

1 *Xanthomonas sontii* sp. nov., a non-pathogenic bacterium isolated from healthy basmati rice
2 (*Oryza sativa*) seeds from India.

3 **Kanika Bansal^{1,¶}, Amandeep Kaur^{1,¶}, Samriti Midha^{1,§}, Sanjeet Kumar^{1,#}, Suresh Korpole¹**
4 **and Prabhu B. Patil^{1,*}**

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6 ¹Bacterial Genomics and Evolution Laboratory, CSIR-Institute of Microbial Technology,
7 Chandigarh, India.

8 [§]Present address: Institute of Infection and Global Health, University of Liverpool, Liverpool, UK.

9 [#]Present address: Department of Archaeogenetics, Max Planck Institute for the Science of Human
10 History, Jena, Germany.

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12 [¶]**Equal contribution**

13 ^{*} Corresponding author

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17 **Running title:** Non-pathogenic *Xanthomonas* from rice plants.

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26 **Data submission:** Whole genome sequences of PPL1, PPL2 and PPL3 strains are submitted to
27 NCBI with accession numbers NQYO, NQYP, NMPO respectively.

28 Address correspondence to Prabhu B. Patil, pbpatil@imtech.res.in

29 **Abstract**

30 Three yellow pigmented, Gram negative, aerobic, rod shaped, motile bacterial strains designated
31 as PPL1, PPL2 and PPL3 were isolated from healthy basmati rice seeds. Phenotypic, biochemical
32 and 16S rRNA gene sequence analysis assigned these strains to the genus *Xanthomonas*. The 16S
33 rRNA gene sequence was having 99.59% similarity with *X. sacchari* CFBP4641^T. However,
34 whole genome based phylogenomic analysis revealed that these strains formed a distinct
35 monophyletic clade with *X. sacchari* CFBP4641^T as their closest neighbour. Taxonogenomic
36 studies based on average nucleotide identity (orthoANI) and digital DNA-DNA hybridization
37 (dDDH) values of these strains with type strains (or representative strains) of different
38 *Xanthomonas* species including *X. sacchari* showed below recommended threshold values of ANI
39 (<96%) and dDDH (70%) for species delineation. Furthermore, at the whole genome level, PPL1
40 and PPL2 were found to be clonal, while PPL3 was not a clonal, but belonging to the same
41 species. Our *in planta* pathogenicity studies revealed that the strains PPL1, PPL2 and PPL3 are
42 non-pathogenic to rice plants. Hence, based on the present study, they form a novel lineage and
43 species associated with rice seeds for which the name *Xanthomonas sontii* sp. nov. is proposed.
44 The type strain for the *X. sontii* sp. nov. is PPL1^T (CFBP8688^T = ICMP23426^T = MTCC12491^T)
45 and strains PPL2 (CFBP8689 = ICMP23427 = MTCC12492) and PPL3 (CFBP8690 = ICMP23428
46 = MTCC12492) as other strains of the species.

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48 **Abbreviations:** OrthoANI, Orthologous average nucleotide identity; dDDH, digital DNA-DNA
49 hybridization; NA, nutrient agar; PSA, peptone sucrose agar; GYCA, glucose yeast extract
50 calcium carbonate agar; PBS, phosphate buffer saline; TSBA, tryptic soy agar; MCS, MiSeq
51 control software.

52

53 **Keywords:** *Xanthomonas sontii*, non-pathogenic, healthy basmati rice seeds, orthoANI, dDDH

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60 **Introduction**

61 *Xanthomonas* is a Gram-negative, yellow-pigmented plant associated bacterium that infects
62 economically important crops such as rice [1], pomegranate [2], citrus [3], pepper, cabbage [4],
63 banana [5] etc. It is a complex genus comprising of 33 species (<http://www.bacterio.net/>), which
64 are further classified into 150 pathovars [6]. In 1997, Vauterin *et al.*, divided these *Xanthomonas*
65 species into three clusters based on 16S rRNA gene sequence phylogenetic analysis [7]. Besides
66 main core *Xanthomonas* cluster, *X. albilineans*, *X. hyacinthi*, *X. theicola*, and *X. translucens*
67 grouped as second cluster, whereas *X. sacchari* formed a distinct phylogenetic cluster. However,
68 advent of next generation sequencing technology and introduction of robust whole genome based
69 tools like orthologous average nucleotide identity (orthoANI) and digital DNA-DNA hybridisation
70 (dDDH) have revolutionized the field of bacterial taxonomy [8-10]. Infact, these methods are
71 refining comprehensive taxonomic framework, which are essential for developing diagnostic
72 strategies and understanding host-pathogen relationships in management of crops [8].

73 *Xanthomonas* is emerging as a serious threat for economically important crops. *X. oryzae* pv.
74 *oryzae*, *X. campestris*, *X. axonopodis* pv. *manihotis* were considered in the top 10 plant pathogenic
75 bacteria [11]. Among these, *X. oryzae* causes bacterial blight disease to rice plants resulting in 30-
76 50% decrease in rice yield every year [12], [13], [14]. Other than pathogenic *Xanthomonas* strains
77 that cause disease in rice plants, some of the non-pathogenic *Xanthomonas* strains have also been
78 identified from rice plants [15], [16]. Most of these non-pathogenic strains reported were largely
79 characterized based on phenotypic and biochemical analysis providing limited information.

