr466.

313 Meier-Kolthoff, J.P., Auch, A.F., Klenk, H.-P., Göker, M., 2013. Genome sequence-based
314 species delimitation with confidence intervals and improved distance functions. *BMC*
315 *Bioinformatics* 14, 60. doi:10.1186/1471-2105-14-60.

316 Meng, Q., Jiang, H., Hao, J.J., 2016. “Effects of *Bacillus velezensis* strain BAC03 in
317 promoting plant growth”. *Biological Control* 98 (Supplement C):18–26.
318 doi:10.1016/j.biocontrol.2016.03.010.

319 Mordini, S., Osera, C., Marini, S., Scavone, F., Bellazzi, R., Galizzi, A., Calvio, C., 2013.
320 “The role of SwrA, DegU and P(D3) in fla/che expression in *B. subtilis*.” *PloS One* 8
321 (12): e85065. doi:10.1371/journal.pone.0085065.

322 Morris, C.E., Monier, J.-M., 2003. “The ecological significance of biofilm formation by plant-
323 associated bacteria.” *Annual Review of Phytopathology* 41: 429–53. doi:
324 10.1146/annurev.phyto.41.022103.134521.

325 Niazi, A., Manzoor, S., Asari, S., Bejai, S., Meijer, J., Bongcam-Rudloff, E., 2014. “Genome
326 analysis of *Bacillus amyloliquefaciens* subsp. *plantarum* UCMB5113: a rhizobacterium
327 that improves plant growth and stress management.” *PloS One* 9 (8): e104651.
328 doi:10.1371/journal.pone.0104651.

329 Norman, T.M., Lord, N.D., Paulsson, J., and Losick, R. 2013. “Memory and Modularity in
330 Cell-Fate Decision Making”. *Nature* 503 (7477): 481–86. doi:10.1038/nature12804.

331 Ongena, M., Jacques, P., 2008. “*Bacillus* lipopeptides: versatile weapons for plant disease
332 biocontrol.” *Trends in Microbiology* 16 (3): 115–25. doi:10.1016/j.tim.2007.12.009.

333 Ongena, M., Jacques, P., Touré, Y., Destain, J., Jabrane, A., Thonart, P., 2005. “Involvement
334 of fengycin-type lipopeptides in the multifaceted biocontrol potential of *Bacillus*
335 *Subtilis*.” *Applied Microbiology and Biotechnology* 69 (1): 29–38. doi:10.1007/s00253-
336 005-1940-3.

337 Pandin, C., Le Coq, D., Canette, A., Aymerich, S., Briandet, R., 2017. “Should the biofilm
338 mode of life be taken into consideration for microbial biocontrol agents?” *Microbial*
339 *Biotechnology*, February, 10(4): 719-734. doi:10.1111/1751-7915.12693.

340 Patel, H., Tscheka, C., Edwards, K., Karlsson, G., Heerklotz, H., 2011. “All-or-none
341 membrane permeabilization by fengycin-type lipopeptides from *Bacillus subtilis*
342 QST713.” *Biochimica Et Biophysica Acta* 1808 (8): 2000–2008.
343 doi:10.1016/j.bbamem.2011.04.008.

344 Punja, Z.K., Rodriguez, G., Tirajoh, A., 2016. « Effects of *Bacillus subtilis* strain QST 713
345 and storage temperatures on post-harvest disease development on greenhouse tomatoes ». *Crop Protection* 84 (juin):98- 104. doi:10.1016/j.cropro.2016.02.011.

346

347 Rodriguez-R, L.M., Konstantinidis, K.T., 2016. The enveomics collection: a toolbox for
348 specialized analyses of microbial genomes and metagenomes. *PeerJ Prepr.* 4, e1900v1.
349 doi:10.7287/peerj.preprints.1900v1.

350 Romero, D., Aguilar, C., Losick, R., Kolter, R., 2010. “Amyloid fibers provide structural
351 integrity to *Bacillus subtilis* biofilms.” *Proceedings of the National Academy of Sciences*
352 107 (5): 2230–34. doi:10.1073/pnas.0910560107.

353 Samuels, G.J., Dodd, S.L., Gams, W., Castlebury, L.A., Petrini, O., 2002. “*Trichoderma*
354 species associated with the green mold epidemic of commercially grown *Agaricus*
355 *bisporus*.” *Mycologia* 94 (1): 146–70. doi: 10.2307/3761854

356 Stein, T., Borchert, S., Conrad, B., Feesche, J., Hofemeister, B., Hofemeister, J., Entian, K.-
357 D., 2002. “Two different lantibiotic-like peptides originate from the ericin gene cluster of
358 *Bacillus subtilis* A1/3.” *Journal of Bacteriology* 184 (6):1703–11.
359 doi:10.1128/JB.184.6.1703-1711.2002.

360 Stein, T., 2005. “*Bacillus subtilis* antibiotics: structures, syntheses and specific functions.”
361 *Molecular Microbiology* 56 (4): 845–57. doi:10.1111/j.1365-2958.2005.04587.x.

362 Vlamakis, H., Chai, Y., Beaugregard, P., Losick, R., Kolter, R., 2013. “Sticking together:
363 building a biofilm the *Bacillus subtilis* way.” *Nature Reviews. Microbiology* 11 (3): 157–
364 68. doi:10.1038/nrmicro2960.

365 Weber, T., Blin, K., Duddela, S., Krug, D., Kim, H.U., Brucocoleri, R., Lee, S.Y., Fischbach,
366 M.A., Müller, R., Wohlleben, W., Breitling, R., Takano, E., Medema, M.H., 2015.
367 antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene
368 clusters. *Nucleic Acids Res.* 43, W237–W243. doi:10.1093/nar/gkv437.

369 Winkelman, J.T., Blair, K.M., Kearns, D.B., 2009. “RemA (YlzA) and RemB (YaaB) regulate
370 extracellular matrix operon expression and biofilm formation in *Bacillus subtilis*.”
371 *Journal of Bacteriology* 191 (12): 3981–91. doi:10.1128/JB.00278-09.

372 Wu, S., Zhu, Z., Fu, L., Niu, B., Li, W., 2011. “WebMGA: a customizable web server for fast
373 metagenomic sequence analysis.” *BMC Genomics* 12 (September): 444.
374 doi:10.1186/1471-2164-12-444.

375 Xu, Z., Zhang, R., Wang, D., Qiu, M., Feng, H., Zhang, N., Shen, Q., 2014. “Enhanced
376 control of cucumber wilt disease by *Bacillus amyloliquefaciens* SQR9 by altering the
377 regulation of its degu phosphorylation.” *Applied and Environmental Microbiology* 80 (9):
378 2941–50. doi:10.1128/AEM.03943-13.

379 Yoon, S.-H., Ha, S.-M., Lim, J., Kwon, S., Chun, J., 2017. A large-scale evaluation of
380 algorithms to calculate average nucleotide identity. *Antonie Van Leeuwenhoek* 110,
381 1281–1286. doi :10.1007/s10482-017-0844-4.

382 Zeriouh, H., de Vicente, A., Pérez-García, A., Romero, D., 2014. “Surfactin triggers biofilm
383 formation of *Bacillus subtilis* in melon phylloplane and contributes to the biocontrol
384 activity.” *Environmental Microbiology* 16 (7): 2196–2211. doi:10.1111/1462-
385 2920.12271.

386 Zhao, X., Kuipers, O.P., 2016. “Identification and classification of known and putative
387 antimicrobial compounds produced by a wide variety of Bacillales species.” *BMC*
388 *Genomics* 17: 882. doi:10.1186/s12864-016-3224-y.

389 Zhou, Y., Liang, Y., Lynch, K.H., Dennis, J.J., Wishart, D.S., 2011. “PHAST: a fast phage
390 search tool.” *Nucleic Acids Research* 39 (Web Server issue): W347-352.
391 doi:10.1093/nar/gkr485.

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TABLE AND FIGURE LEGENDS

Table 1: Comparative genomic analysis of *Bacillus velezensis* QST713 with *Bacillus* genomes. (Footnote: Average nucleotide identity (ANI) and average amino acid identity (AAI) calculation was performed *via* the EDGAR platform and the Kostas lab web server (Blom *et al.* 2009, 2016; Goris *et al.* 2007; Rodriguez-R & Konstantinidis 2016; Yoon *et al.* 2017). Digital DNA–DNA hybridization (dDDH) calculation was performed through the DSMZ webservice, the genome-to-genome-distance calculator version 2.1 (GGDC) was used for genome-based species delineation (Meier-Kolthoff *et al.* 2013) with formula two as described in Fan *et al.* 2017.)

Table 2: Comparative analysis of secondary metabolites clusters of *Bacillus velezensis* QST713 identified in genome with plant-associated strains and reference genomes. (Footnote: Prediction of secondary metabolites clusters of *Bacillus* strains were performed through the antiSMASH web server (Medema *et al.* 2011; Blin *et al.* 2013; Weber *et al.* 2015).

