Pantoea vagans sp. nov., *Pantoea eucalypti* sp. nov., *Pantoea deleyi* sp. nov. and *Pantoea anthophila* sp. nov.

Carrie L. Brady,¹ Stephanus N. Venter,¹ Ilse Cleenwerck,²
Katrien Engelbeen,² Marc Vancanneyt,² Jean Swings²
and Teresa A. Coutinho¹

Correspondence

Teresa A. Coutinho

teresa.coutinho@up.ac.za

¹Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

²BCCM/LMG Bacteria Collection, Ghent University, K. L. Ledeganckstraat 35, B-9000 Ghent, Belgium

Bacteria isolated from eucalyptus leaves and shoots showing symptoms of blight and die-back collected in Uganda, Uruguay and Argentina and from maize displaying brown stalk rot symptoms in South Africa were tentatively placed in the genus *Pantoea* on the basis of phenotypic and biochemical tests. These isolates, together with two strains (LMG 2558 and LMG 2560) previously assigned to *Pantoea agglomerans* based on protein electrophoregrams but later excluded from this species, were further investigated using molecular techniques. 16S rRNA gene sequencing and multilocus sequence analyses (MLSA) revealed that the strains were phylogenetically closely related to *Pantoea agglomerans*, *Pantoea stewartii* and *Pantoea ananatis*. MLSA and amplified fragment length polymorphism analysis placed the strains into four separate clusters, not containing any of the type strains of species of the genus *Pantoea*. DNA–DNA hybridization confirmed the classification of the isolates into four novel species, for which the names *Pantoea vagans* sp. nov. (type strain R-21566^T = LMG 24199^T = BCC 105^T = BD 765^T), *Pantoea eucalypti* sp. nov. (type strain R-25678^T = LMG 24197^T = BCC 076^T = BD 769^T), *Pantoea deleyi* sp. nov. (type strain R-31523^T = LMG 24200^T = BCC 109^T = BD 767^T) and *Pantoea anthophila* sp. nov. (type strain LMG 2558^T = BD 871^T = NCPPB 1682^T) are proposed.

The genus *Pantoea* was described to include several species belonging to the ‘*Erwinia herbicola*–*Enterobacter agglomerans*’ complex (Gavini *et al.*, 1989). Presently, the genus comprises seven species with validly published names: *Pantoea agglomerans* and *Pantoea dispersa* (Gavini *et al.*, 1989), *Pantoea citrea*, *Pantoea punctata* and *Pantoea terrea* (Kageyama *et al.*, 1992) and *Pantoea ananatis* and *Pantoea stewartii* (Mergaert *et al.*, 1993). Strains of *Pantoea* are diverse in their origin and geographical spread, and have been isolated from plants as well as from clinical samples.

Abbreviations: AFLP, amplified fragment length polymorphism; MLSA, multilocus sequence analysis.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of *P. eucalypti* R-25678^T (=LMG 24197^T), *P. anthophila* LMG 2558^T, *P. deleyi* R-31523^T (=LMG 24200^T) and *P. vagans* R-21566^T (=LMG 24199^T) are EF688009–EF688012, respectively, and those of strains LMG 5345, LMG 5343, LMG 2781 and R-35496 are respectively EU216734–EU216737.

Detailed DNA–DNA hybridization results and a UPGMA dendrogram based on AFLP analysis are available as supplementary material with the online version of this paper.

P. ananatis is the causal agent of bacterial blight and die-back of eucalyptus in South Africa (Coutinho *et al.*, 2002). In 2001, *Pantoea*-like strains were isolated from eucalyptus trees exhibiting a similar disease in Uganda, Argentina and Uruguay and were thought to belong to *P. ananatis*. *P. ananatis* was also found to cause brown stalk rot of maize in South Africa (Goszczyńska *et al.*, 2007). Isolated simultaneously with *P. ananatis* from maize were additional *Pantoea*-like strains which also caused brown stalk rot. Multilocus sequence analysis (MLSA) has been shown to separate the isolates from eucalyptus and maize into three clusters, indicating that these strains probably constitute three novel species of *Pantoea* (Brady *et al.*, 2008). Also included in the MLSA study were two strains, LMG 2558 (=NCPBP 1682) and LMG 2560 (=NCPBP 1941), mentioned by Beji *et al.* (1988) as belonging to protein profiling group VII, which were assigned to *P. agglomerans* based on their electrophoregrams, despite never being included in DNA–DNA hybridization experiments with the type strain of *P. agglomerans*. It was suggested by Gavini *et al.* (1989) that strains of protein