80 In the present study, we report isolation and characterization of three creamish-yellow pigmented
81 bacterial strains from healthy basmati rice (*Oryza sativa*) seeds. Genome based polyphasic
82 analysis supported with pathogenicity tests revealed that these strains are non-pathogenic to rice
83 and belong to a novel species, for which we propose *Xanthomonas sontii* sp. nov. These non-
84 pathogenic stains are widely over-looked due to their less economic importance. However, these
85 non-pathogenic isolates were isolated from rice plant, where their pathogenic counterparts (*X.*
86 *oryzae*) causes infection and are devastating worldwide. Hence, identification and detailed
87 analysis of these non-pathogenic strains can provide important insights into the lifestyle adapted
88 by these strains and virulence mechanisms of their pathogenic counterparts.

89

90 **Materials and methods**

91 **Bacterial strain isolation and culture conditions**

92 Strains were isolated from surface sterilized healthy rice seeds (Pusa basmati 1121 variety) that
93 were collected from Fazilka, Punjab, India (30.4036° N, 74.0280° E). For bacterial strain isolation,
94 surface sterilized seeds were partially crushed in 0.85 % NaCl (normal saline) using sterile mortar
95 and pestle. The mixture was then suspended in 50 ml of solution [17]. The solution was incubated
96 for 2 h at 28°C and serial dilutions performed up to 10⁻⁶ and different dilutions (100µl) were
97 plated on media like nutrient agar (NA), peptone sucrose agar (PSA) and glucose yeast extract
98 calcium carbonate agar (GYCA). Plates were incubated at 28°C up to 6 days. Bacterial colonies
99 isolated were grown and maintained on PSA medium.

100 **Phenotypic and biochemical characterisation**

101 We analysed the morphology of strains by observing presence of flagella using transmission
102 electron microscopy. PPL1 strain was grown in nutrient broth and incubated at 28°C for 20 h.
103 Subsequently, cells were harvested by centrifugation at 2000 rpm for 10 minutes. Cell pellet
104 was washed twice with phosphate buffer saline (1X PBS) and finally resuspended in PBS.
105 Bacterial suspension was placed on carbon-coated copper grid (300 mesh, Nisshin EM Co., Ltd.)
106 for 15 minutes. The grid was then negatively stained for 30 seconds with 2% phosphotungstic
107 acid, dried and examined under JEM 2100 transmission electron microscope (JEOL, Tokyo,
108 Japan) operating at 200 kV.

109 Further, biochemical characterization such as carbohydrate utilization, acid production and various
110 enzymatic activities were performed using OMNILOG GEN III system (BIOLOG) according to
111 manufacturer's instructions.

112 **DNA extraction, genome sequencing, assembly and annotation**

113 Genomic DNA extraction was carried out using ZR Fungal/Bacterial DNA MiniPrep kit (Zymo
114 Research, Irvine, CA, USA). Qualitative assessment of DNA was performed using NanoDrop
115 1000 (Thermo Fisher Scientific, Wilmington, DE, USA) and agarose gel electrophoresis.
116 Quantitative test was performed using Qubit 2.0 fluorometer (Life Technologies). Nextera XT
117 sample preparation kits (Illumina, Inc., San Diego, CA, USA) were used to prepare Illumina
118 paired-end sequencing libraries (250 x 2 read length) with dual indexing adapters. In-house
119 sequencing of the Illumina libraries was carried out on Illumina MiSeq platform (Illumina, Inc.,
120 San Diego, CA, USA). Adapter trimming was performed automatically by MiSeq control software
121 (MCS), and remaining adapters were detected by NCBI server and were removed by manual

122 trimming. Sequencing reads were *de novo* assembled into high quality draft genome on CLC
123 Genomics Workbench v7.5 (CLC bio, Aarhus, Denmark) using default settings. Genome
124 annotation was performed by NCBI PGAP pipeline
125 (http://www.ncbi.nlm.nih.gov/genome/annotation_prok).

126 **Phylogenomic and taxonogenomic analysis:**

127 The 16S rRNA sequence of the strains was fetched from genome sequence and its comparison
128 with validly published reference bacteria was carried out using Eztaxon
129 (<https://www.ezbiocloud.net/>). Core genome tree was constructed using PhyML[18]. Core genome
130 alignment was obtained using Roary v3.11.2 [19] with identity cutoff 60%. The core gene
131 alignment was converted into phylip format using SeaView v4.4.2-1 [20] and then, newick tree
132 was obtained using PhyML. *Stenotrophomonas maltophilia* ATCC13637 was used as an outgroup.
133 Taxonogenomic analysis of all type strains or representative strains of *Xanthomonas* was
134 performed using OrthoANI v1.2 [21] values calculated by using USEARCH v5.2.32 [22] and
135 dDDH were calculated using Web tool GGDC 2.0 (<http://ggdc.dsmz.de/distcalc2.php>)

136 ***In planta* pathogenicity test**

137 PPL1, PPL2, PPL3 and BXO1 were grown to saturation in PSA media and inoculated on 30 days
138 old rice plant (PUSA-basmati 1121) variety. Inoculation was performed by dipping scissors in
139 bacterial culture and clipping tips of rice leaves. After 14 days, infection was assessed by
140 measuring length of lesions on leaves. Here, BXO1 was positive control and PBS was used as
141 negative control. Pathogenicity data of each isolate was obtained from 10 inoculated leaves based
142 on two independent experiments.

143 **Results and discussion:**

144 **Phenotypic and biochemical characterisation of PPL1, PPL2 and PPL3**

145 All strains PPL1, PPL2 and PPL3 were isolated from glucose yeast extract calcium carbonate agar
146 (GYCA) media after 24 h of incubation at 28 °C. Colonies appeared as yellow, round, smooth,
147 convex and circular. All strains were Gram-negative, rod shaped bacteria with monopolar flagella,
148 as shown in figure 1.

