IJSEM Papers in Press. Published August 4, 2009 as doi:10.1099/ijs.0.012070-0

Transfer of *Pantoea citrea, Pantoea punctata* and *Pantoea terrea* to the genus *Tatumella* emend. as *Tatumella citrea* comb. nov., *Tatumella punctata* comb. nov., and *Tatumella terrea* comb. nov. (Kageyama *et al.*, 1992) and description of *Tatumella morbirosei* sp. nov.

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Running title: New *Tatumella* species

Subject category: New taxa, *Proteobacteria*

Footnote: The GenBank/EMBL accession numbers for the 16S rRNA gene sequences for *Tatumella ptyseos* LMG 7888^T, *Tatumella punctata* LMG 22050^T, *Tatumella terrea* LMG 22051^T, *Tatumella citrea* LMG 22049^T and *Tatumella morbirosei* LMG

23360^T and LMG 23359 are EU344770, EF688006-EF688008, EU344769 and FJ617235, respectively.

Summary

Pantoea citrea, *Pantoea punctata* and *Pantoea terrea* were described for strains isolated from fruit and soil originating in Japan. These three "Japanese" species have been shown to be phylogenetically distant from the remaining species of the genus *Pantoea*. It has previously been observed using multilocus sequence analysis (MLSA) that the "Japanese" species consistently form a distinct clade with an extended branch length, casting doubt on the inclusion of these species within the genus *Pantoea*. Furthermore, the "Japanese" species are closely related to *Tatumella ptyseos*, strains of which originate from human clinical specimens. DNA-DNA hybridization and phenotypic tests confirmed the observed phylogenetic distance of *P. citrea*, *P. punctata* and *P. terrea* from the genus *Pantoea* and the affiliation of these species with *Tatumella*. In addition, strains causing pink disease of pineapple, previously identified as *P. citrea*, were shown to belong to a separate species by 16S rRNA gene sequence analysis, MLSA and DNA-DNA hybridization data. The name *Tatumella morbirosei* sp. nov. with the type strain as LMG 23360^T (= BD 878^T = NCPPB 4036^T = CMC6^T) is proposed for these strains. The new combinations *Tatumella citrea* (Kageyama *et al.* 1992) comb. nov. with the type strain LMG 22049^T (= BD 875^T = ATCC 31623^T = SHS 2003^T), *Tatumella punctata* (Kageyama *et al*. 1992) comb. nov. with the type strain LMG 22050^T (= BD 876^T = ATCC 31626^T = SHS 2006^T) and *Tatumella terrea* (Kageyama *et al*. 1992) comb. nov. with the type strain LMG

22051^T (= BD 877^T = ATCC 31628^T = SHS 2008^T) are proposed for *P. citrea, P. punctata* and *P. terrea*, respectively.

Introduction

Following the proposal of the novel genus *Pantoea* in 1989 (Gavini *et al*., 1989), but preceding the transfer of *Erwinia ananas* and *Erwinia stewartii* to *Pantoea* (Mergaert *et al*., 1993), three novel *Pantoea* species that produce 2,5-diketo-D-gluconic acid (DKGA) from D-glucose were described from fruit and soil samples in Japan (Kageyama *et al*., 1992). *Pantoea citrea*, *Pantoea punctata* and *Pantoea terrea* were included in the genus *Pantoea* based on general phenotypic data and DNA-DNA hybridization values, despite the inability of the original *Pantoea* species to produce DKGA. Until recently, no phylogenetic study had been performed on all validly published *Pantoea* species, giving no reason to doubt the inclusion of *P. citrea*, *P. punctata* and *P. terrea* in the genus *Pantoea*. However, the most recent edition of Bergey's Manual of Systematic Bacteriology (Grimont & Grimont, 2005) states that more taxonomic work is required to justify the assignment of these three species to the genus *Pantoea*. A recent phylogenetic study of the *Enterobacteriaceae* revealed an *atpD* sequence indel which is specific to *Pantoea* and *Tatumella* (Paradis *et al*., 2005), indicating a close phylogenetic relationship between these two genera. This was in agreement with the initial suggestion of P. Grimont that the "Japanese" species may be more similar to *Tatumella ptyseos* than *Pantoea* in their nutritional patterns (Kageyama *et al*., 1992). The single species genus *Tatumella* was created for clinical strains isolated in North and South America between 1960 and 1980 (Hollis *et al*., 1981). A MLSA scheme based on *gyrB*, *rpoB*, *atpD*, and *infB* genes was recently performed on 102 *Pantoea* strains including the "Japanese" species and *Tatumella*

ptyseos (Brady *et al*., 2008). A concatenated tree constructed from the sequences of the four genes was found to be the most robust approach for revealing phylogenetic relationships amongst *Pantoea* strains. The MLSA study indicated a clear phylogenetic divergence between *P. citrea*, *P. punctata* and *P. terrea* and the remaining *Pantoea* species, and confirmed *Tatumella ptyseos* as a close phylogenetic relative of the "Japanese" species. It was concluded that the "Japanese" species should be transferred to the genus *Tatumella*. A similar study based on multilocus typing of *Pantoea* species using six protein-coding genes, was in agreement regarding the taxonomic position of the "Japanese" species and also suggested the reclassification of these three species as *Tatumella* (Delétoile *et al*., 2008).

Isolation of strains

Strains used in this study were obtained from the BCCM/LMG Bacteria Collection (http://www.belspo.be/bccm) and the Centres for Disease Control, Atlanta, Georgia, U.S.A., and are listed in Table 1. An alkali extraction method (Niemann *et al*., 1997) was used to isolate genomic DNA from the strains which was stored at -20 °C.

16S rRNA gene sequencing

The almost complete 16S rRNA gene was sequenced for the type strains of *P. citrea* (LMG 22049^T), *P. punctata* (LMG 22050^T) and *P. terrea* (LMG 22051^T), and additional *P. citrea* strains (LMG 23359 and LMG 23360), which were found to cause pink disease of pineapple (Cha *et al*., 1997), using the primers and conditions determined by Coenye *et al*. (1999). The sequences were aligned using ClustalX (Thompson *et al.*, 1997) and the overhangs were trimmed. The Modeltest 3.7 programme (Posada & Crandall, 1998) was then applied to determine the best-fit

evolutionary model. Maximum likelihood and neighbour joining analyses were performed using Phyml (Guindon & Gascuel, 2003) and PAUP 4.0b10 (Swofford, 2000) respectively, by applying the models and parameters determined by Modeltest (only Maximum likelihood phylogenetic trees are shown). Bootstrap analysis with 1000 replicates was performed to assess the support for these clusters.

In the 16S rRNA gene sequence tree (Fig. 1) the genus *Pantoea* is phylogenetically split, although this is not unusual as *Pantoea* has been shown to be polyphyletic (Brady *et al*., 2008). The majority of the *Pantoea* "core" species are contained in a cluster supported by high bootstrap support, whilst *P. dispersa* and a *Pantoea* species from Brenner DNA group IV cluster amongst *Erwinia* species. The "Japanese" species are situated in a distinctly separate clade with a different branch point, also with high bootstrap support. These findings support those of Grimont & Grimont (2005), based on 16S rRNA gene and *rpoB* sequence comparisons that the "Japanese" species cluster at a lower level to the *Pantoea* "core" clade. Interestingly, LMG 7888^{T} the type strain of *Tatumella ptyseos* clusters closely with the type strain of *Pantoea terrea*, within the "Japanese" species clade prompting further examination of the relationship of the "Japanese" species with *T. ptyseos*. The additional *P. citrea* strains LMG 23359 and LMG 23360, which cause pink disease of pineapple, do not cluster with the type strain of this species (LMG 22049^{T}), but are found on a separate branch suggesting these strains do not belong to *P. citrea*. The 16S rRNA gene sequence similarity of LMG 23360 was greater than 98 % to the type strains of *P. punctata*, *P. citrea*, *Pantoea* sp. (Brenner DNA group II) and *T. ptyseos*.