Table 1. Strains used in this study

Abbreviations: LMG, BCCM/LMG Bacteria Collection, Ghent University, Belgium; BCC, Bacterial Culture Collection, Forestry and Agricultural Biotechnology Institute, Pretoria, South Africa; BD, Plant Pathogenic and Plant Protecting Bacteria (PPPPB) Culture Collection, ARC-PPRI, Pretoria, South Africa; CDC, Centers for Disease Control, Atlanta, GA, USA; NCPPB, National Collection of Plant Pathogenic Bacteria, York, UK.

Strain	Source	Location
<i>Pantoea agglomerans</i> (Br HG XIII)*		
LMG 1286 ^T	Clinical	Zimbabwe
LMG 2565	Cereal	Canada
LMG 2596	Onion	South Africa
LMG 2660	<i>Wisteria floribunda</i>	Japan
<i>Pantoea ananatis</i> (Br HG VI)*		
LMG 2665 ^T	Pineapple	Brazil
LMG 20103	Eucalyptus	South Africa
LMG 24190	Onion	South Africa
<i>Pantoea stewartii</i> subsp. <i>stewartii</i>		
LMG 2715 ^T	Maize	USA
LMG 2718	Maize	USA
<i>Pantoea stewartii</i> subsp. <i>indologenes</i>		
LMG 2632 ^T	Fox millet	India
LMG 2673	Pineapple	Hawaii, USA
<i>Pantoea dispersa</i> (Br HG III)*		
LMG 2603 ^T	Soil	Japan
LMG 2602	Sorghum	India
LMG 2604	Wild rose	Netherlands
<i>Pantoea citrea</i>		
LMG 22049 ^T	Mandarin orange	Japan
<i>Pantoea punctata</i>		
LMG 22050 ^T	Mandarin orange	Japan
LMG 23562	Mandarin orange	Japan
<i>Pantoea terrea</i>		
LMG 22051 ^T	Soil	Japan
LMG 23564	Soil	Japan
<i>Pantoea anthophila</i> sp. nov. (MLSA group C)		
LMG 2558 ^T = BD 871 ^T = NCPPB 1682 ^T	<i>Impatiens balsamina</i>	India
LMG 2560 = NCPPB 1941	<i>Tagetes erecta</i>	Unknown
<i>Pantoea vagans</i> sp. nov. (MLSA group A)		
BCC 105 ^T = LMG 24199 ^T = BD 765 ^T	Eucalyptus	Uganda
BCC 013 = LMG 24195	Eucalyptus	Uruguay
BCC 015 = LMG 24196	Eucalyptus	Argentina
BD 639 = LMG 24201	Maize	South Africa
BCC 081	Eucalyptus	Uruguay
BCC 072	Eucalyptus	Uruguay
BCC 208	Eucalyptus	Uganda
<i>Pantoea eucalypti</i> sp. nov. (MLSA group B)		
BCC 076 ^T = LMG 24197 ^T = BD 769 ^T	Eucalyptus	Uruguay
BCC 077 = LMG 24198	Eucalyptus	Uruguay
<i>Pantoea deleyi</i> sp. nov. (MLSA group D)		
BCC 109 ^T = LMG 24200 ^T = BD 767 ^T	Eucalyptus	Uganda
<i>Pantoea</i> sp. (Br HG II, MLSA group H)		
LMG 5345 ^R = CDC 3123-70 ^{R†}	Clinical	USA
LMG 24526 = CDC 238-70	Clinical	USA
<i>Pantoea</i> sp. (Br HG IV, MLSA group I)		
LMG 2781 ^R = CDC 1741-71 ^{R†}	Clinical	USA
LMG 24529 = CDC 3638-70	Clinical	USA
<i>Pantoea</i> sp. (Br HG V, MLSA group E)		
LMG 5343 ^R = CDC 3482-71 ^{R†}	Clinical	USA
LMG 24532 = CDC 2928-68	Clinical	USA
<i>Pantoea</i> sp. (Br HG V, MLSA group F)*		
LMG 24534 ^R = CDC 3527-71 ^{R†}	Clinical	USA

Table 1. cont.