149 Major biochemical characteristics of PPL1, PPL2 and PPL3 strains along with their closest
150 neighbour *X. sacchari* NCPPB 4341^T were determined using BIOLOG GEN III MICROPLATE™
151 and compared with *X. albilineans* LMG 494^T [23] (table 1). All three strains grew well between
152 20°C to 37°C with optimum temperature 28°C. No growth observed at 50°C. Further,
153 strains were able to grow at pH 6.0 and up to 4% NaCl whereas no growth observed at pH 5.0

154 and 8% NaCl. In BIOLOG results, all strains PPL1, PPL2 and PPL3 were positive for utilization
155 of D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, α -D-lactose, D-
156 melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, α -D-glucose, D-mannose,
157 D-fructose, D-galactose, L-fucose, glycerol, gelatin, L-alanine, L-aspartic Acid, L-glutamic Acid,
158 pectin, quinic acid, methyl pyruvate, L-lactic acid, citric acid, L-malic acid, tween 40, propionic
159 acid, acetic acid. Strains were resistant to rifamycin SV, lincomycin, vancomycin, tetrazolium
160 violet, tetrazolium blue, lithium chloride. Overall, biochemical characteristics of PPL1, PPL2 and
161 PPL3 strains were in accordance with its close relative *X. sacchari* NCPPB 4341^T. Biochemical
162 characteristics of *X. albilineans* LMG 494^T relative species of *X. sacchari* was taken from
163 literature and included in table 1 [23].

164 **Pathogenicity test:**

165 Pathogenicity was checked by *in planta* inoculation studies. After 14 days of infection, BXO1
166 infected leaves showed approx. 13 cm lesion while, PPL1, PPL2, PPL3 and negative control did
167 not show significant infection (approx. 0.5cm lesion) when compared with BXO1 (figure 2).
168 Hence, this clearly reveals that PPL1, PPL2, PPL3 are non-pathogenic to the host.

169 **In-house whole genome sequencing and assembly**

170 Whole genome sequencing of PPL1, PPL2 and PPL3 strains were carried out using in-house
171 Illumina MiSeq platform. The genome size of all strains was approx. 5Mb with genome coverage
172 ranging from 78x to 109x. Assembly statistics for all the strains are given in table 2.

173 **Phylogenomic analysis:**

174 Core genome tree was constructed using PhyML. For analysis, total 36 species were used
175 (including 32 type and representative strains of different *Xanthomonas* species, along with three
176 strains PPL1, PPL2 and PPL3 isolated in this study). *Stenotrophomonas maltophilia* ATCC13637
177 was used as an outgroup. Out of 36 species, 27 were clubbed in one group as previously reported
178 [7] including *X. pisi*, *X. vesicatoria*, *X. citri*, *X. codiae*, *X. fragariae*, *X. bromi*, *X. campestris*, *X.*
179 *dyei*, *X. phaseoli*, *X. hortorum*, *X. arboricola*, *X. cynarae*, *X. cucurbitae*, *X. vasicola*, *X.*
180 *floridensis*, *X. perforans*, *X. euvesicatoria*, *X. maliensis*, *X. gardneri*, *X. axonopodis*, *X. cassavae*,
181 *X. nasturtii*, *X. alfalfae*, *X. prunicola*, *X. oryzae*, *X. melonis*, and *X. populi*. Whereas 8 strains
182 fallen in second group including PPL1, PPL2, PPL3, *X. sacchari*, *X. theicola*, *X. translucens*, *X.*
183 *hyacinthi*, *X. albilineans*. PPL1^T, PPL2 and PPL3 formed a monophyletic clade distinguishing
184 them from other strains. However, *X. sacchari* is the closest neighbour of these strains. Amongst
185 PPL strains, PPL1 and PPL2 are distinct from PPL3 with 100 bootstrap value (figure 3).

186 **Genome based taxonogenomic status:**

187 The orthoANI (figure 4) and dDDH values (table 3) of PPL1, PPL2 and PPL3 with type and
188 representative strains of genus *Xanthomonas* species were below the cut-off for species
189 delineation. These strains have *X. sacchari* as their closest relative with ANI values of ~
190 94%, establishing novel species status of these strains. All the PPL1, PPL2 and PPL3 strains
191 showed dDDH values of around 55% with *X. sacchari* and less than 35% with other species of the
192 genus *Xanthomonas*. Interestingly, at the whole genome level, PPL1 and PPL2 strains were found
193 to be clonal (ANI- 99.95%, dDDH- 99.5%) whereas, PPL3 was not clonal (ANI- 97.6%, dDDH-
194 ~78%) however, it belonged to the same species.

195 **Description of *Xanthomonas sontii* sp. nov.**

196 *Xanthomonas sontii* (N.L. masc. gen. n. *sontii* named in honour of Ramesh V. Sonti, a renowned
197 Indian bacterial and plant molecular geneticist).