***gyrB, rpoB, atpD,* and *infB* gene sequencing**

MLSA was performed on all strains, as previously described (Brady *et al*., 2008), to provide further support for the removal of the "Japanese" species from *Pantoea*. Sequence analysis and tree construction was performed as described above. Several *Erwinia* species were included in the MLSA study and housekeeping gene sequences for *Erwinia tasmaniensis*, *Escherichia coli*, *Shigella dysenteriae*, *Klebsiella pneumoniae*, *Citrobacter rodentium*, *Citrobacter koseri* and *Cronobacter sakazakii* were obtained from genome sequencing databases (http://www.ncbi.nlm.nih.gov, http://www.sanger.ac.uk, http://asap.ahabs.wisc.edu/asap). In Fig. 2, a MSLA phylogenetic tree based on the concatenated sequences of *gyrB*, *rpoB*, *atpD* and *infB* genes, *Pantoea* strains form a monophyletic cluster within the *Enterobacteriaceae*. This cluster contains two sub lineages which are supported by high bootstrap values of 100 %. The first sub lineage contains the *Pantoea* "core" species including Brenner DNA groups II, IV and V. The second sub lineage consists of the "Japanese" species and the type strain of *T. ptyseos*. The type strain of *T. ptyseos* clusters closely with *P. terrea* strains, specifically with LMG 23565 and its duplicate CCUG 30163. This result indicates that LMG 23565 (= CCUG 30163) was erroneously classified and in fact belongs to *T. ptyseos*. LMG 23359 and LMG 23360, two supposed *P. citrea* strains causing pink disease of pineapple referred to as MLSA group J (Brady *et al*., 2008) , group with LMG 22049^{T}, the type strain of *P. citrea* but are situated on a separate branch with a long branch length. This supports the probability that these two strains do not belong to *P. citrea*, but to a novel species. All species clusters within both sub lineages of *Pantoea* are supported with 100 % bootstrap values. All four housekeeping- and 16S rRNA-gene sequences were examined for heterogenous nucleotides which could be used as signature nucleotide positions to

differentiate between *Tatumella* and *Pantoea*. Eight signature nucleotides were identified in the 16S rRNA gene sequences which differ between *Tatumella* and *Pantoea*. The gene sequences of *atpD* revealed the most heterogeneity with 23 signature nucleotides which are conserved in *Tatumella* species and differ from all *Pantoea* species. The signature nucleotides for the 16S rRNA- and *atpD*-genes are listed in Supplementary Table S1, available on IJSEM online. The *E. coli* numbering positions are used to designate the nucleotide positions (Brosius *et al*., 1978, http://www.ncbi.nlm.nih.gov).

DNA-DNA hybridizations

High quality DNA for DNA-DNA hybridization of strains was prepared by the method of Wilson (1987), with minor modifications (Cleenwerck *et al*., 2002). DNA-DNA hybridizations were performed using the microplate method (Ezaki *et al*., 1989) with some modifications (Cleenwerck *et al*., 2002). The hybridization temperature was 45 °C ± 1 °C, reciprocal reactions (A x B and B x A) were performed for every DNA pair from all strains and their variation was within the limits of this method (Goris *et al*., 1998). The values presented are based on a minimum of four replicates. Representative strains from each "Japanese" *Pantoea* species were selected for hybridization based on the 16S rRNA gene sequence- and MLSA- phylogenetic trees. The type strains of the "Japanese" species were hybridized amongst each other, and with the type strain of *Tatumella ptyseos*, their closest phylogenetic neighbour, as well as with the type strains of *P. agglomerans*, *P. ananatis*, *P. vagans*, *P. stewartii* ssp. *stewartii* and *P. dispersa*. A summary of the hybridization results is presented in Table 2. The DNA relatedness between the type strains of *P. citrea* LMG 22049^T, *P. punctata* LMG 22050^T and *P. terrea* LMG 22051^T ranges from 13 to 21 %, which

is considerably lower than the 28-43 % reported by Kageyama *et al*. (1992) and could be due to different hybridization methods used. LMG 23359 and LMG 23360, the strains which can cause pink disease of pineapple (Cha *et al*., 1997) shared 96 % DNA relatedness when hybridized against each other, whilst LMG 23360 displayed only 42 % DNA similarity with the type strain of *P. citrea* LMG 22049^T. These results together with the 16S rRNA gene sequence- and MLSA-data prove that LMG 23360 and LMG 23359 do not belong to *P. citrea*.

Pantoea citrea LMG 22049^T and *P. punctata* LMG 22050^T displayed 14 and 21 % DNA relatedness when hybridized to *T. ptyseos* LMG 7888^T, respectively. In contrast, the *T. ptyseos* type strain shared 66 % DNA relatedness with *P. terrea* LMG 22051^T, and 87 % with LMG 23565, originally considered to be *P. terrea*. LMG 23565 demonstrated only 55 % DNA similarity, when hybridized to *P. terrea* LMG 22051^T. These results are in favour of the reclassification of LMG 23565 (= CCUG 30163) as *T. ptyseos* and confirm the close phylogenetic relationship between *P. terrea* and *T. ptyseos*, observed in both the 16S rRNA gene sequence- and MLSA- phylogenetic trees (Figs. 1 & 2). The DNA relatedness between the type strains of the "Japanese" *Pantoea* species and the type strains of *P. agglomerans*, *P. ananatis*, *P. vagans*, *P. stewartii* and *P. dispersa* was below 10 %. These low hybridization values are also reflected in the phylogenetic distance between the "Japanese" species and the *Pantoea* "core" species in both Figures 1 and 2.

G + C content

The mole % G + C content of the type strains, determined by HPLC (Mesbah *et al*., 1989), are as follows: *Pantoea citrea* (LMG 22049^T) = 49.8 mol %; MLSA group J

(LMG 23360^T) = 50.2 mol %; *Pantoea punctata* (LMG 22050^T, LMG 22098) = 50.7 mol %, *Pantoea terrea* (LMG 22051^T, LMG 23564) = 52.6-52.8 mol % and *Tatumella ptyseos* (LMG 7888T, LMG 23565) = 51.7-52.1 mol %.