†Reference strain.

*Br HG, Brenner hybridization group.

profiling group VII should be excluded from *P. agglomerans*, but that they should be included provisionally in *Pantoea* until their correct classification was determined. The MLSA results (Brady *et al.*, 2008) indicated that strains LMG 2558 and LMG 2560 of Beji protein profiling group VII constitute another novel species belonging to *Pantoea*, as recommended by Gavini *et al.* (1989).

Isolation of strains

Isolates were obtained from eucalyptus leaves showing typical bacterial blight symptoms including leaf spots and water-soaked lesions. The leaves were surface-sterilized and crushed in sterile water and the resulting suspension was streaked on nutrient agar and incubated at 30 °C for 3 days. Single colonies were obtained by restreaking and incubation under the same conditions. Isolates from diseased maize plants were received from Dr T. Goszczynska (Plant Protection Research Institute, South Africa) (Goszczynska *et al.*, 2007). Additional strains used in this study were obtained from the BCCM/LMG Bacteria Collection (<http://www.belspo.be/bccm>) and the Centers for Disease Control, Atlanta, GA, USA. The strains used in this study are listed in Table 1.

Amplified fragment length polymorphism (AFLP) analysis

Genomic DNA was extracted from all strains using the DNeasy Tissue kit (Qiagen). AFLP analysis was performed according to the method described previously (Brady *et al.*, 2007) using the selective primer combination Eco-C/Mse-GC. Band patterns were analysed with BioNumerics 4.0 (Applied Maths) and compared with a database containing profiles of reference strains of all *Pantoea* species with validly published names. A UPGMA dendrogram was constructed using Pearson's correlation coefficient. The isolates from eucalyptus and maize were divided into three clusters by AFLP analysis and the two strains from the study of Beji *et al.* (1988) formed a separate cluster (see Supplementary Fig. S1, available in IJSEM Online). These AFLP clusters did not contain any reference strains, suggesting that the strains belonged to novel species.

16S rRNA gene sequencing

Almost-complete 16S rRNA gene sequences were determined for selected strains from each AFLP cluster using the primers and conditions described by Coenye *et al.* (1999). The sequences were aligned using CLUSTAL_X (Thompson *et al.*, 1997) and overhangs were trimmed. The program MODELTEST 3.7 (Posada & Crandall, 1998) was then applied to the datasets 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 on the trees to assess the reliability of the clusters. The 16S rRNA gene sequence similarity of strains of the four novel species was greater than 98% to *P. agglomerans*, *P. ananatis*, *P. stewartii* and *P. dispersa*. In the 16S rRNA gene phylogenetic tree, the four novel species cluster within the *Pantoea* 'core' group, each on a separate branch, along with *P. agglomerans*, *P. stewartii* and *P. ananatis* (Fig. 1). The bootstrap support within the *Pantoea* cluster was generally quite low, although this can be explained by the high level of homoplasy in the 16S rRNA gene sequences of members of the *Enterobacteriaceae* (Stephan *et al.*, 2007). *Pantoea* has also been shown to be polyphyletic, making it difficult to resolve taxonomic issues within the genus (Brady *et al.*, 2008).

gyrB, *rpoB*, *atpD* and *infB* sequences

In order to provide stronger support for the description of the four novel *Pantoea* species, MLSA based on *gyrB*, *rpoB*, *atpD* and *infB* gene sequences was performed on the strains (Brady *et al.*, 2008). Sequence analysis and tree construction was performed as described above. MLSA revealed that the isolates from eucalyptus and maize and the strains from Beji protein profiling group VII form four well-supported clusters in the concatenated tree (Fig. 2), which were referred to as MLSA groups A, B, C and D (Brady *et al.*, 2008). The four novel species could also be differentiated clearly from Brenner's hybridization groups II, IV and V (Brenner *et al.*, 1984), referred to as MLSA groups E, F, H and I in the *Pantoea* MLSA study (Brady *et al.*, 2008) (Figs 1 and 2) and belonging to *Pantoea* according to Grimont & Grimont (2005).