198 Cells are Gram-negative, aerobic, rod shape, motile and form yellow, round, smooth, convex and
199 circular colonies after 24hrs. Cells can grow on nutrient agar (NA), peptone sucrose agar (PSA)
200 and glucose yeast extract calcium carbonate agar (GYCA) media. Optimum temperature for
201 growth is 28 °C. They are able to utilize of D-maltose, D-trehalose, D-cellobiose, gentiobiose,
202 sucrose, D-turanose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-
203 glucosamine, α -D-glucose, D-mannose, D-fructose, D-galactose, L-fucose, glycerol, gelatin, L-
204 alanine, L-aspartic acid, L-glutamic acid, pectin, quinic acid, methyl pyruvate, L-lactic acid, citric
205 acid, L-malic acid, , tween 40, propionic acid, acetic acid. Strains were able to grow at pH 6.0 and
206 resistant to 1% NaCl, 1% sodium lactate, and antibiotics like rifamycin SV, lincomycin,
207 vancomycin, tetrazolium violet, tetrazolium blue, lithium chloride. Taxonogenomic and
208 phylogenomic analysis revealed distinctness of these species with orthoANI and dDDH values
209 below established cutoff values i.e. 96% for ANI and 70% for dDDH. Core genome tree analysis
210 showed separate grouping PPL1, PPL2 and PPL3 from other *Xanthomonas* strains. Further,
211 amongst PPL strains PPL3 differ at clone level forming distinct clade than PPL1 and PPL2.
212 Therefore, we propose PPL1, PPL2 and PPL3 as novel species *X. sontii* of the genus *Xanthomonas*
213 with PPL1 as type strain PPL1^T (CFBP8688^T = ICMP23426^T = MTCC12491^T).

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221 rice and its Microbiome” (MLP0020).

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276 **Figure legends**

277 **Figure 1:** Transmission electron microscopy image of PPL1^T strain with monopolar flagella.

278 **Figure 2:** *In planta* infected leaves of rice (**Pusa Basmati 1121**) (a) leaves showing symptoms of
279 disease after 14 dpi (b) lesion length measured in cm for positive (BXO1), negative (PBS) control
280 and PPL strains. Error bar indicates standard deviation of readings from 10 inoculated leaves and
281 from two independent experiments.

282 **Figure 3:** Whole genome based phylogeny considering all type strains and representative strains
283 of genus *Xanthomonas*. The scale bar shows the number of nucleotide substitution per site. PPL1^T,
284 PPL2 and PPL3 strains (highlighted in coloured box) formed a distinct cluster. *S. maltophilia*
285 ATCC1637 was used as an outgroup.

286 **Figure 4:** Heat map showing ANI strains values of PPL1^T, PPL2 and PPL3 with type and
287 representative strains of the genus *Xanthomonas*.

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296 **Tables**

297 **Table 1:** Comparison of biochemical characteristics of PPL1^T, PPL2, PPL3, and their closest
 298 neighbor *X. sacchari* NCPPB 4341^T. Symbols represents; + : positive, - : negative, +/- :
 299 borderline, § : *X. albilineans* LMG 494^T strain characteristics already reported in [23], NA : data
 300 not available in literature.

	PPL1 ^T	PPL2	PPL3	<i>X. sacchari</i> NCPPB 4341 ^T	<i>X. albilineans</i> [§] LMG 494 ^T
Dextrin	+	+	+	+	-
D-Maltose	+	+	+	+	-
D-Trehalose	+	+	+	+	-
D-Cellobiose	+	+	+	+	+
Gentiobiose	+	+	+	+	-
Sucrose	+	+	+	+	+
D-Turanose	+	+	+	+	-
pH 6	+	+	+	+	NA
D-Raffinose	-	-	-	-	-
α-D-Lactose	+	+	+	+	-
D-Melibiose	+	+	+	+	-
β-Methyl-D-Glucoside	+	+	+	+	-
D-Salicin	+	+	+	+	NA
N-Acetyl-D-Glucosamine	+	+	+	+	+
N-Acetyl-β-D-Mannosamine	-	-	-	+/-	*
N-Acetyl-D-Galactosamine	+	+	+/-	+/-	-
N-Acetyl Neuraminic Acid	-	-	-	-	NA
1% NaCl	+	+	+	+	NA
4% NaCl	+	+	+	+	NA
8% NaCl	-	-	-	-	NA
α-D-Glucose	+	+	+	+	+
D-Mannose	+	+	+	+	+
D-Fructose	+	+	+	+	+
D-Galactose	+	+	+	+	-
L-Fucose	+	+	+	+	+
L-Rhamnose	-	-	-	+/-	-
Inosine	-	-	-	-	-
1% Sodium Lactate	+	+	-	+	NA
Fusidic Acid	-	-	-	-	NA
D-Sorbitol	-	-	-	-	-
D-Mannitol	-	-	-	-	-
D-Arabitol	-	-	-	-	-
Glycerol	+	+	+/-	+	-
D-Aspartic Acid	-	-	-	-	NA

Strain			PPL1 ^T	PPL2	PPL3
Rifamycin SV	+	+	+	+	NA
Minocycline	-	-	-	-	NA
Gelatin	+	+	+	+	NA
L-Alanine	+	+	+	+	-
L-Arginine	-	-	-	+/-	NA
L-Aspartic Acid	+	+	+	+	-
L-Glutamic Acid	+	+	+	+	+/-
L-Pyroglutamic acid	-	-	-	-	-
Lincomycin	+	+	+	+	NA
Pectin	+	+	+	+	NA
D-Gluconic Acid	-	-	-	-	-
Quinic Acid	+	+	+	+	-
D-Saccharic Acid	-	-	-	-	-
Vancomycin	+	+	+	+	NA
Tetrazolium Violet	+	+	+	+	NA
Tetrazolium blue	+	+	+	+	NA
p-Hydroxy Phenylacetic acid	-	-	-	+	-
Methyl Pyruvate	+	+	+/-	+	+
D-Lactic Acid Methyl Ester	-	-	-	-	NA
L-Lactic Acid	+	+	+	+	+
Citric Acid	+	+	+	+	-
L-Malic Acid	+	+	+	+	NA
Bromo-Succinic acid	+	+	+	+	-
Lithium Chloride	+	+	+	+	NA
Tween 40	+	+	+	+	-
Propionic Acid	+	+	+	+	-
Acetic Acid	+	+	+	+	-
Aztreonam	+/-	+	+	+	NA

301

302 **Table 2:** Genome assembly statistics of PPL1^T, PPL2 and PPL3 strains.