Phenotypic assays

Differences between the *Pantoea* "core" species and the "Japanese" species have been previously noted, not only phylogenetically but also phenotypically (Grimont & Grimont, 2005, Delétoile *et al*., 2008). API 20 E, API 50 CHB/E, Biotype 100 (bioMérieux) and GN2 MicroPlate (Biolog) tests were performed on all *Tatumella* and *Pantoea* strains used in this study, to verify that the phenotypic data agrees with those available in literature. Cell suspensions were prepared from strains grown on tryptic soy agar for 12 hours. All phenotypic test strips and plates were incubated for 24-48 hours at 28 °C, except the Biotype 100 strips which were incubated for up to six days. Scoring was performed according to the manufacturer's instructions. Phenylalanine deaminase activity was determined by adding 10 % aqueous $FeCl_3$ to 24 hour cultures grown on (D)-phenylalanine agar (Merck). The development of a green colour indicated a positive reaction. A high correlation was observed between the phenotypic results generated in this study, the phenotypic data presented in Bergey's Manual of Systematic Bacteriology (Grimont & Grimont, 2005) and the original species descriptions of *P. citrea*, *P. punctata*, *P. terrea* (Kageyama *et al*., 1992) and *Tatumella ptyseos* (Hollis *et al*., 1981). *T. ptyseos* and the "Japanese" species can be distinguished from the genus *Pantoea* by a positive reaction for arginine dihydrolase (except *P. terrea* and *T. ptyseos*) and 2-ketogluconate dehydrogenase, their inability to produce acid from arbutin, *myo*-inositol and L-rhamnose and their inability to utilize D-galacturonic acid, D-glucoronic acid, *myo*-

inositol, β-methyl-D-glucoside, L-rhamnose, D-sacccharic acid and *meso*-tartrate (except *T. ptyseos*). A summary of the most useful phenotypic and biochemical characteristics for differentiating *T. ptyseos* and the "Japanese" species from *Pantoea* species is presented in Table 3. Table 3 was assembled using data generated in this study (except for DKGA), of which the majority agrees with that previously published.

A summary of biochemical and phenotypic characteristics which can differentiate between *T. ptyseos*, the "Japanese" species and the pink disease-causing strains LMG 23360 and LMG 23359 is listed in Table 4. The strains causing pink disease of pineapple can be differentiated from *P. citrea* by a positive phenylalanine deaminase reaction, acid production from amidon, their ability to utilise adonitol and trigonelline, and their inability to utilize gentiobiose and lactulose. *P. terrea* can be differentiated from *T. ptyseos*, its closest phylogenetic neighbour, by negative phenylalanine deaminase reaction, the ability to utilize formic acid and pyruvic acid methyl ester, and the inability to utilize quinic acid and L-tartrate.

A selection of 50 phenotypic characteristics was used to construct a UPGMA dendrogram (Fig. 3) in PAUP 4.0b10 (Swofford, 2000). The dendrogram shows a clear distinction of *T. ptyseos* and the "Japanese" species from the *Pantoea* "core" species, lending further support for the re-classification of these three species in the genus *Tatumella*, and the description of a novel species for the strains causing pink disease of pineapple.

Conclusions

The many previous re-arrangements seen in the "*Erwinia herbicola-Enterobacter agglomerans* complex" were, for the most part, based on DNA-DNA hybridization data, biochemical characterization and protein-profiling. When *P. citrea*, *P. punctata* and *P. terrea* were described as belonging to the genus *Pantoea*, molecular techniques such as 16S rRNA gene sequencing and MLSA were not readily accessible. With rapid gene sequencing now a reality, it is possible to observe true phylogentic relationships and to resolve evident taxonomic issues.

The 16S rRNA gene- and MLSA-trees show a clear division of the *Pantoea* "core" species from the "Japanese" species and *T. ptyseos*. Furthermore, MLSA group J (strains causing pink disease of pineapple) was shown to cluster independently from the type strain of *P. citrea* in both phylogenetic trees. These results were supported equally by DNA-DNA hybridization values, which share a high correlation with MLSA data (Brady *et al*., 2008), and phenotypic data. Although the genus *Tatumella* is reported to have few distinguishing phenotypic properties (Farmer, 2005), a number of biochemical characteristics were identified which are shared by the "Japanese" species and which can be used to differentiate these species from *Pantoea* (see Table 3).

An important characteristic distinguishing *P. citrea*, *P. punctata*, *P. terrea*, *T. ptyseos* and MLSA group J from *Pantoea* species is their ability to produce 2-ketogluconate dehydrogenase which oxidizes 2-ketogluconate to DKGA. The production of DKGA is responsible for the discolouration of fruit tissue typical of pink disease of pineapple (Pujol & Kado, 2000), and therefore plays an important role in disease expression.

Noticeably, not one *Pantoea* "core" species has this ability (Bouvet *et al*., 1989). Several objections for not including the "Japanese" species in the genus *Tatumella* were stated in the original description, despite a personal communication from P. Grimont suggesting that the "Japanese" species were phenotypically similar to *Tatumella* (cited by Kageyama *et al*., 1992). These included acid production from D-xylose and L-arabinose, arginine dihydrolase and phenylalanine deaminase activity, methyl red and Voges-Proskauer reaction, esculin hydrolase activity, citrate utilization and lower G + C content. However, closer examination of all available data revealed that all taxa are positive for acid production from D-xylose and L-arabinose, methyl red and Voges-Proskauer reactions and citrate utilization. *T. ptyseos and P. terrea* are both negative for arginine dihydrolase activity, whilst *P. citrea* and *P. punctata* are both positive. The G + C content of *T. ptyseos* is 53-54 mol % which is slightly higher compared to the "Japanese" species which ranges from 49.7 to 51.9 mol %. However, the G + C contents of *Pantoea* "core" species range from 53 to 61 mol %, which is considerably higher. Therefore the current data, both phylogenetic and phenotypic, supports the transfer of the "Japanese" species from the genus *Pantoea* to the genus *Tatumella*.

We propose to transfer *P. citrea*, *P. punctata* and *P. terrea* to the genus *Tatumella* as *Tatumella citrea* comb. nov., *Tatumella punctata* comb. nov. and *Tatumella terrea* comb. nov. We further propose *Tatumella morbirosei* sp. nov. for strains LMG 23359 and LMG 23360, the causal agent of pink disease of pineapple.

Emended description of the genus *Tatumella* Hollis, Hickman & Fanning, 1982

(Ta.tum.el'la. M.L. dim. Neut. –*ella* ending; M.L. fem. n. *Tatumella* named to honour Harvey Tatum, an American bacteriologist who made many contributions to our understanding of the classification and identification of fermentative and nonfermentative bacteria of medical importance.) The description below is based on the data of Hollis *et al*. (1981), Kageyama *et al*. (1992) and this paper.

Gram-negative, non-capsulated, non-sporeforming small rods that are 0.6-1.2 x 0.9-3.0 μm in size. Cells are motile by means of polar, subpolar or lateral flagella or non-moltile at 36 °C. Facultatively anaerobic, fermentative, catalase positive (weak and slow), oxidase negative. Non-pigmented, or pale beige to pale orange. Glucose dehydrogenase, gluconate dehydrogenase and 2-ketogluconate dehydrogenase are produced. Reduce nitrate to nitrite. Indole, urease and gelatin tests are negative. Positive for Voges-Proskauer (Coblentz), methyl red and citrate (Simmons); phenylalanine, arginine dihydrolase and ONPG tests are variable. Negative for H_2S (TSI), lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase, KCN test, lipase and DNase. Acid is produced from L-arabinose, D-galactose, D-glucose, glycerol, D-mannitol, D-mannose, melibiose, D-ribose, D-trehalose and D-xylose (variable reaction for *T. morbirosei*), but not from amygdalin, dulcitol, erythritol, glutarate, glycogen, histamine, *myo*-inositol, α-methyl-D-glucoside, propionate, L-rhamnose, sorbitol and L-sorbose. *N*-acetyl-D-glucosamine, 4-aminobutyrate, L-aspargine, L-aspartic acid, bromosuccinic acid, D-fructose, fumarate, β-galactoppyranoside, D-gluconic acid, α-D-glucose-1-phosphate, α-D-glucose-6-phosphate, L-glutamic acid, glycerol, inosine, 5-ketogluconate, D-mannose, L-proline, D-psicose, D-ribose, succinic acid, D-trehalose, thymidine and uridine are

utilized as sole sources of carbon and energy. Susceptible to many antibiotics. Isolated from human clinical samples, fruit and soil. The G + C content of the DNA ranges from 49.8 to 53 mol %. The type species is *Tatumella ptyseos* Hollis, Hickman & Fanning, 1982.