418 **Table 3:** Comparative analysis of genes involved in biofilm formation in *B. velezensis*
419 QST713 and *B. velezensis* FZB42. (*) represents the longest nucleotide sequence taken as a
420 basis for BLAST comparison.

421

422 **Table S1:** Prophage regions of *Bacillus velezensis* QST713 genome.

423 (Footnote: Prophage regions were identified using PHASTER web server (Zhou *et al.* 2011;
424 Arndt *et al.* 2016).

425

426 **Table S2:** Comparative analysis of gene clusters encoding secondary metabolites in *B.*
427 *velezensis* QST713 with *Bacillus* strains. (*) represents the longest nucleotide sequence taken
428 as a basis for BLAST comparison.

429

430 **Fig. 1:** Neighbor-joining phylogenetic tree constructed from the core genomes of 30 *B.*
431 *subtilis*, *B. amyloliquefaciens* and *B. velezensis* strains. The position of *Bacillus velezensis*
432 QST713 in the tree is marked by a yellow dot. EDGAR platform was used to obtain
433 alignments in NEXUS format and SeaView 4.5.4 software to construct phylogenetic tree
434 using maximum-parsimony method (Edgar 2004a, 2004b; Blom *et al.* 2009, 2016; Gouy *et al.*
435 2009).

436

437 **Fig. 2:** Circular map of genomic features of the whole genome of *Bacillus velezensis* QST713.
438 Circles display from the inner to outside: (1) GC Skew ; (2) GC Content ; (3) Predictive
439 secondary metabolites clusters ; (4) Predictive prophages clusters; (5) rRNA (black), tRNA
440 (red), ncRNA (green); (6) Predicted CDSs transcribed in clockwise direction; (7) Predicted
441 CDSs transcribed in the counterclockwise direction; (8, 9, 10, 11) Blast comparison of
442 QST713 genome with *Bacillus* strains, SQR9, FZB42, NCIB3610 and 168 respectively.

443 Circular map and blast comparison were performed with BLAST Ring Image Generator
444 software (BRIG) (Alikhan *et al.* 2011).

445

446 **Fig. 3:** Blast comparison of NRPS, TransATPKS and lantipeptide clusters in QST713
447 (above), FZB42, A13 or CC09 (below). Square indicate the differences between strain
448 sequences.

449

450 **Fig. 4:** Phenotypic comparisons of *B. velezensis* QST713 with *Bacillus* species. Strains are *B.*
451 *subtilis* 168, *B. subtilis* NCIB3610, *B. velezensis* SQR9, *B. velezensis* FZB42 and *B.*
452 *velezensis* QST713. Biofilm formation was evaluated as macrocolonies morphology, pellicles
453 formation and submerged biofilms. To visualize colony architecture, 5 µl of an overnight
454 culture in TSB were spotted on 1.5% Tryptone Soya Agar (TSA, Biomérieux, France) with 40
455 µg.ml⁻¹ of Congo red to visualize matrix elements (Jones and Wozniak 2017). For pellicles
456 visualisation, 10 µl of an overnight culture in TSB were used to inoculate 2 ml of TSB in 24-
457 well plates (TPP, Switzerland). Plates were then incubated at 25°C for 72h, macrocolonies
458 and pellicles formation were recorded at 72h and digital pictures were taken. Submerged
459 biofilm formation was performed in 96-well microtiter plates (Greiner µClear®, Germany).
460 Briefly, for each strain, 200 µl of an overnight culture in TSB standardized to an OD_{600nm} of
461 0.01 were added to the wells, then incubated at 25°C for 90 min for attachment. The
462 supernatant was removed to eliminate non-adherent bacteria and 200 µl of sterile TSB was
463 added. Plates were then incubated for 24h at 25°C, experiment was repeated six times.
464 SYTO9® (Invitrogen, France), a green-fluorescent nucleic acid marker was used to tag the
465 cells fluorescently for submerged-biofilm observations by confocal laser scanning microscopy
466 (Leica SP8, Leica Microsystems, Germany). Swarming motility of *Bacillus* strains was
467 determined by the spread of bacteria on TSA 0.8% agar plates at 25° for 24h, 10 µl of an

468 overnight culture were inoculated at the centre of the 9 cm agar plates dried for 15 min and
469 incubated at 25°C for 24h. Experiments was repeated three times.

470

471 **Fig. 5:** Biocontrole effect of *Bacillus velezensis* QST713 against *T. aggressivum* f.
472 *europaeum*. (A) Button mushroom yields of *A. bisporus* when the culture compost is
473 contaminated or not by *T. aggressivum* (T. a) and treated or not by the QST713 strain: (+)
474 Presence of; (-) Absence of. *Agaricus bisporus* was seeded at a rate of 0,8% of compost
475 weight (Amycel Delta, white hybrid variety, Amycel, Vendôme). Treatment with *B.*
476 *velezensis* QST713: compost was homogenized with suspension of *B. velezensis* QST713 at a
477 rate of 0.1 g.kg⁻¹ of product (Serenade Max ®, AMM No. 2100162, BayerCropScience,
478 France) corresponding at 5.10⁶ CFU.gr⁻¹ of compost. Inoculation with *T. aggressivum* with
479 2000 spores in a central spot in pot of 9 kg of compost. Yield data correspond at the number
480 in kg per m² of button mushroom whole feets collected form a complete culture cycle of 2
481 months. Experiment was repeated 6 times. (B) Antagonism test of *T. aggressivum* by *B.*
482 *velezensis* QST713: (a) *T. aggressivum* alone; (b) *T. aggressivum* vs *B. velezensis* QST713.
483 The fungal pathogen was inoculated with an agar plug taken from a 72 h fungal culture that
484 was deposited on the center of YMEA medium plate (yeast extract 2g.L⁻¹, malt extract 20g.L⁻¹,
485 agar 15g.L⁻¹). 5 µl of sterile water (control) or of an overnight culture of *B. velezensis*
486 QST713 in TSB was inoculated in three spots at 3 cm of *T. aggressivum* spot. Petri dish were
487 incubated at 25°C and observations are performed 5 days after by measuring the inhibition
488 zone of *T. aggressivum*. Experiment was repeated 3 times. Differences among treatments
489 were determined by performing a one-way analysis of variance ($P < 0.05$) and Tukey's
490 honestly significant difference (HSD) procedure ($P < 0.05$) with Statgraphics Centurion
491 software (Statpoint Technologies, United States). Letters a and b on the graph represent
492 significant differences ($P < 0.05$).

493

494 **Fig. S1:** Classification of genes into orthologous groups (COG) in *B. velezensis* QST713.

495 Distribution of *B. velezensis* QST713 coding sequences (71.7%) symbolized in percentages of

496 genes classified into COG. Genes not found in the cog annotation are classified in the

497 category "not in COG" in black. The functional classification of protein-coding genes was

498 performed using RPS-BLAST with COG database and classified into categories *via* the

499 WebMGA server (Wu *et al.* 2011).

500

501

Table 1: Comparative genomic analysis of *Bacillus velezensis* QST713 with *Bacillus* genomes.