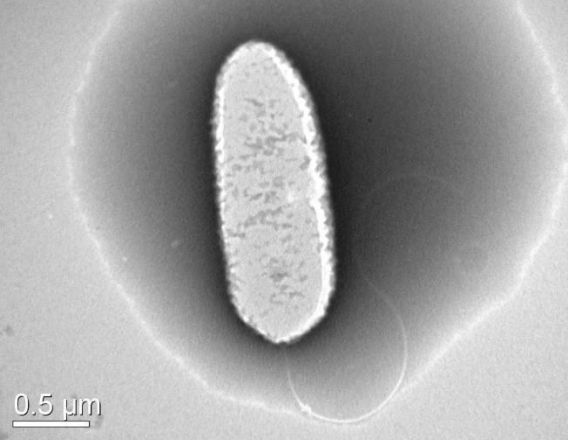
303

S. N.	Strain Name	Completeness/ Contamination	Fold (X)	N50 (kb)	Contigs	Genome Size	GC (%)	CDS	rRN A+ tRNA	Isolation source	Accessio n No.
1	PPL1 ^T	96.31/0.22	78	32.9	332	4.8	69	4149	3+51	Rice seeds	NQYO
2	PPL2	95.79/0.07	109	48.1	200	4.9	68.8	4105	2+50	Rice seeds	NQYP
3	PPL3	98.56/0.55	80	40.3	231	4.8	68.8	4106	3+52	Rice seeds	NMPO

304

305 **Table 3:** The dDDH values of strains PPL1^T, PPL2 and PPL3 with other *Xanthomonas* strains.

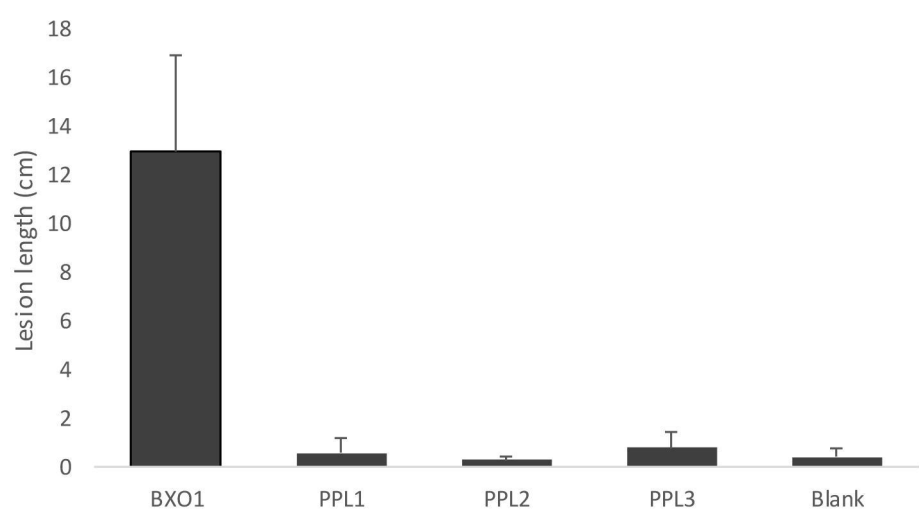
306	<i>X. theicola</i> CFBP4691	32.4	32.4	32.5
	<i>X. translucens</i> DSM18974 ^T	33	33	33
307	<i>X. hyacinthi</i> CFBP1156	33.6	33.6	33.4
	<i>X. albilineans</i> CFBP2523 ^T	28.5	28.4	28.4
308	<i>X. sacchari</i> CFBP4641 ^T	55.1	55.3	55.2
309	PPL3	78.2	78.7	100
	PPL1 ^T	100	99.5	78.2
	PPL2	99.5	100	78.7
	<i>X. maliensis</i> LMG27592 ^T	23.1	23.1	23.1
	<i>X. campestris</i> ATCC33913 ^T	23	23	23.1
	<i>X. cucurbitae</i> CFBP2542 ^T	23.2	23.2	23
	<i>X. cassavae</i> CFBP4642 ^T	23.4	23.4	23.3
	<i>X. floridensis</i> WHRI8848 ^T	23.4	23.4	23.4
	<i>X. codiae</i> CFBP4690	23.6	23.6	23.7
	<i>X. melonis</i> CFBP4644	23.4	23.4	23.4
	<i>X. vesicatoria</i> LMG911 ^T	22.9	22.8	22.8
	<i>X. pisi</i> DSM18256	23.1	23	23.3
	<i>X. dyei</i> CFBP7245 ^T	22.9	22.9	23
	<i>X. fragariae</i> PD885	22.5	22.4	22.4
	<i>X. arboricola</i> CFBP2528 ^T	23.6	23.5	23.4
	<i>X. populi</i> CFBP1817 ^T	22.7	22.6	22.4
	<i>X. hortorum</i> MO81	22.9	22.8	22.8
	<i>X. cynarae</i> CFBP4188 ^T	23	23	22.9
	<i>X. gardneri</i> ICMP7383	23.1	23	22.9
	<i>X. nasturtii</i> WHRI8853 ^T	23.1	23.1	23.1
	<i>X. bromi</i> CFBP1976 ^T	23	23	23
	<i>X. prunicola</i> CFBP8353 ^T	22.9	22.9	22.9
	<i>X. axonopodis</i> DSM3585 ^T	23.1	23.1	23
	<i>X. citri</i> LMG9322 ^T	23.3	23.3	23.3
	<i>X. phaseoli</i> CFBP412	23	23.1	23
	<i>X. perforans</i> 91-118	23	23	23
	<i>X. euvesicatoria</i> LMG27970	23.6	23.6	23.6
	<i>X. alfalfae</i> LMG495 ^T	23.4	23.4	23.3
	<i>X. vasicola</i> NCPPB2417 ^T	22.8	22.8	22.9
	<i>X. oryzae</i> ATCC35933 ^T	22.9	22.8	23
	<i>S. maltophilia</i> ATCC13637 ^T	22.9	22.9	22.9