Description of *Tatumella citrea* (Kageyama, Nakae, Yagi & Sonoyama 1992) comb. nov.

Tatumella citrea (ci′tre.a. M.L. adj. *citrea*, of citrus)

Cells are Gram-negative, short rods (0.8-1.2 x 1.0-3.0 μm) occurring singly or in pairs, non-motile and non-sporeforming. Colonies are pale beige to pale orange, round, convex and smooth with entire margins. Nicotinic acid or nicotinamide are required for growth. Facultatively-anaerobic, oxidase negative, catalase positive, glucose dehydrogenase, gluconate dehydrogenase and 2-ketogluconate dehydrogenase are produced. Indole, urease and phenylalanine deaminase are negative, whilst arginine dihydrolase is positive. Reduce nitrate to nitrite. Acid is produced from: L-arabinose, D-fucose, D-galactose, D-glucose, glycerol, maltose, D-mannose, D-mannitol, D-tagatose and D-trehalose, but not from amidon, D-raffinose or sucrose. The following carbon sources are utilized at 28 °C: *N*-acetyl-D-glucosamine, *cis*-aconotic acid, L-arabinose, L-aspargine, L-aspartic acid, citrate, dextrin, erythritol, formic acid, D-fructose, D-galactose, gentiobiose (weak), D-gluconic acid, D-glucose, 5-ketogluconate, lactose, lactulose, D-malate, D-maltose, maltotriose, D-mannitol, pyruvic acid methyl ester, succinic acid and D-tagatose. The following carbon sources are not utilized at 28 °C: D-adonitol, L-alanine, D-arabinose, betaine, dulcitol, L-fucose, α-methyl-D-glucoside, β-methyl-D-glucoside, D-galacturonic acid, D-

glucoronic acid, glutarate, histdine, *myo*-inositol, D-melibiose, L-proline, propionate, quinic acid, D-raffinose, L-rhamnose, D-sorbitol, L-serine, sucrose, L-tartrate, *meso*-tartrate, and trigonelline. The G + C content of the type strain is 49.8 mol %. The type strain is LMG 22049^T (= BD 875^T = ATCC 31623^T = SHS 2003^T) and was isolated from mandarin orange in Japan.

Description of *Tatumella punctata* (Kageyama, Nakae, Yagi & Sonoyama 1992) comb. nov.

Tatumella punctata (punc.ta′ta. L. N. *punctum*, a point; M.L. adj. *punctata*, full of points)

Cells are Gram-negative, short rods (1.1-1.2 x 1.3-2.3 μm) occurring singly or in pairs, non-motile and non-sporeforming. Colonies are pale beige to pale orange, round, convex and smooth with entire margins. Nicotinic acid or nicotinamide are required for growth. Facultatively-anaerobic, oxidase negative, catalase positive, glucose dehydrogenase, gluconate dehydrogenase and 2-ketogluconate dehydrogenase are produced. Indole, urease and phenylalanine deaminase are negative, whilst arginine dihydrolase is positive. Reduce nitrate to nitrite. Acid is produced from: L-arabinose, D-fructose, D-fucose, D-galactose, D-glucose, glycerol, D-mannose, D-raffinose, sucrose and D-trehalose, but not from amidon or D-mannitol. The following carbon sources are utilized at 28 °C: *N*-acetyl-D-glucosamine, D-arabinose, L-aspargine, L-aspartic acid, cellobiose (variable), citrate, D-fructose, D-galactose, gentiobiose, D-gluconic acid, D-glucose, 5-ketogluconate, D-mannitol, D-mannose, succinic acid, sucrose and D-trehalose. The following carbon sources are not utilized at 28 °C within three to six days: *cis*-aconotic acid, D-adonitol, L-alanine, L-

arabinose, D-arabitol, L-arabitol, betaine, dextrin, dulcitol, erythritol, formic acid, L-fucose, D-galacturonic acid, D-glucoronic acid, α-methyl-D-glucoside, β-methyl-D-glucoside, glutarate, histidine, *myo*-inositol, lactose, lactulose, D-maltose, maltotriose, D-melibiose, L-proline, propionate, pyruvic acid methyl ester, quinic acid, D-raffinose, L-rhamnose, D-sorbitol, L-serine, L-tartrate, *meso*-tartrate and trigonelline. The G + C content of the type strain is 50.7 mol %. The type strain is LMG 22050^T (= BD 876^T = ATCC 31626^T = SHS 2006^T) and was isolated from mandarin orange in Japan.

Description of *Tatumella terrea* (Kageyama, Nakae, Yagi & Sonoyama 1992) comb. nov.

Tatumella terrea (ter′re.a. L. n. *terra*, soil; L. adj. *terrea*, of soil)

Cells are Gram-negative, short rods (0.8-0.9 x 1.2-2.0 μm) occurring singly or in pairs, motile by means of one or two lateral flagella and non-sporeforming. Colonies are pale beige to pale orange, round, convex and smooth with entire margins. Nicotinic acid or nicotinamide are required for growth. Facultatively-anaerobic, oxidase negative, catalase positive, glucose dehydrogenase, gluconate dehydrogenase and 2-ketogluconate dehydrogenase are produced. Indole, urease, phenylalanine deaminase and arginine dihydrolase are negative. Reduce nitrate to nitrite. Acid is produced from: L-arabinose, D-fructose, D-galactose, D-glucose, glycerol, D-mannose, sucrose and D-trehalose, but not from amidon, D-mannitol or D-raffinose. The following carbon sources are utilized at 28 °C: *N*-acetyl-D-glucosamine, L-aspargine, L-aspartic acid, citrate, D-fructose, formic acid, D-galactose, D-gluconic acid, D-glucose, 5-ketogluconate, D-mannose, pyruvic acid methyl ester, succinic

399 acid and D-trehalose. The following carbon sources are not utilized at 28 °C: *cis*-
400 aconotic acid, D-adonitol, L-alanine, D-arabinose, L-arabinose, D-arabitol, L-arabitol,
401 betaine, cellobiose, dextrin, dulcitol, erythritol, L-fucose, D-galacturonic acid,
402 gentiobiose, D-glucoronic acid, α-methyl-D-glucoside, β-methyl-D-glucoside,
403 glutarate, histidine, *myo*-inositol, lactose, lactulose, D-maltose, maltotriose, D-
404 melibiose, L-proline, propionate, quinic acid, D-raffinose, L-rhamnose, D-sorbitol, L-
405 serine, sucrose, L-tartrate and trigonelline. The G + C content of the type strain is 52.8
406 mol %. The type strain is LMG 22051^T (= BD 877^T = ATCC 31628^T = SHS 2008^T)
407 and was isolated from soil in Japan.
408
409 **Description of *Tatumella morbirosei* sp. nov.**
410 *Tatumella morbirosei* (mor.bi.ró.se.i. L.N. *morbus*, disease; L.Adj. *roseus*, rosy,
411 pink. N.L. gen. N. *morbirosei*, of the pink disease, referring to the causal agent of
412 pink disease of pineapple)
413
414 Cells are Gram-negative, short rods (0.8-1.2 x 1.0-3.0 μm) occurring singly or in
415 pairs, non-motile and non-sporeforming. Colonies are pale beige, round, convex and
416 smooth with entire margins. Facultatively-anaerobic, oxidase negative, catalase
417 positive, glucose dehydrogenase, gluconate dehydrogenase and 2-ketogluconate
418 dehydrogenase are produced. Indole and urease are negative, whilst phenylalanine
419 deaminase is positive and arginine dihydrolase is weakly positive. Reduce nitrate to
420 nitrite. Acid is produced from: amidon, L-arabinose, D-fucose, D-fructose, D-
421 galactose, D-glucose, glycerol, 5-ketogluconate, melibiose, D-mannitol, D-mannose,
422 D-tagatose and D-trehalose but not from D-raffinose or sucrose. The following carbon
423 sources are utilized at 28 °C: *N*-acetyl-D-glucosamine, D-adonitol, D-arabinose, L-