Strains	Genbank accession N°	dDDH % (\pm C.I.)	ANI (%)	AAI (%)	GC (%)	bp	Source
<i>Bacillus velezensis</i>							
QST713	CP025079	100 \pm 0.0	100	100	45.9	4233757	Commercial strain used in agriculture (Serenade® : Ref : Bayer, SERENE100/40)
CFSAN034339	NZ_LYNB00000000	99.5 \pm 0.3	99.96	99.89	45.9	4209526	Agricultural soil
Bs006	NZ_LJAU00000000	96.4 \pm 1.3	99.97	99.88	45.8	4173094	Banana roots
UMAF6639	NZ_CP006058	92.0 \pm 2.1	98.93	99.24	46.3	4034636	Unknown
UCMB5036	NC_020410	92.7 \pm 2.0	98.74	99.13	46.6	3910324	Inner tissues of the cotton plant
CC09	NZ_CP015443	91.2 \pm 2.2	98.80	98.92	46.1	4167153	Camphor leaves
AS43 3	NC_019842	88.1 \pm 2.5	98.37	98.87	46.6	3961368	Surface of a wheat spike
UCMB5113	NC_022081	88.9 \pm 2.4	98.23	98.82	46.7	3889532	Soil from Karpaty mountains
TrigoCor1448	NZ_CP007244	88.3 \pm 2.4	98.38	98.81	46.5	3957904	Wheat rhizosphere
SB1216	CP015417	88.2 \pm 2.5	98.14	98.79	46.8	3814720	Soil
FZB42	NC_009725	88.3 \pm 2.5	98.11	98.77	46.5	3918589	infested sugar beet
G341	NZ_CP011686	88.4 \pm 2.4	98.17	98.54	46.5	4009746	Korean ginseng rhizosphere
UCMB5033	NC_022075	87.8 \pm 2.5	97.92	98.53	46.2	4071167	Cotton rhizosphere
JTYP2	NZ_CP020375	83.4 \pm 2.8	97.79	98.50	46.5	3929789	Crassulaceae leaf surface
LS69	NZ_CP015911	83.4 \pm 2.8	97.81	98.49	46.5	3917759	isolated from the rice field
S3 1	NZ_CP016371	83.4 \pm 2.8	97.79	98.49	46.5	3929772	Cucumber rhizosphere
SYBC H47	NZ_CP017747	81.2 \pm 2.9	97.42	98.36	46.4	3884433	Honey
D2 2	NZ_CP014990	79.6 \pm 2.9	97.32	98.24	46.7	3921833	Unknown
SQR9	NZ_CP006890	82.9 \pm 2.8	97.61	98.11	46.1	4117023	Cucumber rhizosphere
Y2	NC_017912	83.6 \pm 2.8	97.62	98.09	45.9	4238624	Wheat rhizosphere
YAUB9601 Y2	NC_017061	83.6 \pm 2.8	97.62	98.09	45.9	4242767	Wheat rhizosphere
IT 45	NC_020272	79.8 \pm 3.0	97.21	98.07	46.6	3928855	Commercial strain used in horticulture
NJN 6	NZ_CP007165	79.3 \pm 2.9	97.44	98.06	46.6	4052546	Banana rhizosphere
M75	NZ_CP016395	79.6 \pm 2.9	97.27	98.06	46.6	4007450	Cotton waste
CAUB946	NC_016784	78.9 \pm 2.9	97.22	97.97	46.5	4019858	Rice rhizosphere
<i>Bacillus amyloliquefaciens</i>							
DSM 7	NC_014551	55.7 \pm 2.7	93.29	95.77	46.1	3980199	Soil, fermentation plant
TA208	NC_017188	55.1 \pm 2.7	93.17	95.53	45.8	3937511	Lab stock, overproducing guanosine
<i>Bacillus subtilis</i>							
NDmed	NZ_JPVW00000000	20.5 \pm 2.4	76.98	79.97	43.7	4059981	Endoscope washer-disinfector
NCIB 3610	NZ_CP020102	20.9 \pm 2.4	76.43	81.00	43.5	4215607	Soil
168	NZ_CP010052	20.9 \pm 2.4	76.43	81.00	43.5	4215619	Laboratory strain

(Footnote: Average nucleotide identity (ANI) and average amino acid identity (AAI) calculation was performed via the EDGAR platform and the Kostas lab web server (Blom *et al.* 2009, 2016; Goris *et al.* 2007; Rodriguez-R & Konstantinidis 2016; Yoon *et al.* 2017). Digital DNA–DNA hybridization (dDDH) calculation was performed through the DSMZ webserver, the genome-to-genome-distance calculator version 2.1 (GGDC) was used for genome-based species delineation (Meier-Kolthoff *et al.* 2013) with formula two as described in Fan *et al.* 2017.)

Table 2: Comparative analysis of secondary metabolites clusters of *Bacillus velezensis* QST713 identified in genome with plant-associated strains and reference genomes.

<i>Bacillus velezensis</i> QST713						Presence (+) or absence (-) of secondary metabolites clusters in <i>Bacillus</i> strains			
Cluster number	Synthetase	Metabolites	MIBiG ID (% of genes show similarity)	Predicted large cluster position	bp	FZB42	SQR9	3610	168
1	NRPS	Surfactin	BGC0000433_c1 (86%)	347609 - 413022	65414	+	+	+	+
2	TransATPKS	Macrolactin	BGC0000181_c1 (100%)	1440778 - 1526670	85893	+	+	-	-
3	TransATPKS-NRPS	Bacillaene	BGC0001089_c1 (100%)	1756070 - 1858741	102672	+	+	+	+
4	NRPS	Bacillomycin D	BGC0001090 (66%)	1936517 - 1981185	44669	+	+	-	-
5	TransATPKS-NRPS	Fengycin	BGC0001095_c1 (100%)	1989975 - 2039517	49543	+	+	+	+
6	TransATPKS	Difficidin	BGC0000176_c1 (100%)	2460543 - 2560999	100457	+	+	-	-
7	Bacteriocin-NRPS	Bacillibactin	BGC0001185_c1 (100%)	3272524 - 3339313	66790	+	+	+	+
8	NRPS	Bacilysin	BGC0000309_c1 (100%)	3895380 - 3953631	58252	+	+	+	+
9	TransATPKS-NRPS	Rhizocticin	BGC0000926_c (22%)	191893 - 269628	77736	-	-	-	-
10	Lantipeptide	Subtilin-like / Ericin	BGC0000511_c1 (100%)	3485394 - 3500516	15123	-	-	-	-
11	NRPS	-	-	3625021 - 3693450	68430	-	-	-	-
12	OtherKS	-	-	986643 - 1027887	41245	+	+	-	-
13	T3PKS	-	-	2166999 - 2208099	41101	+	+	+	+
14	Terpene	-	-	1110586 - 1131326	20741	+	+	+	+
15	Terpene	-	-	2080722 - 2102605	21884	+	+	+	+

(Footnote: Prediction of secondary metabolites clusters of *Bacillus* strains were performed through the antiSMASH web server (Medema *et al.* 2011; Blin *et al.* 2013; Weber *et al.* 2015).)

Table 3: Comparative analysis of genes involved in biofilm formation in *B. velezensis* QST713 with *B. velezensis* FZB42. (*) represents the longest nucleotide sequence taken as a basis for BLAST comparison.