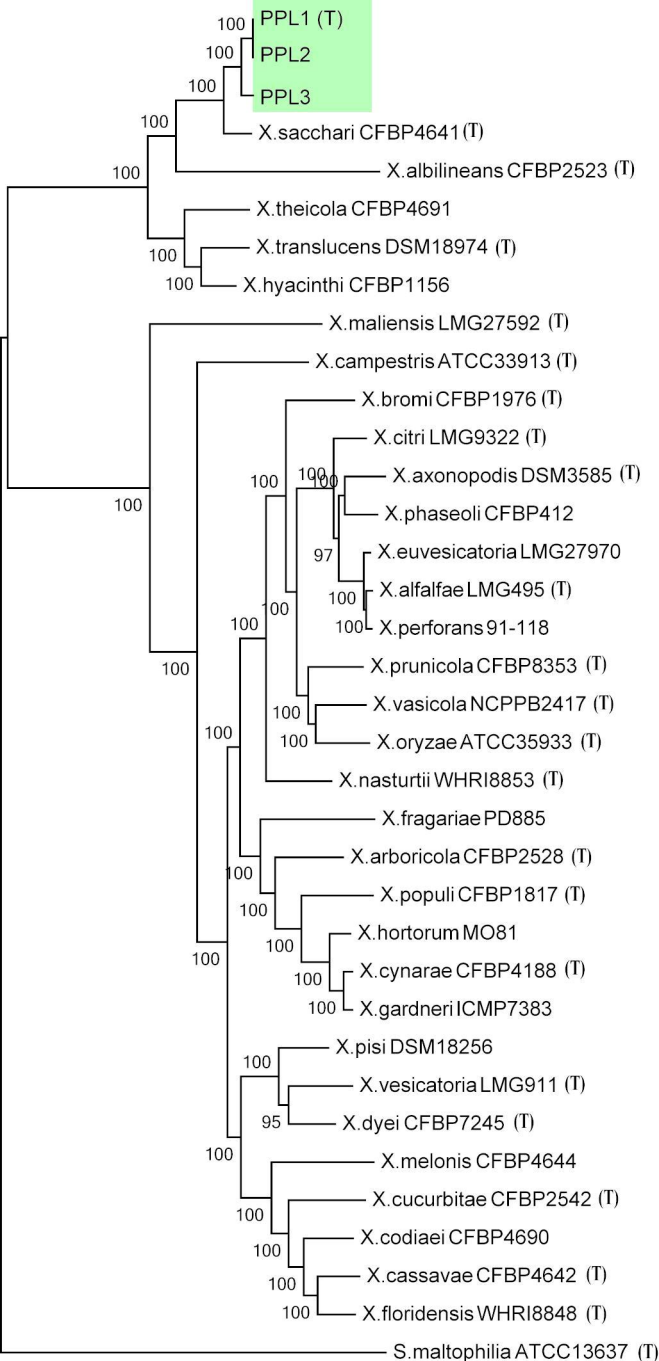
0.5 μm



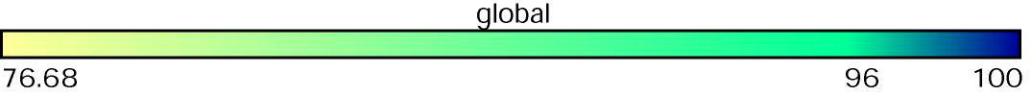
(A)



(B)