DNA–DNA hybridizations

High-quality DNA for DNA–DNA hybridization 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 ± 1 °C. Reciprocal reactions (A × B and B × 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 MLSA groups

A, B, C and D were selected and hybridized to the type strains of *P. agglomerans* (LMG 1286^T), *P. ananatis* (LMG 2665^T), *P. stewartii* (LMG 2715^T) and *P. dispersa* (LMG 2603^T) and among each other. DNA–DNA hybridization was also performed with strains from other species of the genus *Pantoea* with validly published names as well as with strains of Brenner's hybridization groups II, IV and V. These results are available in Supplementary Table S1. The level of DNA–DNA binding between representative strains of MLSA groups A–D and the type strain of *P. agglomerans* was less than 68 %, less than 30 % to the type strains of *P. ananatis* and *P. dispersa* and less than 15 % to the type strain of *P. stewartii*. The strains of MLSA groups A–D exhibited less than 44 % DNA relatedness when hybridized to strains from Brenner's hybridization groups II, IV and V. When seven strains from MLSA group A, isolated from eucalyptus and maize, were hybridized with each other (LMG 24199^T, LMG 24195, LMG 24196, LMG 24201, BCC 072, BCC 081 and BCC 427), they exhibited levels of DNA relatedness ranging from 83 to 103 % (data presented in part in Supplementary Table S1). The hybridization values between strains LMG 24197^T and LMG 24198 (MLSA group B), also isolated from eucalyptus, and LMG 2558^T and LMG 2560 (MLSA group C) were even higher, at 99 and 105 %, respectively.

DNA G+C content

The ranges of G+C content of DNA of the four novel species, determined by HPLC (Mesbah *et al.*, 1989), are as

Fig. 1. Maximum-likelihood tree based on 16S rRNA gene sequences of *Pantoea* strains. Bootstrap values after 1000 replicates are expressed as percentages. The sequence of *Pectobacterium carotovorum* LMG 2404^T was included as an outgroup. Bar, fraction of substitutions per site.

follows: MLSA group A (LMG 24199^T, LMG 24195, LMG 24196, LMG 24201, BCC 072, BCC 081 and BCC 427), 55.2–55.8 mol%; MLSA group B (LMG 24197^T and LMG 24198), 54.3–54.5 mol%; MLSA group D (LMG 24200^T), 58.6 mol%; and MLSA group C (LMG 2558^T and LMG 2560), 57.4–57.5 mol%.

Phenotypic assays

Physiological and biochemical tests were performed on selected isolates using API 20E, API 50CHB/E and Biotype-100 strips (bioMérieux) as well as Biolog GN plates. The samples were observed for 6 days, although the majority of reactions occurred after 3 days. Results are given in the species descriptions. The four novel species can be differentiated from their closest phylogenetic neighbours by their ability to utilize L-ornithine (differentiation from *P. agglomerans*, *P. ananatis*, *P. dispersa* and *P. stewartii*), Tweens 40 and 80 (differentiation from *P. agglomerans*, *P. ananatis* and *P. dispersa*) and L-tartrate (differentiation from *P. agglomerans*, *P. stewartii* and *P. anthophila*) and by their inability to utilize lactose (differentiation from *P. ananatis*, *P. dispersa*, *P. stewartii* and *P. eucalypti*). The following characteristics can be used to differentiate the four novel species from each other: utilization of D-

Fig. 2. Maximum-likelihood tree based on concatenated *gyrB*, *rpoB*, *atpD* and *infB* sequences of selected *Pantoea* strains. Bootstrap values after 1000 replicates are expressed as percentages. Sequences from *Shigella dysenteriae* M131649 were obtained from the genome sequencing database of the Sanger Institute (<http://www.sanger.ac.uk>) and included as an outgroup. Bar, fraction of substitutions per site.

arabitol, gentiobiose, 5-ketogluconate, lactose, malonic acid and L-pyroglutamic acid. A summary of the most distinguishing phenotypic characteristics from the Biotype-100 and Biolog systems, which can differentiate the four novel species from their closest phylogenetic neighbours and each other, is presented in Table 2.