<i>Bacillus velezensis</i> QST713					<i>B. velezensis</i> FZB42 Genbank accession n°	
Genes	Product	Accession n°	Position	bp	Coverage / Identity with QST713	
<i>epsO</i>	Operon for capsular biosynthesis	BVQ_17985	3557349 - 3558314	966	RBAM_RS15740	100% / 98%
<i>epsN</i>		BVQ_17990	3558293 - 3559465	1173	RBAM_RS15745	100% / 99%
<i>epsM</i>		BVQ_17995	3559470 - 3560117	648	RBAM_RS15750	100% / 99%
<i>epsL</i>		BVQ_18000	3560114 - 3560722	609	RBAM_RS15755	100% / 99%
<i>epsK</i>		BVQ_18005	3560719 - 3562236	1518	RBAM_RS15760	100% / 99%
<i>epsJ</i>		BVQ_18010	3562233 - 3563267	1035	RBAM_RS15765	100% / 98%
<i>epsI</i>		BVQ_18015	3563264 - 3564340	1077	RBAM_RS15770	100% / 98%
<i>epsH</i>		BVQ_18020	3564345 - 3565382	1038	RBAM_RS15775	100% / 99%
<i>epsG</i>		BVQ_18025	3565401 - 3566504	1104	RBAM_RS15780	100% / 99%
<i>epsF</i>		BVQ_18030	3566508 - 3567644	1137	RBAM_RS15785	100% / 99%
<i>epsE</i>		BVQ_18035	3567637 - 3568479	843	RBAM_RS15790	100% / 99%
<i>epsD</i>		BVQ_18040	3568476 - 3569615	1140	RBAM_RS15795	100% / 98%
<i>epsC</i>		BVQ_18045	3569631 - 3571424	1794	RBAM_RS15800	100% / 99%
<i>epsB</i>		BVQ_18050	3572351 - 3571671	681	RBAM_RS15805	100% / 99%
<i>epsA</i>	BVQ_18055	3573064 - 3572357	708	RBAM_RS15810	100% / 99%	
<i>comA</i>	Response regulator in the two-component regulatory system ComP/ComA involved in a major quorum response pathway that regulates the development of genetic competence	BVQ_16475	3266368 - 3265724	645	RBAM_RS14365	100% / 99%
<i>pgcA (yhxB)</i>	Operon for poly-γ-glutamate synthesis	BVQ_05065	982326 - 984068	1743	RBAM_RS04780	100% / 99%
<i>pgsA (capA)</i>		BVQ_18760	3749291 - 3748143	1149	RBAM_RS16480	100% / 99%
<i>pgsB (capB)</i>		BVQ_18770	3750955 - 3749774	1182	RBAM_RS16490	100% / 99%
<i>pgsC (capC)</i>		BVQ_18765	3749759 - 3749310	450	RBAM_RS16485	100% / 99%
<i>sinI</i>	SinR antagonist	BVQ_12985	2626360 - 2626533	174	RBAM_RS11410	100% / 99%
<i>sinR</i>	Regulator of biofilm formation	BVQ_12990	2626567 - 2626902	336	RBAM_RS11415*	98% / 99%
<i>tasA</i>	Operon for amyloid fibers biosynthesis and essential for biofilm formation	BVQ_12995	2627735 - 2626950	786	RBAM_RS11420	100% / 99%
<i>sipW</i>		BVQ_13000	2628384 - 2627800	585	RBAM_RS11425	100% / 99%
<i>tapA (yqxM)</i>		BVQ_13005	2629027 - 2628356	672	RBAM_RS11430	100% / 99%
<i>blsA (yuaB)</i>	major amphiphilic protein that mediates adherence and forms a highly hydrophobic coat around biofilms	BVQ_15970	3168030 - 3168569	540	RBAM_RS14060	100% / 99%
<i>spo0A</i>	Regulator of initiation of sporulation	BVQ_12800	2593194 - 2592394	801	RBAM_RS11225	100% / 99%
<i>degU</i>	Two-component response regulator	BVQ_18575	3701900 - 3701211	690	RBAM_RS16295	100% / 99%
<i>degQ</i>	Degradation enzyme regulation protein	BVQ_18580	3701977 - 3703140	1164	RBAM_RS16300	100% / 99%
<i>kinA</i>	Kinases involved in multicomponent phosphorelay system	BVQ_07360*	1407114 - 1408934	1821	RBAM_RS06875	100% / 99%
<i>kinB</i>		BVQ_16365	3244655 - 3245938	1284	RBAM_RS14255	100% / 99%
<i>kinC</i>		BVQ_07600	1448464 - 1449768	1305	RBAM_RS07105	100% / 99%
<i>kinD</i>		BVQ_07170*	1370427 - 1368910	1518	RBAM_RS06695	98% / 99%
<i>abrB</i>	Transition state regulator	BVQ_00230	45895 - 45611	285	RBAM_RS00230	100% / 99%
<i>slrA</i>	Transcriptional regulator	BVQ_19965	3965724 - 3965885	162	RBAM_RS17715	100% / 100%
<i>slrR</i>	Transcriptional regulator	BVQ_18060	3573308 - 3573763	456	RBAM_RS15815	99% / 99%
<i>remA</i>	activation of the matrix biosynthesis operons	BVQ_08245	1620674 - 1620943	270	RBAM_RS07740	100% / 100%
<i>lys (ypdA)</i>	Sensor histidine kinase	BVQ_14910	2974431 - 2972650	1782	RBAM_RS12940	100% / 99%
<i>srfAA</i>	Surfactin synthetases	BVQ_01790	367609 - 378366	10758	RBAM_RS01840	100% / 99%
<i>srfAB</i>		BVQ_01795	378388 - 389151	10764	RBAM_RS01845	100% / 99%
<i>srfAC</i>		BVQ_01800	389186 - 393022	3837	RBAM_RS01850	100% / 98%
<i>srfAD</i>		BVQ_01805	393042 - 393773	732	RBAM_RS01855	100% / 99%
<i>sfp</i>	Phosphopantetheinyl transferase necessary for surfactin synthesis	BVQ_01815	395915 - 395241	675	RBAM_RS01880	99% / 99%
<i>swrA</i>	Swarming protein	BVQ_18440	3677165 - 3676830	336	RBAM_RS16160	100% / 95%
<i>swrB</i>	Swarming protein	BVQ_08655	1696313 - 1696780	468	RBAM_RS08150	100% / 99%
<i>swrC</i>	Multidrug efflux pump	BVQ_03840	744422 - 747565	3144	RBAM_RS03555	100% / 99%
<i>sigH</i>	Sigma factor H	BVQ_00560	111395 - 112051	657	RBAM_RS00625	100% / 99%
<i>sigW</i>	ECF sigma factor W	BVQ_01060	188349 - 188912	564	RBAM_RS01130	100% / 99%
<i>motA</i>	Flagellar motor rotation protein	BVQ_07185	1372681 - 1371866	816	RBAM_RS06710	100% / 99%
<i>motB</i>	Flagellar motor rotation protein	BVQ_07180	1371894 - 1371109	786	RBAM_RS06705	100% / 99%
<i>fla-che</i>	Operon for flagellar synthesis and chemotaxis	BVQ_08500 - BVQ_08655	1670445 - 1696780	26335	RBAM_RS07995 - RBAM_RS08150	100% / 99%
<i>codY</i>	Transcription regulator	BVQ_08495	1669312 - 1670091	780	RBAM_RS07990	100% / 99%
<i>ecsA</i>	ABC transporter ATP-binding protein	BVQ_05445	1050844 - 1051587	744	RBAM_RS05140	100% / 99%
<i>ecsB</i>	ABC transporter permease	BVQ_05450	1051580 - 1052806	1227	RBAM_RS05145	100% / 99%
<i>ecsC</i>	ABC transporter-associated protein	BVQ_05455	1052849 - 1053553	705	RBAM_RS05150	100% / 99%
<i>yusV</i>	Protein involved in swarming/biofilm formation	BVQ_17175	3397437 - 3396613	825	RBAM_RS15000	100% / 99%