arabinose, L-aspargine, L-aspartic acid, citrate, dextrin, erythritol, formic acid (weak), D-fructose, D-galactose, D-gluconic acid, D-glucose, 5-ketogluconate, D-malate, D-maltose, maltotriose, D-mannitol, D-mannose, pyruvic acid methyl ester (weak), succinic acid, D-tagatose, D-trehalose and trigonelline. The following carbon sources are not utilized at 28 °C: *cis*-aconotic acid, L-alanine, L-arabitol, betaine, cellobiose, dulcitol, L-fucose, gentiobiose, α-methyl-D-glucoside, β-methyl-D-glucoside, D-galacturonic acid, D-glucoronic acid, glutarate, histidine, *myo*-inositol, lactose, lactulose, D-melibiose, L-proline, propionate, quinic acid, D-raffinose, L-rhamnose, D-sorbitol, L-serine, L-tartrate and *meso*-tartrate. The G + C content of the type strain is 50.2 mol %. The type strain is LMG 23360^T (= BD 878^T = NCPPB 4036^T = CMC6^T) and was isolated from pineapple in the Philippines.

Acknowledgements

This study was partially supported by the South African-Flemish Bilateral Agreement, the National Research Foundation (NRF), the Tree Protection Co-operative Programme (TPCP) and the THRIP support programme of the Department of Trade and Industry, South Africa. The BCCM/LMG Bacteria collection is supported by the Federal Public Planning Service-Science Policy, Belgium. The authors wish to thank Katrien Engelbeen for technical assistance and Dr J.P. Euzeby for suggesting the name “morbirosei”.

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560 **Table 1**: Strains of *Tatumella* and *Pantoea* used in this study, LMG = BCCM/LMG Bacteria Collection, Ghent University, Belgium, ATCC =

561 American Type Culture Collection, Rockville, Maryland, U.S.A., CCUG = Culture Collection, University of Göteborg, Sweden, BD = Plant

562 Pathogenic and Plant Protecting Bacteria (PPPPB) Culture Collection, ARC-PPRI, Pretoria, South Africa,

563 ^{T} = type strain, ^{a} = Genbank accession numbers, Br HG = Brenner hybridization group

Species	**Strain**	**Source**	**Location**	***gyrB*[a]**	***rpoB*[a]**	***atpD*[a]**	***infB*[a]**
Tatumella citrea	LMG 22049^{T} = BD 875^{T}	Mandarin orange	Japan	EF988802	EF988974	EF988715	EF988888
Tatumella morbirosei	LMG 23360^{T} = BD 878^{T}	Pineapple	Philippines	EU344760	EU344768	EU344756	EU344764
	LMG 23359 = NCPPB 4035	Pineapple	Philippines	EU344759	EU344767	EU344755	EU344763
Tatumella punctata	LMG 22050^{T} = BD 876^{T}	Mandarin orange	Japan	EF988803	EF988975	EF988716	EF988889
	LMG 22097	Mandarin orange	Japan	EF988805	EF988977	EF988718	EF988891
	LMG 22098	Persimmon	Japan	EF988806	EF988978	EF988719	EF988892
	LMG 23562	Mandarin orange	Japan	EF988807	EF988979	EF988720	EF988893
	LMG 23563	Mandarin orange	Japan	EF988808	EF988980	EF988721	EF988894
	CCUG 30157	Mandarin orange	Japan	EF988795	EF988967	EF988708	EF988881
	CCUG 30160	Mandarin orange	Japan	EF988796	EF988968	EF988709	EF988882
Tatumella terrea	LMG 22051^{T} = BD 877^{T}	Soil	Japan	EF988804	EF988976	EF988717	EF988890
	LMG 23564	Soil	Japan	EF988809	EF988981	EF988722	EF988895
	CCUG 30162	Soil	Japan	EF988797	EF988969	EF988710	EF988883
Tatumella ptyseos	LMG 7888^{T} = ATCC 33301^{T}	Human	USA	EU145260	EU145292	EU145244	EU145276
	LMG 23565	Soil	Japan	EU344758	EU344766	EU344754	EU344762
	CCUG 30163	Soil	Japan	EU344757	EU344765	EU244753	EU344761
Pantoea agglomerans	LMG 1286^{T}	Human	Zimbabwe	EF988798	EF988970	EF988711	EF988884
	LMG 2660	*Wisteria floribunda*	Japan	EF988823	EF988995	EF988736	EF988909
Pantoea ananatis	LMG 2665^{T}	Pineapple	Brazil	EF988824	EF988996	EF988737	EF988910
	LMG 20103	Eucalyptus	South Africa	EF988799	EF988971	EF988712	EF988885
Pantoea stewartii ssp. *stewartii*	LMG 2715^{T}	Maize	USA	EF988831	EF989003	EF988744	EF988917
	LMG 2718	Maize	USA	EF988832	EF989004	EF988745	EF988918
Pantoea stewartii ssp. *indologenes*	LMG 2632^{T}	Fox millet	India	EF988822	EF988994	EF988735	EF988908
	LMG 2673	Pineapple	Hawaii	EF988827	EF988999	EF988740	EF988914
Pantoea dispersa	LMG 2603^{T}	Soil	Japan	EF988818	EF988990	EF988731	EF988904

	LMG 2604	Wild rose	Netherlands	EF988819	EF988991	EF988732	EF988905
Pantoea anthophila	LMG 2558^{T}	*Impatiens balsamina*	India	EF988812	EF988984	EF988725	EF988898
	LMG 2560	*Tagetes erecta*	Unknown	EF988813	EF988985	EF988726	EF988899
Pantoea vagans	LMG 24199^{T}	Eucalyptus	Uganda	EF988768	EF988940	EF988715	EF988854
	LMG 24201	Maize	South Africa	EF988792	EF988964	EF988705	EF988878
Pantoea eucalypti	LMG 24197^{T}	Eucalyptus	Uruguay	EF988762	EF988934	EF988675	EF988848
	LMG 24198	Eucalyptus	Uruguay	EF988763	EF988935	EF988676	EF988849
Pantoea deleyi	LMG 24200^{T}	Eucalyptus	Uganda	EF988770	EF988950	EF988683	EF988856
Pantoea sp. (Br HG II)	LMG 5345^{T}	Human, stool	New Jersey, USA	EU145272	EU145304	EU145256	EU145288
	LMG 24526	Human, blood	New York, USA	EU145261	EU145293	EU145245	EU145277
Pantoea sp. (Br HG IV)	LMG 2781^{T}	Human, trachea	Connecticut, USA	EU145271	EU145303	EU145255	EU145287
	LMG 24529	Human, cyst	Georgia, USA	EU145264	EU145296	EU145248	EU145280
Pantoea sp. (Br HG V)	LMG 5343^{T}	Human, urethra	Montana, USA	EU145270	EU145302	EU145254	EU145286
	LMG 24532	Human, sputum	Wisconsin, USA	EU145267	EU145299	EU145251	EU145283
Pantoea sp. (Br HG V)	LMG 24534^{T}	Human, blood	Paris, France	EU145269	EU145301	EU145253	EU145285
Erwinia billingiae	LMG 2613^{T}	Pear	UK	EU145275	EU145307	EU145259	EU145291
Erwinia psidii	LMG 7034	Guava	Brazil	FJ187834	FJ187844	FJ187829	FJ187839
Erwinia rhapontici	LMG 2688^{T}	Rhubarb	UK	EF988838	EF989010	EF988751	EF988924
Erwinia toletana	LMG 24162^{T}	Olive tree	Spain	EU145274	EU145306	EU145258	EU145290