0.050



S. maltophilia ATCC13637 (T)	PPL1 (T)	PPL2	PPL3	X.sacchari CFBP4641 (T)	X.hyacinthi CFBP1156	X.translucens DSM18974 (T)	X.theicola CFBP4691	X.albilineans CFBP2523 (T)	X.campestris ATCC33913 (T)	X.vesicatoria LMG911 (T)	X.pisi DSM18256	X.dyei CFBP7245 (T)	X.codiaei CFBP4690	X.floridensis WHRI8848 (T)	X.cassavae CFBP4642 (T)	X.cucurbitae CFBP2542 (T)	X.melonis CFBP4644	X.fragariae PD885	X.arboricola CFBP2528 (T)	X.hortorum MO81	X.cynarae CFBP4188 (T)	X.gardneri ICMP7383	X.populi CFBP1817 (T)	X.citri LMG9322 (T)	X.phaseoli CFBP412	X.euvesicatoria LMG27970	X.perforans 91-118	X.alfalfae LMG495 (T)	X.axonopodis DSM3585 (T)	X.bromi CFBP1976 (T)	X.vasicola NCPPB2717 (T)	X.oryzae ATCC35933 (T)	X.prunicola CFBP8353 (T)	X.nasturtii WHRI8853 (T)	X.maliensis LMG27592 (T)
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100	79.17	79.21	79.04	79.05	79.07	79.22	78.89	76.68	77.76	77.06	77.6	77.19	78.1	77.33	77.69	77.59	77.65	76.69	77.63	77.05	77.24	77.53	77.14	77.16	77.25	77.37	77.32	77.34	77.28	77.19	76.71	77.11	77.25	77.63	77.16
79.17	100	99.95	97.6	94.14	87.68	87.03	86.99	84.33	79.42	79.1	79.14	79.21	79.94	79.63	79.79	79.88	79.76	78.67	79.98	79.16	79.32	79.27	78.97	79.16	79.11	79.27	79.26	79.32	78.88	79.05	78.6	78.9	78.98	79.22	79.75
79.21	99.95	100	97.66	94.23	87.55	87.02	86.8	84.49	79.48	79.15	79.41	79.17	80.11	79.76	79.67	79.56	79.79	78.63	79.97	79.27	79.39	79.33	79.02	79.13	79.3	79.28	79.34	79.21	79.14	78.65	78.9	79.02	79.4	79.65	
79.04	97.6	97.66	100	94.14	87.6	87.14	87.05	84.43	79.35	79	79.47	79.22	80.15	79.65	79.76	79.76	79.7	78.55	79.85	79.32	79.39	79.28	79.03	79.1	79.15	79.33	79.43	79.35	79.06	79.15	78.56	78.89	78.87	79.32	79.56
79.05	94.14	94.23	94.14	100	87.65	87.21	86.84	84.16	79.34	78.96	79.31	79.18	79.84	79.58	79.69	79.56	79.91	78.64	79.95	79.17	79.13	79.21	78.77	79.06	79.26	79.19	79.27	79.42	79	78.92	78.72	78.69	78.89	79.41	79.61
79.07	87.68	87.55	87.6	87.65	100	92.53	90.68	83.69	79.84	79.52	79.83	79.6	80.38	80.08	80.05	79.86	79.88	78.78	80.38	79.75	79.88	79.71	79.12	79.42	79.49	79.31	79.41	79.67	79.33	79.42	79.05	79.13	79.18	79.72	79.65
79.22	87.03	87.02	87.14	87.21	92.53	100	90.13	83.61	79.82	79.69	79.75	79.72	80.41	79.98	80.05	79.79	80.19	78.81	80.38	79.74	79.8	79.74	79.45	79.4	79.56	79.7	79.69	79.63	79.56	79.59	79.24	79.42	79.44	79.77	79.71
78.89	86.99	86.8	87.05	86.84	90.68	90.13	100	83.31	79.55	79.27	79.58	79.52	80.11	79.62	79.74	79.6	79.96	78.48	79.99	79.21	79.44	79.28	78.84	79.26	79.33	79.28	79.4	79.59	79.27	79.22	78.6	79.08	79.09	79.4	79.48
76.68	84.33	84.49	84.43	84.16	83.69	83.61	83.31	100	77.41	77.22	77.63	77.51	77.71	77.48	77.53	76.98	77.79	76.78	77.7	77.05	77.43	77.28	76.73	77.23	77.22	77.09	77.26	77.5	77.04	77	76.94	77.29	76.9	77.18	77.48
77.76	79.42	79.48	79.35	79.34	79.84	79.82	79.55	77.41	100	84.99	85.5	85.42	85.51	85.49	85.59	85.16	84.97	84.92	86.11	85.53	85.81	85.84	84.97	85.09	85.07	85.19	85.2	85.2	84.92	85.06	84.89	84.74	84.89	85.53	82.66
77.06	79.1	79.15	79	78.96	79.52	79.69	79.27	77.22	84.99	100	90.29	90.61	87.18	87.9	87.56	86.56	86.02	85.64	86.73	86.51	86.18	86.25	85.62	86.22	85.94	86.18	86.07	86.17	85.74	86.78	85.91	85.79	86.18	87.36	82.37
77.6	79.14	79.41	79.47	79.31	79.83	79.75	79.58	77.63	85.5	90.29	100	91.34	87.39	88.96	87.61	86.94	86.47	86.01	87.78	87.09	86.78	86.97	86.19	86.47	86.35	86.46	86.5	86.54	86.17	86.85	86.11	86.13	87.58	87.38	82.56
77.19	79.21	79.17	79.22	79.18	79.6	79.72	79.52	77.51	85.42	90.61	91.34	100	87.13	88.05	87.36	86.5	86.17	85.96	86.92	86.68	86.6	86.74	85.98	86.27	86.21	86.22	86.18	86.25	85.85	86.81	86	85.93	86.49	87.41	82.4
78.1	79.94	80.11	80.15	79.84	80.38	80.41	80.11	77.71	85.51	87.18	87.39	87.13	100	91.55	91.68	89.55	88.15	85.56	86.71	86.08	86.15	86.18	85.61	86.3	86.47	86.38	86.36	86.46	86.06	86.43	85.85	86.18	86.05	86.88	82.99