Fig. 1

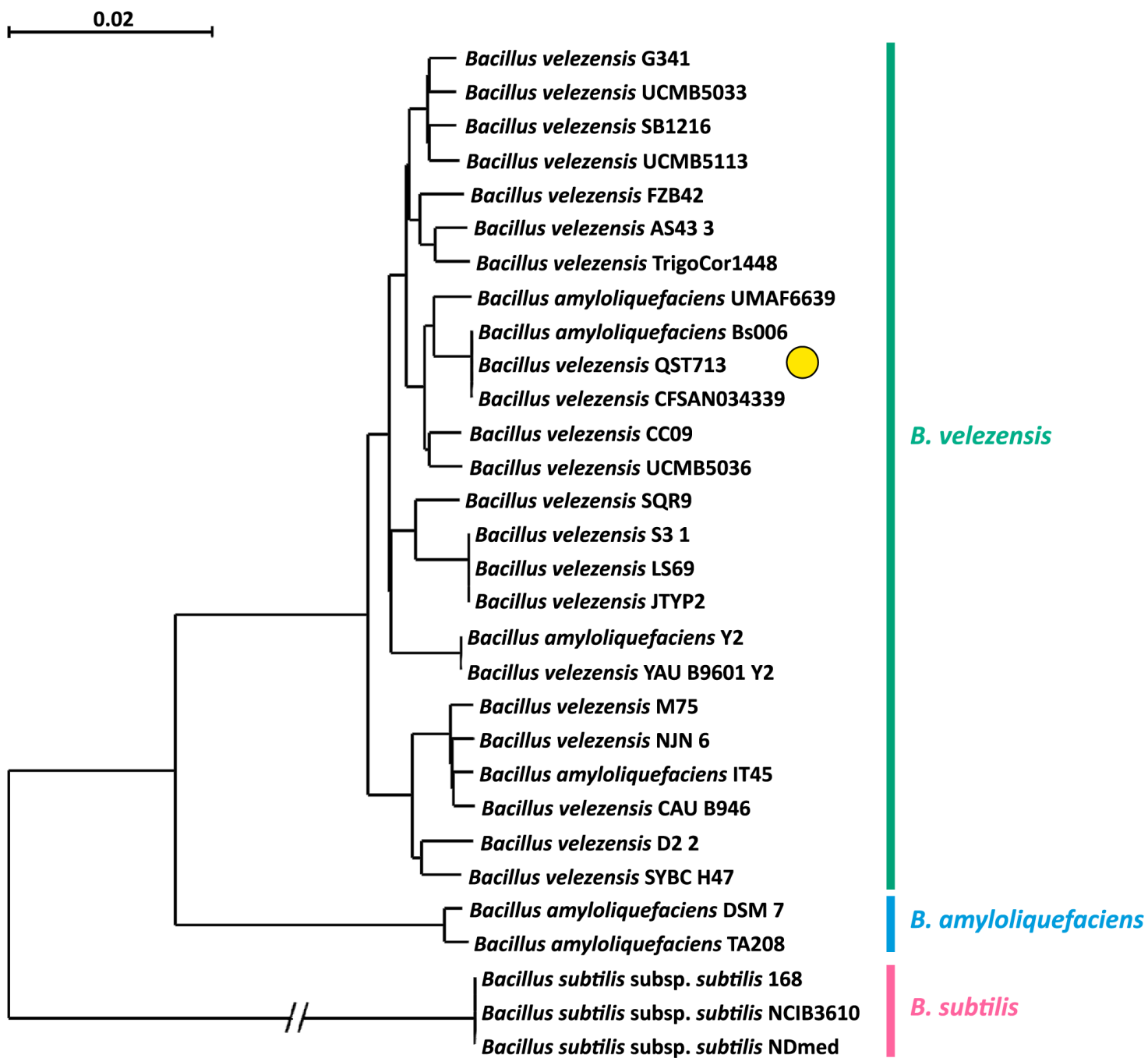


Fig. 2

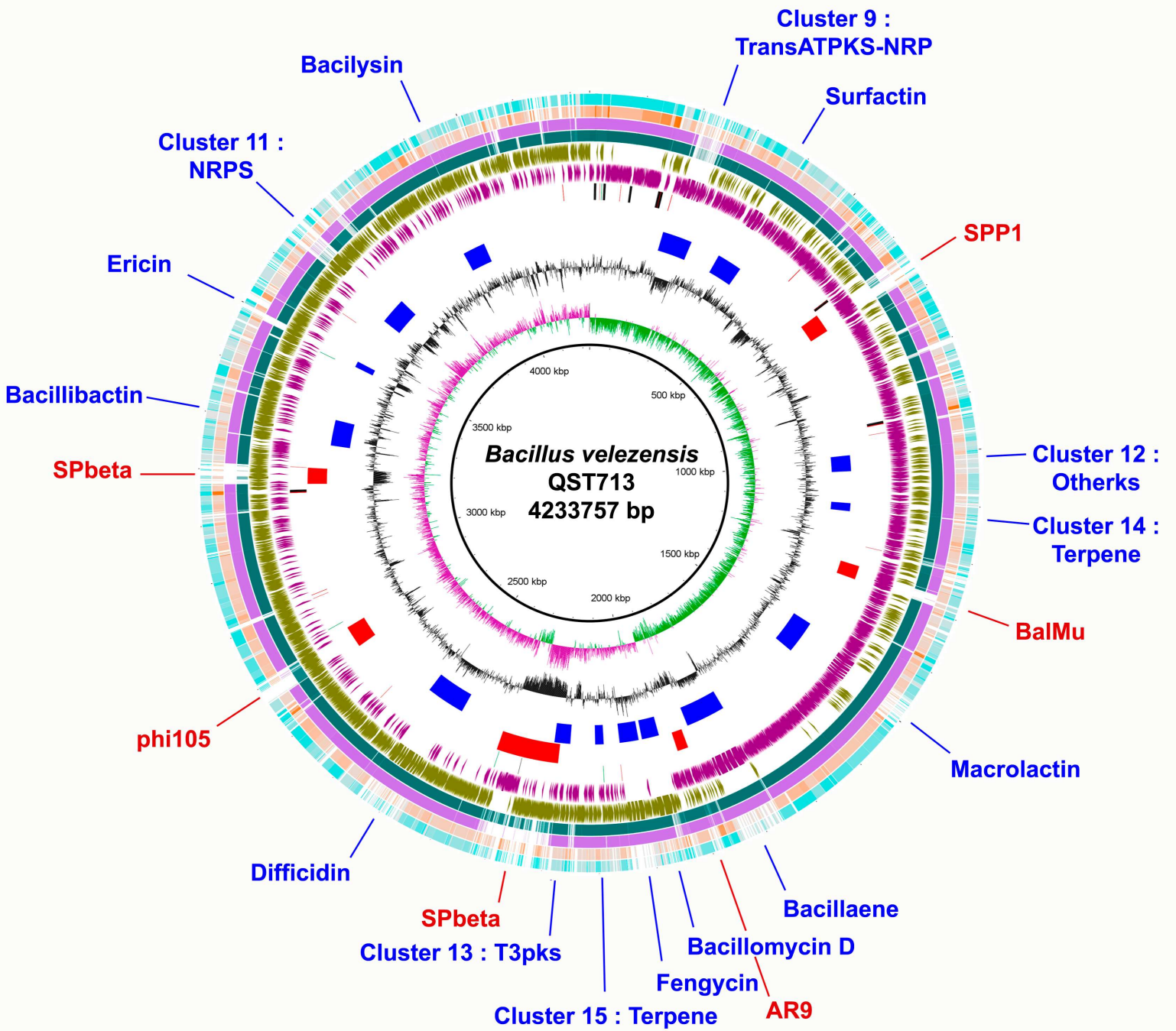


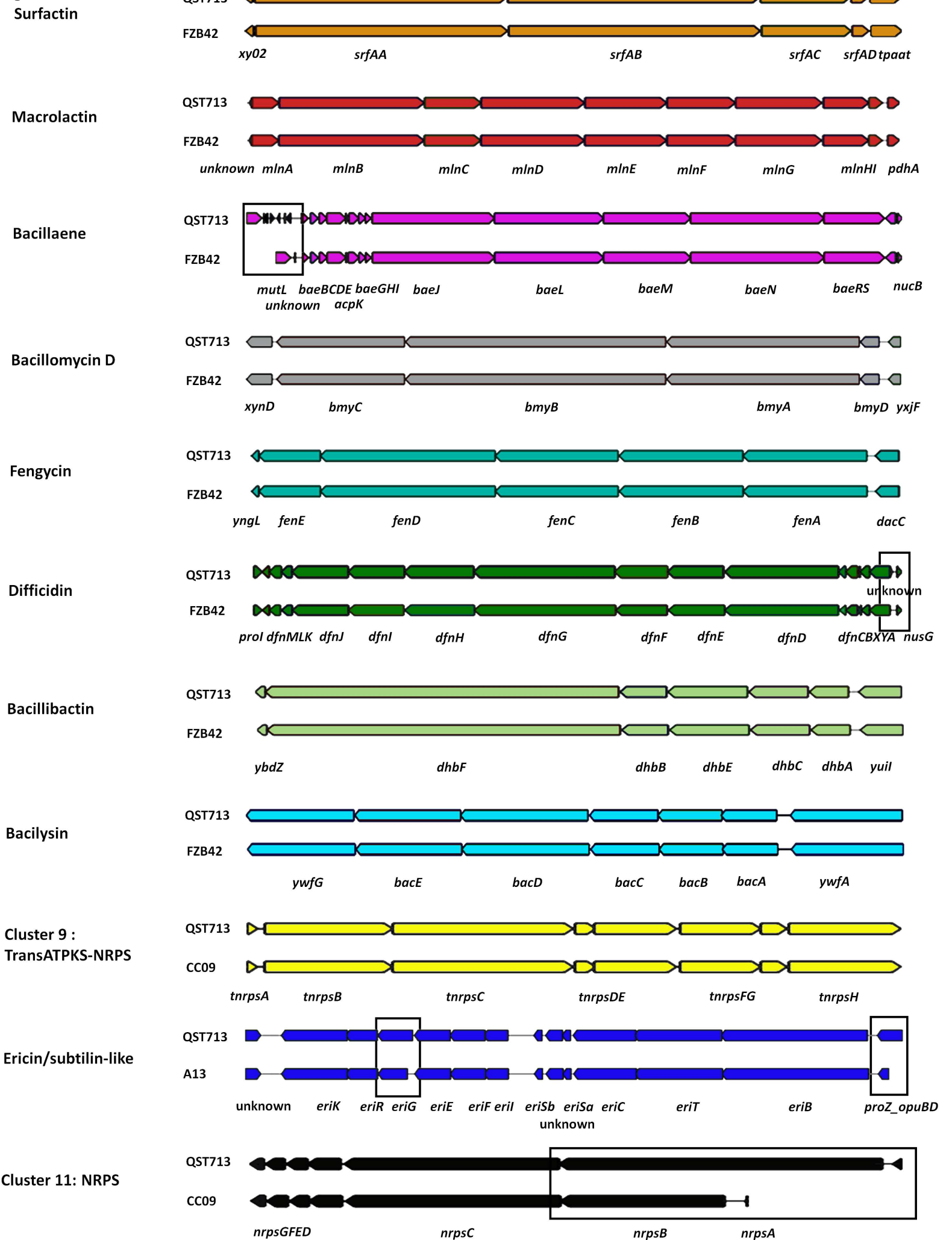
Fig. 3

Fig. 4

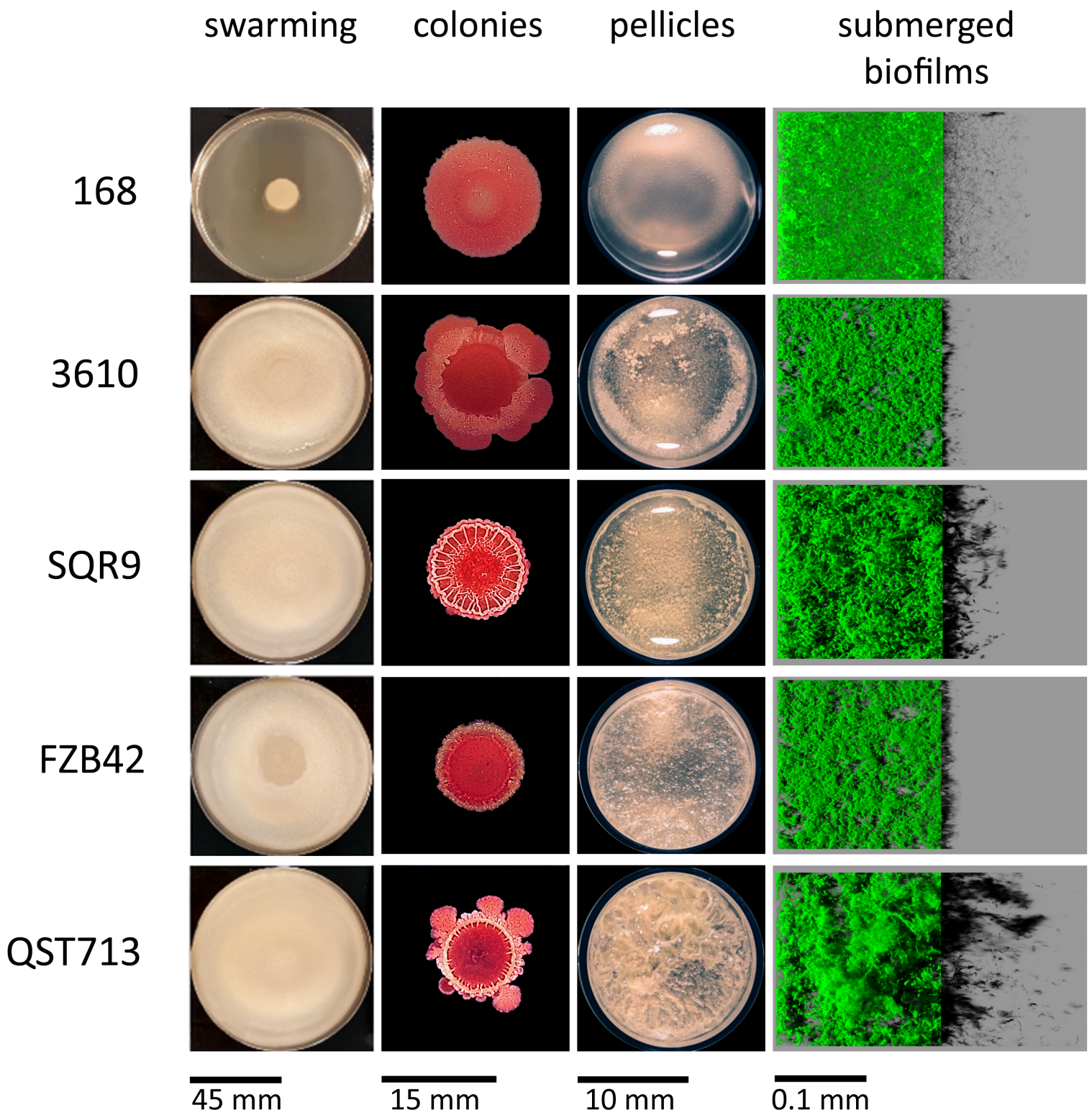
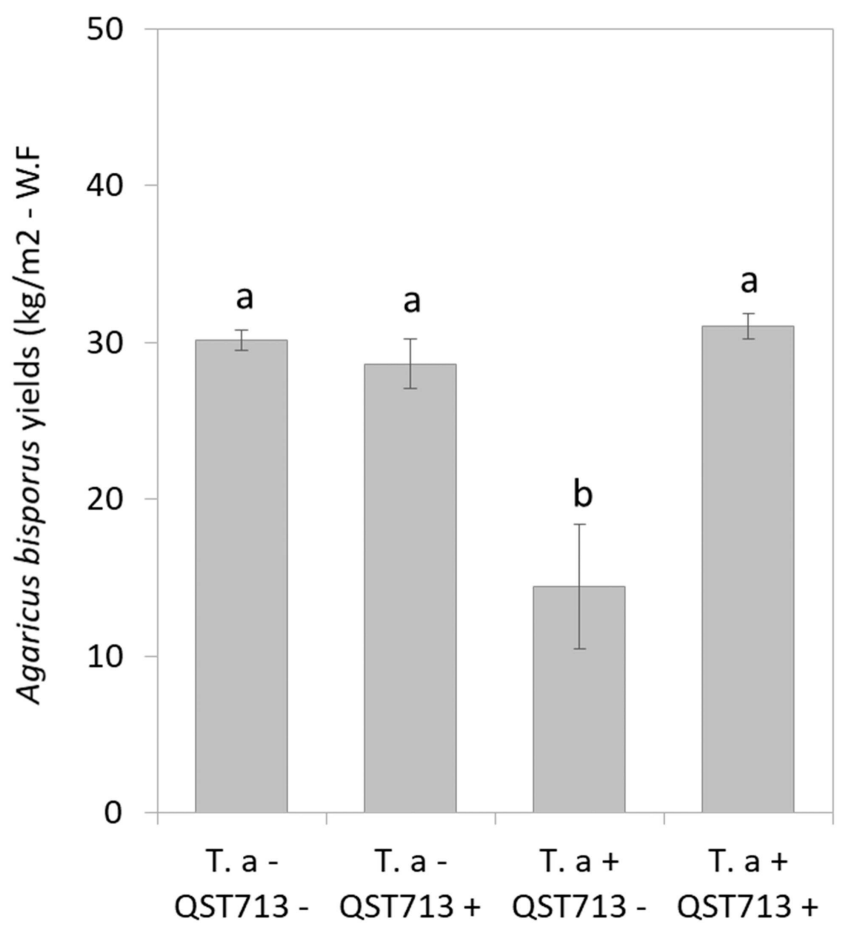
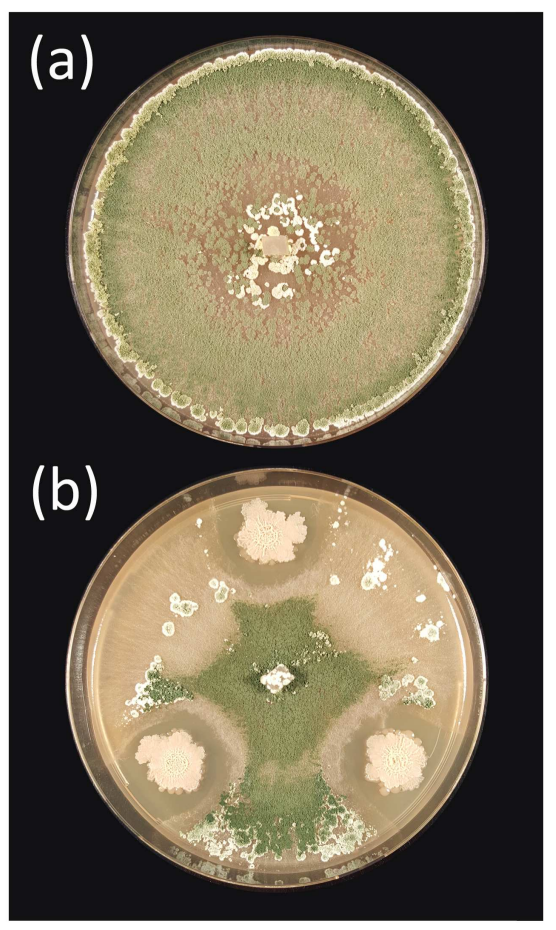


Fig. 5

A



B



1 Abstract

2 *Bacillus subtilis* QST713 is extensively used as a biological control agent in agricultural fields
3 including in the button mushroom culture, *Agaricus bisporus*. This last use exploits its inhibitory
4 activity against microbial pathogens such as *Trichoderma aggressivum* f. *europaeum*, the main
5 button mushroom green mould competitor. Here, we report the complete genome sequence of the
6 QST713 biocontrol strain with a genome size of 4 233 757 bp, 4263 predicted genes and an
7 average GC content of 45.9%. Based on phylogenomic analyses, the QST713 strain is finally
8 designated as *Bacillus velezensis*. Genomic analyses revealed two clusters encoding potential
9 new antimicrobials with NRPS and TransATPKS synthetase. *B. velezensis* QST713 genome also
10 harbours several genes previously described as being involved in surface colonization and
11 biofilm formation. This strain shows a strong ability to form *in vitro* spatially organized biofilm
12 and to antagonize *T. aggressivum*. The availability of this genome sequence could bring new
13 elements to understand the interactions with micro or/and macroorganisms in crops.

14 **Keywords** : *Bacillus velezensis*, Biofilm, Genome, Biocontrol, Secondary metabolites.

15

Table S1

[Click here to download Supplementary File: Table S1 Pandin.docx](#)

Table S2

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Fig. S1

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Table S1: Prophage regions of *Bacillus velezensis* QST713 genome.