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Table 2: DNA-DNA hybridization values between *T. citrea* comb. nov., *T. morbirosei* sp. nov., *T. punctata* comb. nov., *T. terrea* comb. nov., *T. ptyseos* and selected species belonging to *Pantoea*.

		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**
Tatumella citrea	1. LMG 22049^T	100													
Tatumella morbirosei	2. LMG 23360^T	42	100												
	3. LMG 23359		96	100											
Tatumella punctata	4. LMG 22050^T	21	17		100										
	5. LMG 22098	16			93	100									
Tatumella terrea	6. LMG 22051^T	13	11		17	18	100								
	7. LMG 23564						82	100							
Tatumella ptyseos	8. LMG 7888^T	14	15		21		66		100						
	9. LMG 23565	15	13		20		55	54	87	100					
Pantoea agglomerans	10. LMG 1286^T	6			8		8				100				
Pantoea ananatis	11. LMG 2665^T	5			6		6				21	100			
Pantoea vagans	12. LMG 24199^T	5			7		8				65	20	100		
Pantoea stewartii ssp. *stewartii*	13. LMG 2715^T	2			3		3				6	20	9	100	
Pantoea dispersa	14. LMG 2603^T	7			7	7	8				24	20	19	22	100

Table 3: Selected phenotypic characteristics useful for distinguishing *Tatumella* species from *Pantoea* species. 1 = *Tatumella ptyseos* (1 strain), 2 = *Tatumella citrea* comb. nov. (1 strain), 3 = *Tatumella morbirosei* sp. nov. (2 strains), 4 = *Tatumella punctata* comb. nov. (7 strains), 5 = *Tatumella terrea* comb. nov. (3 strains), 6 = *Pantoea agglomerans* (3 strains), 7 = *Pantoea ananatis* (4 strains), 8 = *Pantoea anthophila* (2 strains), 9 = *Pantoea deleyi* (1 strain), 10 = *Pantoea dispersa* (2 strains), 11 = *Pantoea eucalypti* (2 strains), 12 = *Pantoea stewartii* ssp. *stewartii* (1 strain), 13 = *Pantoea stewartii* ssp. *indologenes* (2 strains), 14 = *Pantoea vagans* (7 strains). All data presented was generated during this study, except for 2-ketogluconate dehydrogenase for which the results were taken from Kageyama *et al*., 1992 and Bouvet *et al*., 1989.

+, positive; -, negative; (+), weakly positive; +/-, variable reaction, ND, not determined

* *T. ptyseos* is non-motile at 36 °C but many strains are motile at 25 °C. Flagella of *Tatumella* species are polar, sub-polar or lateral rather than peritrichous like *Pantoea* species.

[a] API 50 CHB/E, [b] Biotype 100, GN2 MicroPlate

Characteristic	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**
motility (36 °C)*	-	-	-	-	+	+	+	-	-	+	-	-	+	-
arginine dihydrolase	-	+	(+)	+	-	-	-	-	-	-	-	-	-	-
2-ketogluconate dehydrogenase	+	+	+	+	+	-	-	ND	ND	-	ND	-	-	ND
Acid from [a]:														
arbutin	-	-	-	-	-	+	+	+	-	+	+	+	+	+
myo-inositol	-	-	-	-	-	(+)	+	+	-	+	+	-	+	+

L-rhamnose	-	-	-	-	-	+	+	+	+	+	+	-	+	+
Utilization of [b]:														
cis-aconitic acid	-	+	-	-	-	+	+	+	+	+	+	+	+	+
D-alanine	-	-	-	-	-	+	+	+	+	+	+	+	+	+
L-alanine	-	-	-	-	-	+	+	+	+	+	+	+	+	+
cellobiose	-	-	-	+/-	-	+	+	+	+	+	+	+	+	+
D-galacturonic acid	-	-	-	-	-	+	+	+	+	+	+	+	+	+
D-glucoronic acid	-	-	-	-	-	+	+	+	+	+	+	+	+	+
L-histidine	-	-	-	-	-	+	+	+	+	+	+	+	+	+
myo-inositol	-	-	-	-	-	+	+	+	+	+	+	+	+	+
D,L-lactic acid	-	-	-	-	-	+	+	+	+	+	+	+	+	+
maltose	-	+	+	-	-	+	+	+	+	+	+	-	+	+
β-methyl-D-glucoside	-	-	-	-	-	+	+	+	+	+	+	+	+	+
L-proline	-	-	-	-	-	+	+	+	+	+	+	+	+	+
L-rhamnose	-	-	-	-	-	+	+	+	+	+	+	+	+	+
D-saccharic acid	-	-	-	-	-	+	+	+	+	+	+	+	+	+
L-serine	-	-	-	-	-	+	+	+	+	+	+	+	+	+
meso-tartrate	(+)	-	-	-	-	+	+	+	+	+	+	+	+	+

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588 **Table 4:** Phenotypic characteristics distinguishing *T. citrea* comb. nov., *T. morbirosei*

589 sp. nov., *T. punctata* comb. nov. and *T. terrea* comb. nov. from each other and from

590 *T. ptyseos*

591 1 = *T. ptyseos* LMG 7888^T, LMG 23565, 2 = *T. citrea* LMG 22049^T,

592 3 = *T. morbirosei* LMG 23360^T, LMG 23359, 4 = *T. punctata* LMG 22050^T,

593 LMG 22097, LMG 22098, LMG 23563, 5 = *T. terrea* LMG 22051^T, LMG 23564.

594 +, positive; (+), weakly positive; -, negative

595 All data presented was generated during this study.

Characteristic	**1**	**2**	**3**	**4**	**5**
arginine dihydrolase	-	+	(+)	+	-
phenylalanine deaminase	+	-	+	-	-
Acid from:					
amidon (starch)	-	-	+	-	-
D-mannitol	-	+	+	-	-
D-raffinose	-	-	-	+	-
sucrose	+	-	-	+	+
Utilization of:					
adonitol	-	-	+	-	-
L-arabinose	-	+	+	-	-
dextrin	-	+	+	-	-
erythritol	-	+	+	-	-
formic acid	-	+	(+)	-	+
gentiobiose	-	(+)	-	+	-
lactulose	-	+	-	-	-
pyruvic acid methyl ester	-	(+)	(+)	-	+
quinic acid	+	-	-	-	-
L-tartrate	+	-	-	-	-
trigonelline	-	-	+	-	-

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Supplementary Table S1: Signature nucleotides of the 16S rRNA- and *atpD*-gene sequences for the differentiation of *Tatumella* species from *Pantoea* species. *E. coli* numbering positions are used.