77.33	79.63	79.76	79.65	79.58	80.08	79.98	79.62	77.48	85.49	87.9	88.96	88.05	91.55	100	93.2	89.54	87.9	85.59	87.14	86.45	86.29	86.4	85.76	86.49	86.53	86.57	86.45	86.52	86.15	86.84	85.97	86.05	86.39	87.16	83.02
77.69	79.79	79.67	79.76	79.69	80.05	80.05	79.74	77.53	85.59	87.56	87.61	87.36	91.68	93.2	100	89.5	87.76	85.68	87.54	86.46	86.49	86.56	85.78	86.62	86.72	86.84	86.89	87.03	86.41	86.81	86.18	86.24	86.39	87.21	82.85
77.59	79.88	79.56	79.76	79.56	79.86	79.79	79.6	76.98	85.16	86.56	86.94	86.5	89.55	89.54	89.5	100	87.82	84.87	86.3	85.62	85.51	85.65	84.94	85.8	85.9	85.89	85.87	86.04	85.49	85.87	85.39	85.4	85.55	86.24	82.74
77.65	79.76	79.79	79.7	79.91	79.88	80.19	79.96	77.79	84.97	86.02	86.47	86.17	88.15	87.9	87.76	87.82	100	84.88	86.23	85.5	85.48	85.54	84.89	85.76	85.76	85.93	85.81	85.89	85.46	85.7	85.39	85.45	85.52	86	82.67
76.69	78.67	78.63	78.55	78.64	78.78	78.81	78.48	76.78	84.92	85.64	86.01	85.96	85.56	85.59	85.68	84.87	84.88	100	87.4	87.37	87.37	87.47	87.12	85.92	85.87	85.88	85.97	86.05	85.72	86.09	85.95	85.93	85.89	86.67	82
77.63	79.98	79.97	79.85	79.95	80.38	80.38	79.99	77.7	86.11	86.73	87.78	86.92	86.71	87.14	87.54	86.3	86.23	87.4	100	89.49	89.53	89.5	88.52	87.06	86.94	87.02	87.03	86.98	86.58	86.9	86.76	86.64	87.1	87.68	83.23
77.05	79.16	79.27	79.32	79.17	79.75	79.74	79.21	77.05	85.53	86.51	87.09	86.68	86.08	86.45	86.46	85.62	85.5	87.37	89.49	100	95.87	95.75	90.71	86.54	86.37	86.45	86.47	86.67	86.17	86.58	86.42	86.47	86.44	87.56	82.41
77.24	79.32	79.39	79.39	79.13	79.88	79.8	79.44	77.43	85.81	86.18	86.78	86.6	86.15	86.29	86.49	85.51	85.48	87.37	89.53	95.87	100	98.31	90.71	86.58	86.37	86.59	86.38	86.62	86.13	86.55	86.43	86.42	86.39	87.45	82.52
77.53	79.27	79.33	79.28	79.21	79.71	79.74	79.28	77.28	85.84	86.25	86.97	86.74	86.18	86.4	86.56	85.65	85.54	87.47	89.5	95.75	98.31	100	90.78	86.59	86.4	86.63	86.54	86.62	86.19	86.57	86.36	86.33	86.58	87.45	82.49
77.14	79.16	79.13	79.1	79.06	79.42	79.4	79.26	77.23	84.97	85.62	86.19	85.98	85.61	85.76	85.78	84.94	84.89	87.12	88.52	90.71	90.71	90.78	100	85.9	85.83	85.85	85.92	85.91	85.69	85.85	85.87	85.73	85.82	86.57	82.06
77.16	79.16	79.13	79.1	79.06	79.42	79.4	79.26	77.23	85.09	86.22	86.47	86.27	86.3	86.49	86.62	85.8	85.76	85.92	87.06	86.54	86.58	86.59	85.9	100	93.67	94.04	94.28	94.14	93.07	89.32	89.91	89.93	89.81	88.83	82.61
77.25	79.11	79.3	79.15	79.26	79.49	79.56	79.33	77.22	85.07	85.94	86.35	86.21	86.47	86.53	86.72	85.9	85.76	85.87	86.94	86.37	86.37	86.4	85.83	93.67	100	94.14	94.06	94.11	93.16	89.15	89.52	89.65	89.58	88.63	82.78
77.37	79.27	79.28	79.33	79.19	79.31	79.7	79.28	77.09	85.19	86.18	86.46	86.22	86.38	86.57	86.84	85.89	85.93	85.88	87.02	86.45	86.59	86.63	85.85	94.04	94.14	100	98.58	98.54	92.96	89.26	90.15	90.07	89.77	88.73	82.89
77.32	79.26	79.34	79.43	79.27	79.41	79.69	79.4	77.26	85.2	86.07	86.5	86.18	86.36	86.45	86.89	85.87	85.81	85.97	87.03	86.47	86.38	86.54	85.92	94.28	94.06	98.58	100	98.78	93.07	89.15	90.06	90.08	89.76	88.82	82.89
77.34	79.32	79.21	79.35	79.42	79.67	79.63	79.59	77.5	85.2	86.17	86.54	86.25	86.46	86.52	87.03	86.04	85.89	86.05	86.98	86.67	86.62	86.62	85.91	94.14	94.11	98.54	98.78	100	93.17	89.33	90.06	90.09	89.85	88.99	82.96
77.28	78.88	79.14	79.06	79	79.33	79.56	79.27	77.04	84.92	85.74	86.17	85.85	86.06	86.15	86.41	85.49	85.46	85.72	86.58	86.17	86.13	86.19	85.69	93.07	93.16	92.96	93.07	93.17	100	89.31	89.64	89.64	89.43	88.58	82.77
77.19	79.05	79.14	79.15	78.92	79.42	79.59	79.22	77	85.06	86.78	86.85	86.81	86.43	86.84	86.81	85.87	85.7	86.09	86.9	86.58	86.55	86.57	85.85	89.32	89.15	89.26	89.15	89.33	89.31	100	89.52	89.43	89.61	88.93	82.36
76.71	78.6	78.65	78.56	78.72	79.05	79.24	78.6	76.94	84.89	85.91	86.11	86	85.85	85.97	86.18	85.39	85.39	85.95	86.76	86.42	86.43	86.36	85.87	89.91	89.52	90.15	90.06	90.06	89.64	89.52	100	91.3	91.11	88.78	82.34
77.11	78.9	78.9	78.89	78.69	79.13	79.42	79.08	77.29	84.74	85.79	86.13	85.93	86.18	86.05	86.24																				