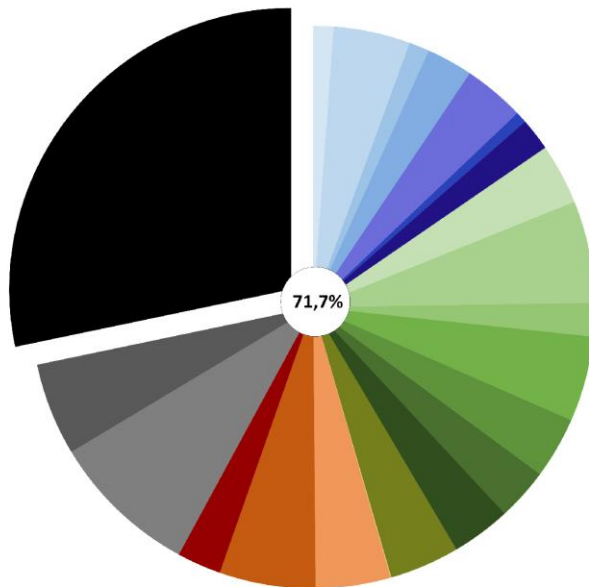
Region	Region length	Completeness	Number of CDS	Phage Hit protein	Hypothetical protein	Specific Keyword	Region_position	Possible phage	G+C percentage
1	44.8Kb	questionable	71	45	26	integrase, terminase, portal, capsid, tail	630065-674933	PHAGE_Bacill_SPP1_NC_004166	43.88%
2	32.8Kb	questionable	45	32	13	terminase, head, capsid, tail, portal, plate	1260401-1293209	PHAGE_Bacill_BalMu_1_NC_030945	46.83%
3	26.4Kb	incomplete	11	8	3	tail, recombinase	1876725-1903221	PHAGE_Bacill_AR9_NC_031039	41.48%
4	150.2Kb	incomplete	180	112	68	virion, tail, recombinase	2192669-2342879	PHAGE_Bacill_SPbeta_NC_001884	36.62%
5	52.5Kb	questionable	53	41	12	integrase, portal	2760236-2812785	PHAGE_Bacill_phi105_NC_004167	43.51%
6	38.5Kb	questionable	30	22	8	tail, head, capsid, portal	3173273-3211799	PHAGE_Bacill_SPbeta_NC_001884	36.03%

(Footnote: Prophage regions were identified using PHASTER web server (Zhou *et al.* 2011; Arndt *et al.* 2016).)

Table S2: Comparative analysis of gene clusters encoding secondary metabolites in *B. velezensis* QST713 with *Bacillus* strains. (*) represents the longest nucleotide sequence taken as a basis for BLAST comparison.

<i>Bacillus velezensis</i> QST713							Genbank accession number Blast Coverage / Identity nt sequence QST713 with <i>Bacillus</i> species	
Cluster number	Metabolites	Synthetase	Main genes	Accession	Position	bp	<i>B. velezensis</i> FZB42	
1	Surfactin	NRPS	<i>xy02</i>	BVQ_01785	367201 - 367425	225	RBAM_RS01835	100% / 99%
			<i>srfAA</i>	BVQ_01790	367609 - 378366	10758	RBAM_RS01840	100% / 99%
			<i>srfAB</i>	BVQ_01795	378388 - 389151	10764	RBAM_RS01845	100% / 99%
			<i>srfAC</i>	BVQ_01800	389186 - 393022	3837	RBAM_RS01850	100% / 98%
			<i>srfAD</i>	BVQ_01805	393042 - 393773	732	RBAM_RS01855	100% / 99%
			<i>tpaat</i>	BVQ_01810	393895 - 395205	1311	RBAM_RS01860	100% / 99%
2	Macrolactin	TransATPKS	unknown	BVQ_07650	1458250 - 1458449	200	RBAM_RS07155	98% / 99%
			<i>mInA</i>	BVQ_07655	1458450 - 1460756	2307	RBAM_RS07160	100% / 99%
			<i>mInB</i>	BVQ_07660	1460778 - 1473032	12255	RBAM_RS07165*	100% / 99%
			<i>mInC</i>	BVQ_07665	1473032 - 1477804	4773	RBAM_RS07170	100% / 98%
			<i>mInD</i>	BVQ_07670	1477851 - 1486559	8709	RBAM_RS07175	100% / 99%
			<i>mInE</i>	BVQ_07675	1486552 - 1493556	7005	RBAM_RS07180	100% / 99%
			<i>mInF</i>	BVQ_07680	1493580 - 1499291	5712	RBAM_RS07185	100% / 99%
			<i>mInG</i>	BVQ_07685	1499291 - 1506670	7380	RBAM_RS07190	100% / 99%
			<i>mInH</i>	BVQ_07690	1506721 - 1510569	3849	RBAM_RS07195*	100% / 98%
			<i>mInI</i>	BVQ_07695	1510602 - 1511693	1092	RBAM_RS07200	100% / 99%
	<i>pdhA</i>	BVQ_07700	1512163 - 1513278	1116	RBAM_RS07205	100% / 99%		
3	Bacillaene	TransATPKS-NRPS	<i>mutL</i>	BVQ_08940*	1760813 - 1762687	1875	RBAM_RS08435	99% / 99%
			unknown	BVQ_08945	1762739 - 1762888	150	-	-
			unknown	BVQ_08950	1762848 - 1763354	507	-	-
			unknown	BVQ_08955	1763792 - 1764094	303	-	-
			unknown	BVQ_08960	1764573 - 1764782	210	-	-
			unknown	BVQ_08965*	1765319 - 1765528	210	RBAM_RS08440	99% - 97%
			unknown	BVQ_08970	1765615 - 1766136	522	-	-
			unknown	BVQ_08975	1767460 - 1767675	216	-	-
			<i>baeB</i>	BVQ_08980	1767659 - 1768336	678	RBAM_RS08445	100% / 99%
			<i>baeC</i>	BVQ_08985	1768651 - 1769520	870	RBAM_RS08450	100% / 99%
			<i>baeD</i>	BVQ_08990	1769657 - 1770631	975	RBAM_RS08455	100% / 99%
			<i>baeE</i>	BVQ_08995	1770633 - 1772873	2241	RBAM_RS08460	100% / 99%
			<i>acpK</i>	BVQ_09000	1772939 - 1773187	249	RBAM_RS08465	100% / 99%
			<i>baeG</i>	BVQ_09005	1773239 - 1774501	1263	RBAM_RS08470	100% / 98%
			<i>baeH</i>	BVQ_09010	1774498 - 1775271	774	RBAM_RS08475	100% / 99%
			<i>baeI</i>	BVQ_09015	1775281 - 1776030	750	RBAM_RS08480	100% / 100%
			<i>baeJ</i>	BVQ_09020*	1776070 - 1791021	14952	RBAM_RS08485	100% / 98%
			<i>baeL</i>	BVQ_09025	1791023 - 1804429	13407	RBAM_RS08490*	100% / 98%
			<i>baeM</i>	BVQ_09030	1804447 - 1814982	10536	RBAM_RS08495	100% / 98%
			<i>baeN</i>	BVQ_09035	1814972 - 1831270	16299	RBAM_RS08500*	100% / 98%
<i>baeR</i>	BVQ_09040*	1831284 - 1838741	7458	RBAM_RS08505	100% / 98%			
<i>baeS</i>	BVQ_09045	1840089 - 1838878	1212	RBAM_RS08510	100% / 99%			
	<i>nucB</i>	BVQ_09050	1840378 - 1840812	435	RBAM_RS08515	100% / 99%		
4	Bacillomycin D	NRPS	<i>xynD</i>	BVQ_09605	1937867 - 1939405	1539	RBAM_RS09060	99% / 94%
			<i>bmyC</i>	BVQ_09610	1939730 - 1947586	7857	RBAM_RS09065*	100% / 68%
			<i>bmyB</i>	BVQ_09615	1947675 - 1963763	16089	RBAM_RS09070*	100% / 82%
			<i>bmyA</i>	BVQ_09620	1963808 - 1975756	11949	RBAM_RS09075	100% / 99%
			<i>bmyD</i>	BVQ_09625	1975776 - 1976978	1203	RBAM_RS09080	100% / 97%
			<i>yxjF</i>	BVQ_09635	1977536 - 1978321	786	RBAM_RS09085	100% / 98%
5	Fengycin	TransATPKS-NRPS	<i>yngL</i>	BVQ_09740	1999440 - 1999820	381	RBAM_RS09190	100% / 99%
			<i>fenE</i>	BVQ_09745	2003696 - 1999893	3804	RBAM_RS09195	100% / 98%
			<i>fenD</i>	BVQ_09750	2014490 - 2003715	10776	RBAM_RS09200	100% / 99%
			<i>fenC</i>	BVQ_09755	2022165 - 2014516	7650	RBAM_RS09205	100% / 98%
			<i>fenB</i>	BVQ_09760	2029878 - 2022181	7698	RBAM_RS09210	100% / 98%
			<i>fenA</i>	BVQ_09765	2037562 - 2029904	7659	RBAM_RS09215	100% / 98%
	<i>dacC</i>	BVQ_09775	2039517 - 2038042	1476	RBAM_RS09220	100% / 98%		
6	Difficidin	TransATPKS	<i>prol</i>	BVQ_12475	2476320 - 2477159	840	RBAM_RS10905	100% / 99%
			<i>dfnM</i>	BVQ_12480	2477942 - 2477196	747	RBAM_RS10910	100% / 98%
			<i>dfnL</i>	BVQ_12485	2479249 - 2478002	1248	RBAM_RS10915	99% / 99%
			<i>dfnK</i>	BVQ_12490	2480461 - 2479307	1155	RBAM_RS10920	100% / 99%
			<i>dfnJ</i>	BVQ_12495	2486758 - 2480543	6216	RBAM_RS10925	100% / 99%
			<i>dfnI</i>	BVQ_12500	2492907 - 2486755	6153	RBAM_RS10930	100% / 99%
			<i>dfnH</i>	BVQ_12505	2500648 - 2492930	7719	RBAM_RS10935	100% / 98%
	<i>dfnG</i>	BVQ_12510	2516267 - 2500653	15615	RBAM_RS10940	100% / 98%		