E.coli numbering position	***Tatumella***	***Pantoea***
16S rRNA gene signature nucleotides:		
136	T	C
593	C	T
619	C	T
624	C	T
637	C	T
652	A	T
1115	C	T
1366	T	C
atpD gene signature nucleotides:		
198	C	T
201	T	G
204	G	M
207	G	H
330	T	A
338	A	C
351	T	C
360	A	T
361	A	T
366	C	T
374	T	A
376	G	T
385	A	C
387	T	G
549	A	Y
603	G	C
613	C	A
615	G	C
693	T	C
699	T	G
739	G	A
804	T	R
828	A	S

Figure 1: Maximum likelihood tree based on 16S rRNA gene sequences of *Tatumella* species. Bootstrap values after 1000 replicates are expressed as percentages. *Escherichia coli* was included as an outgroup.

Figure 2: Maximum likelihood tree based on the concatenated nucleotide sequences of *gyrB, rpoB, atpD* and *infB* genes of *Tatumella* and *Pantoea* strains. Bootstrap values after 1000 replicates are expressed as percentages. *Cronobacter sakazakii* was included as an outgroup. Gene sequences for *Erwinia tasmaniensis*, *Escherichia coli*, *Shigella dysenteriae*, *Klebsiella pneumoniae*, *Citrobacter rodentium*, *Citrobacter koseri* and *Cronobacter sakazakii* were obtained from genome sequencing databases (http://www.ncbi.nlm.nih.gov, http://www.sanger.ac.uk, http://asap.ahabs.wisc.edu/asap).

Figure 3: UPGMA dendrogram constructed from 50 phenotypic characteristics useful for the differentiation of the "core" *Pantoea* species from species of the genus *Tatumella*.


DSM 4484T|Erwinia rhapontici|AJ233417
LMG 11254T|Erwinia persicinus|Z96086
CECT 5263T|Erwinia toletana|AF130910
LMG 2613T|Erwinia billingiae|Y13249
ICMP 14143T|Erwinia pyrifoliae|EF122435
LMG 2024T|Erwinia amylovora|Z96088
LMG 2781R|Pantoea sp.|EU216736
LMG 2603T|Pantoea dispersa|DQ504305
LMG 2708T|Erwinia mallotivora|AJ233414
CFBP 5189T|Erwinia papayae|AY131237
LMG 7034|Erwinia psidii|Z96085
LMG 2906T|Erwinia tracheiphila|Y13250
LMG 24534R|Pantoea sp.|EU216737
LMG 24200T|Pantoea deleyi|EF688011
LMG 5343R|Pantoea sp.|EU216735
LMG 24199T|Pantoea vagans|EF688012
NCTC 9381T|Pantoea agglomerans|AJ251466
LMG 24197T|Pantoea eucalypti|EF688009
LMG 2558T|Pantoea anthophila|EF688010
LMG 2665T|Pantoea ananatis|Z96081
LMG 2715T|Pantoea stewartii ssp. stewartii|Z96080
LMG 2632T|Pantoea stewartii ssp. indologenes|Y13251
LMG 5345R|Pantoea sp.|EU216734
LMG 7888T|Tatumella ptyseos|EU344770
LMG 22051T|Tatumella terrea|EF688007
LMG 22050T|Tatumella punctata|EF688006
LMG 23359|Tatumella morbirosei|FJ617235
LMG 23360T|Tatumella morbirosei|EU344769
LMG 22049T|Tatumella citrea|EF688008
ATCC 51113T|Citrobacter braakii|AF025368
ATCC 51118T|Citrobacter murliniae|AF025369
ATCC 51114T|Citrobacter werkmanii|AF025373
DSM 30039T|Citrobacter freundi|AJ233408
ATCC 51603T|Kluyvera georgiana|AF047186
ATCC 33433T|Kluyvera ascorbata|AF008579
ATCC 51609T|Kluyvera cochleae|AF047187
ATCC 14239T|Kluyvera cryocrescens|Y07651
LMG 10245T|Enterobacter nimipressuralis|Z96077
ATCC 35953T|Enterobacter asburiae|AB004744
LMG 2693T|Enterobacter cancerogenus|Z96078
ATCC 49162T|Enterobacter hormaechei|AJ508302
ATCC 13047T|Enterobacter cloacae|AJ251469
CCUG 45998T|Enterobacter cowanii|AJ508303
ATCC 11775T|Escherichia coli|X80725
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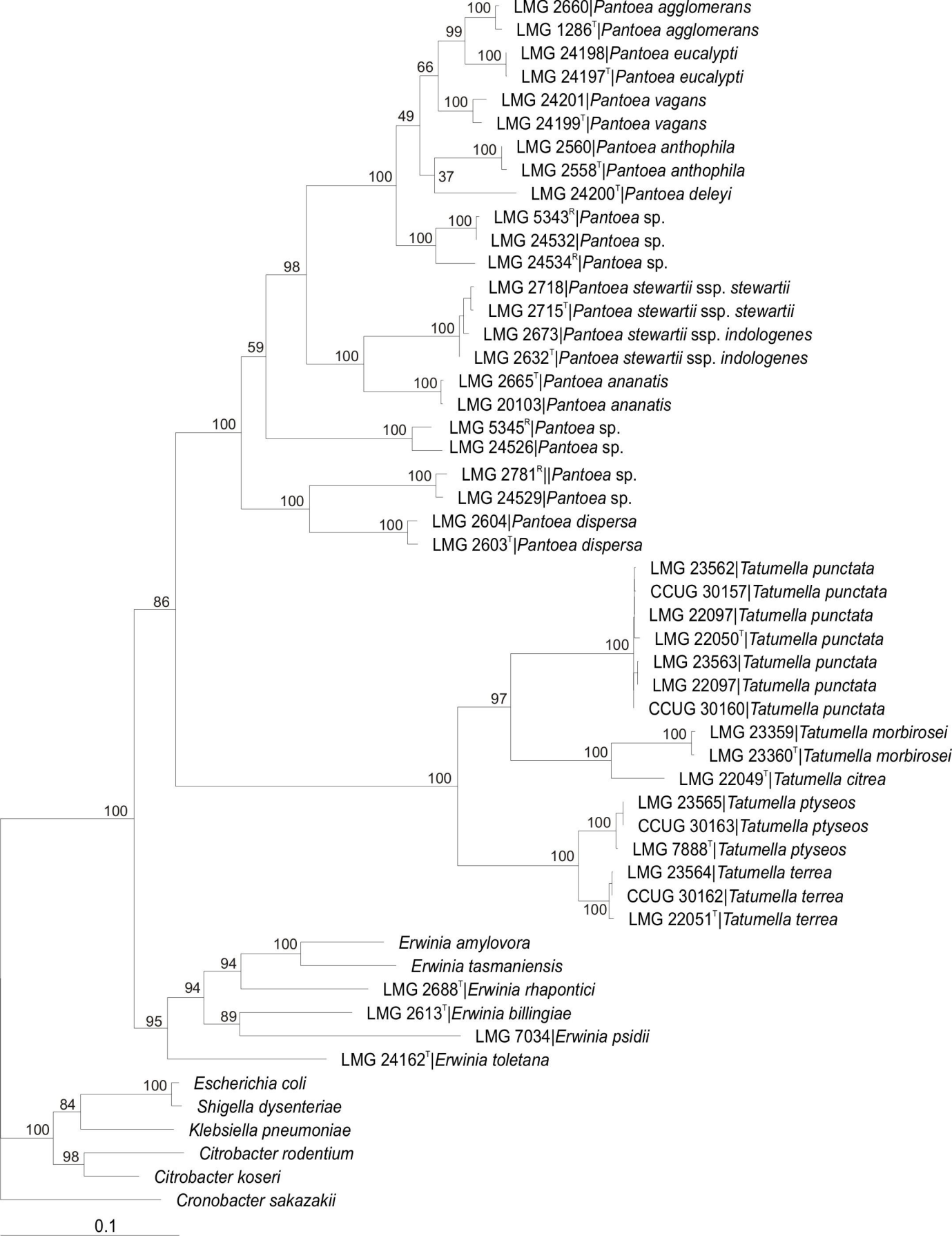
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LMG 1286T|Pantoea agglomerans
LMG 24198|Pantoea eucalypti
LMG 24197T|Pantoea eucalypti
LMG 24201|Pantoea vagans
LMG 24199T|Pantoea vagans
LMG 2560|Pantoea anthophila
LMG 2558T|Pantoea anthophila
LMG 24200T|Pantoea deleyi
LMG 5343R|Pantoea sp.
LMG 24532|Pantoea sp.
LMG 24534R|Pantoea sp.
LMG 2718|Pantoea stewartii ssp. stewartii
LMG 2715T|Pantoea stewartii ssp. stewartii
LMG 2673|Pantoea stewartii ssp. indologenes
LMG 2632T|Pantoea stewartii ssp. indologenes
LMG 2665T|Pantoea ananatis
LMG 20103|Pantoea ananatis
LMG 5345R|Pantoea sp.
LMG 24526|Pantoea sp.
LMG 2781R||Pantoea sp.
LMG 24529|Pantoea sp.
LMG 2604|Pantoea dispersa
LMG 2603T|Pantoea dispersa
LMG 23562|Tatumella punctata
CCUG 30157|Tatumella punctata
LMG 22097|Tatumella punctata
LMG 22050T|Tatumella punctata
LMG 23563|Tatumella punctata
LMG 22097|Tatumella punctata
CCUG 30160|Tatumella punctata
LMG 23359|Tatumella morbirosei
LMG 23360T|Tatumella morbirosei
LMG 22049T|Tatumella citrea
LMG 23565|Tatumella ptyseos
CCUG 30163|Tatumella ptyseos
LMG 7888T|Tatumella ptyseos
LMG 23564|Tatumella terrea
CCUG 30162|Tatumella terrea
LMG 22051T|Tatumella terrea
Erwinia amylovora
Erwinia tasmaniensis
LMG 2688T|Erwinia rhapontici
LMG 2613T|Erwinia billingiae
LMG 7034|Erwinia psidii
LMG 24162T|Erwinia toletana
Escherichia coli
Shigella dysenteriae
Klebsiella pneumoniae
Citrobacter rodentium
Citrobacter koseri
Cronobacter sakazakii
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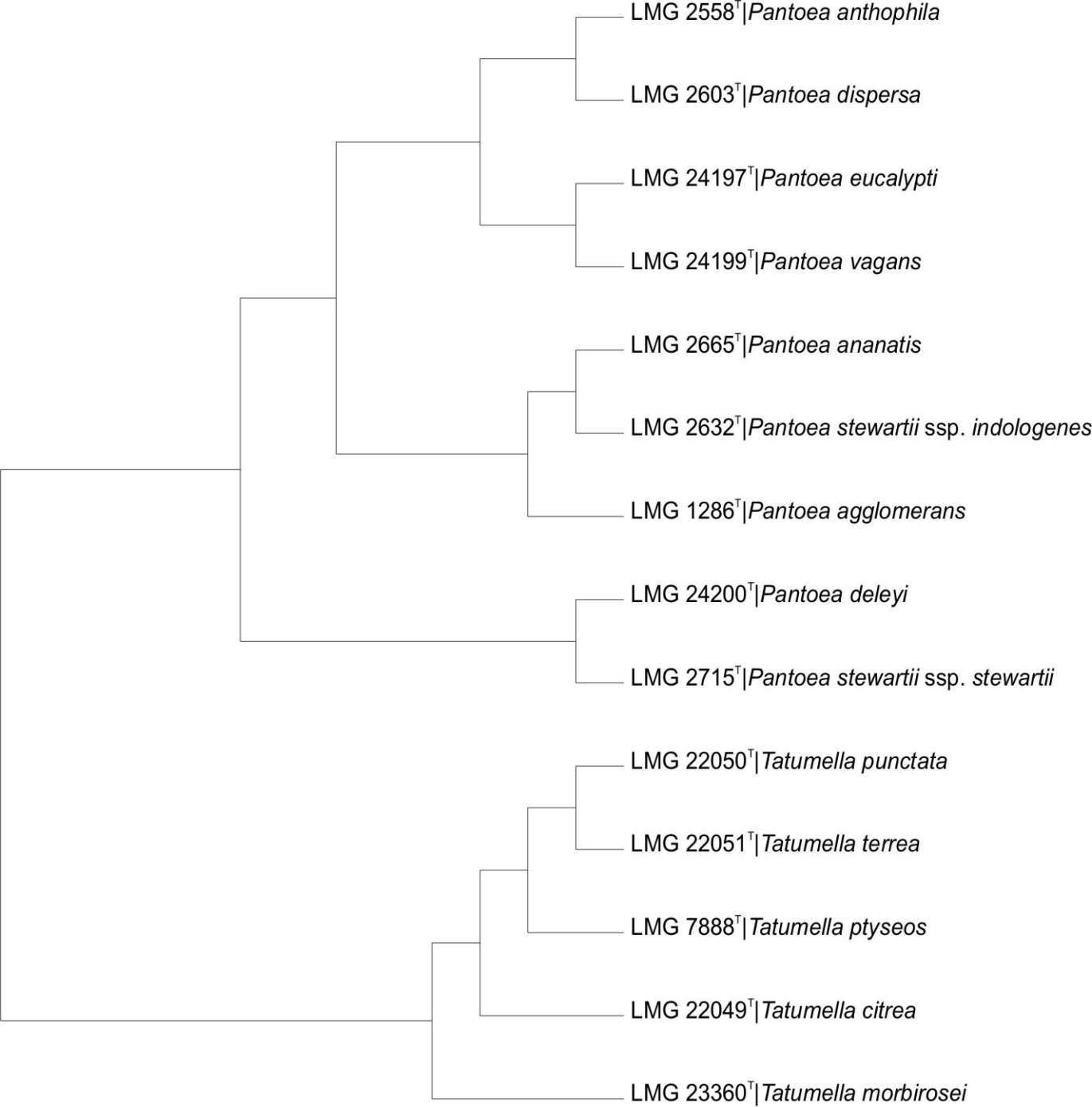
LMG 2558T|Pantoea anthophila
LMG 2603T|Pantoea dispersa
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LMG 24199T|Pantoea vagans
LMG 2665T|Pantoea ananatis
LMG 2632T|Pantoea stewartii ssp. indologenes
LMG 1286T|Pantoea agglomerans
LMG 24200T|Pantoea deleyi
LMG 2715T|Pantoea stewartii ssp. stewartii
LMG 22050T|Tatumella punctata
LMG 22051T|Tatumella terrea
LMG 7888T|Tatumella ptyseos
LMG 22049T|Tatumella citrea
LMG 23360T|Tatumella morbirosei