			<i>dfnF</i>	BVQ_12515	2522045 - 2516319	5727	RBAM_RS10945	100% / 98%
			<i>dfnE</i>	BVQ_12520	2528381 - 2522085	6297	RBAM_RS10950	100% / 98%
			<i>dfnD</i>	BVQ_12525*	2540999 - 2528400	12600	RBAM_RS10955	100% / 98%
			<i>dfnC</i>	BVQ_12530	2541776 - 2541039	738	RBAM_RS10960	100% / 99%
			<i>dfnB</i>	BVQ_12535	2543155 - 2541791	1365	RBAM_RS10965	100% / 99%
			<i>dfnX</i>	BVQ_12540	2543424 - 2543152	273	RBAM_RS10970	100% / 99%
			<i>dfnY</i>	BVQ_12545	2544429 - 2543449	981	RBAM_RS10975	100% / 99%
			<i>dfnA</i>	BVQ_12550	2546728 - 2544470	2259	RBAM_RS10980	100% / 99%
			unknown	BVQ_12555	2546772 - 2546957	186	-	-
			<i>nusG</i>	BVQ_12560	2547462 - 2547992	531	RBAM_RS10985	100% / 99%
7	Bacillibactin	NRPS	<i>ybdZ</i>	BVQ_16605	3292505 - 3292290	216	RBAM_RS14485	100% / 98%
			<i>dhbF</i>	BVQ_16610	3299651 - 3292524	7128	RBAM_RS14490	100% / 99%
			<i>dhbB</i>	BVQ_16615	3300592 - 3299666	927	RBAM_RS14495	100% / 98%
			<i>dhbE</i>	BVQ_16620	3302235 - 3300610	1626	RBAM_RS14500	100% / 99%
			<i>dhbC</i>	BVQ_16625	3303450 - 3302254	1197	RBAM_RS14505	100% / 99%
			<i>dhbA</i>	BVQ_16630	3304259 - 3303474	786	RBAM_RS14510	100% / 99%
			<i>yuil</i>	BVQ_16635	3305264 - 3304395	870	RBAM_RS14515	100% / 99%
8	Bacilysin	NRPS	<i>ywfg</i>	BVQ_19710	3914189 - 3912990	1200	RBAM_RS17415	100% / 99%
			<i>bacE</i>	BVQ_19715	3914202 - 3915383	1182	RBAM_RS17420	100% / 99%
			<i>bacD</i>	BVQ_19720	3915380 - 3916798	1419	RBAM_RS17425	100% / 99%
			<i>bacC</i>	BVQ_19725	3917577 - 3916816	762	RBAM_RS17430	100% / 99%
			<i>bacB</i>	BVQ_19730	3918284 - 3917574	711	RBAM_RS17435	100% / 100%
			<i>bacA</i>	BVQ_19735	3918888 - 3918274	615	RBAM_RS17440	100% / 99%
			<i>ywfA</i>	BVQ_19740	3920287 - 3919049	1239	RBAM_RS17445	100% / 99%
Cluster number	Metabolites	Synthetase	genes	Accession	Position	Bp	B. velezensis CC09	
9	Unknown	TransATPKS-NRPS	<i>tnrpsA</i>	BVQ_01170	210823 - 211518	696	A1D33_RS08065	100% / 99%
			<i>tnrpsB</i>	BVQ_01175	211893 - 219515	7623	A1D33_RS08060	100% / 99%
			<i>tnrpsC</i>	BVQ_01180	219475 - 230232	10758	A1D33_RS08055	100% / 99%
			<i>tnrpsD</i>	BVQ_01185	230315 - 231568	1254	A1D33_RS08050	100% / 99%
			<i>tnrpsE</i>	BVQ_01190	231492 - 236384	4893	A1D33_RS08045	100% / 99%
			<i>tnrpsF</i>	BVQ_01195	236569 - 241359	4791	A1D33_RS08040	100% / 99%
			<i>tnrpsG</i>	BVQ_01200	241381 - 242904	1524	A1D33_RS08035	100% / 99%
			<i>tnrpsH</i>	BVQ_01205*	243002 - 249628	6627	A1D33_RS08030	100% / 99%
Cluster number	Metabolites	Synthetase	genes	Accession	Position	bp	Bacillus subtilis strain A13	
10	Subtilin-like/Ericin	Lantipeptide	unknown	BVQ_17650	3486343 - 3486663	321	AAL15576	100% / 100%
			<i>eriK</i>	BVQ_17655	3488531 - 3487212	1374	AAL15574*	98% / 100%
			<i>eriR</i>	BVQ_17660	3489238 - 3488576	663	AAL15573	100% / 100%
			<i>eriG</i>	BVQ_17665*	3490026 - 3489256	771	AAL15575	79% / 100%
			<i>eriE</i>	BVQ_17670	3490783 - 3490028	756	AAL15572	100% / 100%
			<i>eriF</i>	BVQ_17675	3491496 - 3490780	717	AAL15571*	96% / 100%
			<i>eriL</i>	BVQ_17680	3492004 - 3491498	507	AAL15570	100% / 100%
			<i>eriSb</i>	BVQ_17685	3492726 - 3492556	171	AAL15569	100% / 100%
			unknown	BVQ_17690	3492828 - 3493160	333	AAL15568*	93% / 100%
			<i>eriSa</i>	BVQ_17695	3493315 - 3493154	162	AAL15567*	94% / 100%
			<i>eriC</i>	BVQ_17700	3494713 - 3493388	1326	AAL15566	100% / 100%
			<i>eriT</i>	BVQ_17705	3496530 - 3494686	1845	AAL15565	100% / 100%
			<i>eriB</i>	BVQ_17710	3499613 - 3496521	3093	AAL15564	100% / 100%
			<i>proZ/opuBD</i>	BVQ_17715*	3500498 - 3499827	672	AAL15578	33% / 99%
Cluster number	Metabolites	Synthetase	genes	Accession	Position	bp	B. velezensis CC09	
11	Unknown	NRPS	<i>nrpsG</i>	BVQ_18400	3640781 - 3640056	726	A1D33_RS12065*	93% / 99%
			<i>nrpsF</i>	BVQ_18405	3641902 - 3640832	1071	A1D33_RS12060	100% / 99%
			<i>nrpsE</i>	BVQ_18410	3643049 - 3641988	1062	A1D33_RS12055	100% / 99%
			<i>nrpsD</i>	BVQ_18415	3644824 - 3643082	1743	A1D33_RS12050	100% / 99%
			<i>nrpsC</i>	BVQ_18420	3656339 - 3645021	11319	A1D33_RS12045	100% / 99%
			<i>nrpsB</i>	BVQ_18425*	3673450 - 3656351	17100	A1D33_RS12040	63% / 98%
			<i>nrpsA</i>	BVQ_18430*	3674486 - 3673957	530	A1D33_RS12035	86% / 99%
Cluster number	Metabolites	Synthetase	genes	Accession	Position	bp	B. velezensis FZB42	
12	-	OtherKS	-	BVQ_05095 - BVQ_05305	986643 - 1027887	41245	RBAM_RS04810 - RBAM_RS05005	100% / 99%
13	-	T3PKS	-	BVQ_10520 - BVQ_10820	2166999 - 2208099	41101	RBAM_RS09935 - RBAM_RS08595	65% / 99%
14	-	Terpene	-	BVQ_05725 - BVQ_05840	1110586 - 1131326	20741	RBAM_RS05415 - RBAM_RS05525	89% / 99%
15	-	Terpene	-	BVQ_09985 - BVQ_10100	2080722 - 2102605	21884	RBAM_RS09450	92% / 99%



POORLY CHARACTERIZED

- General function prediction only
- Function unknown
- Not in COGs

CELLULAR PROCESSES & SIGNALING

- Cell cycle control, cell division, chromosome partitioning
- Cell wall/membrane/envelope biogenesis
- Cell motility
- Post-translational modification, protein turnover, chaperones
- Signal transduction mechanisms
- Intracellular trafficking, secretion, and vesicular transport
- Defense mechanisms

METABOLISM

- Energy production and conversion
- Amino acid transport and metabolism
- Nucleotide transport and metabolism
- Carbohydrate transport and metabolism
- Coenzyme transport and metabolism
- Lipid transport and metabolism
- Inorganic ion transport and metabolism
- Secondary metabolites biosynthesis, transport and catabolism

INFORMATION STORAGE & PROCESSING

- RNA processing and modification
- Chromatin structure and dynamics
- Translation, ribosomal structure and biogenesis
- Transcription
- Replication, recombination and repair