Conclusions

The data presented in this study indicate that the strains isolated from eucalyptus and maize and the strains from protein profiling group IV (Beji *et al.*, 1988) form four distinct genetic groups. These genetic groups are supported by AFLP, nucleotide sequence analysis and DNA–DNA hybridization values. The DNA–DNA relatedness between strains of *P. agglomerans* and MLSA group A (*Pantoea vagans* sp. nov.) may be considered borderline, as the values are just below the recommended species demarcation of 70% (Wayne *et al.*, 1987). However, both 16S rRNA gene sequencing and MLSA support the phylogenetic delineation of *P. vagans* from *P. agglomerans*. Past studies have highlighted the difficulties in identifying *Pantoea* strains based on phenotypic data (Beji *et al.*, 1988; Brenner *et al.*, 1984; Mergaert *et al.*, 1984; Verdonck *et al.*, 1987), and it has been suggested that caution be exercised when basing identification solely on commercial phenotypic identification systems (Gavini *et al.*, 1989). Despite the high phenotypic similarity within the genus *Pantoea*, several biochemical characteristics were recognized that could distinguish the four novel species from each other and from their closest phylogenetic neighbours. Therefore, we propose to classify the four novel species identified in this study as *Pantoea vagans* sp. nov. (MLSA group A) for strains isolated from eucalyptus and maize, *Pantoea eucalypti* sp. nov. (MLSA group B) for strains

isolated from eucalyptus in Uruguay, *Pantoea deleyi* sp. nov. (MLSA group D) for the strain isolated from eucalyptus in Uganda and *Pantoea anthophila* sp. nov. (MLSA group C) for the two strains belonging to Beji protein profiling group VII (Brady *et al.*, 2008).

Description of *Pantoea vagans* sp. nov.

Pantoea vagans (va'gans. L. part. adj. *vagans* roaming, referring to the wide distribution of the species).

Cells are Gram-negative, short rods ($0.9 \times 1.5\text{--}3.0\ \mu\text{m}$) occurring singly or in pairs, motile and non-spore-forming. Colonies are beige to yellow, round, convex and smooth with entire margins. Facultatively anaerobic and oxidase-negative. Acetoin and β -galactosidase are produced. Indole, H_2S and urease are not produced. Acid is produced from L-arabinose, D-ribose, D-xylose, L-rhamnose, inositol, D-mannitol, N-acetylglucosamine, lactose (weak), sucrose, D-lyxose and D-fucose. The following carbon sources are utilized at $28\ ^\circ\text{C}$ within 3–6 days: L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, maltotriose, L-rhamnose, inositol, aesculin, D-mannitol, maltose, trehalose, cellobiose, sucrose, glycerol, L-tartrate, succinate, fumarate, L-aspartate, L-glutamate, *cis*- and *trans*-aconitate, L-proline, D- and L-alanine, L-serine, malonic acid, Tweens 40 and 80, D-lyxose (weak), gentiobiose (weak) and citric acid (weak). The following carbon sources are not utilized at $28\ ^\circ\text{C}$ within 3–6 days: erythritol, D-adonitol, L-sorbose, dulcitol, D-sorbitol, amygdalin, inulin, raffinose, lactose, lactulose, glycogen, xylitol, turanose, D-tagatose, L-arabitol, 2-ketogluconate, 5-ketogluconate, L-fucose, 3-O-methyl-D-glucopyranose, D-tartrate, L-tryptophan, L-histidine, glutarate, malonate, propionate and L-tyrosine. The G + C content of the type strain is 55.4 mol%.

Table 2. Characteristics that distinguish the novel species from each other and from their closest phylogenetic neighbours

Species/subspecies: 1, *P. agglomerans* (3 strains); 2, *P. ananatis* (4); 3, *P. dispersa* (1); 4, *P. stewartii* subsp. *stewartii* (1); 5, *P. stewartii* subsp. *indologenes* (1); 6, *P. vagans* sp. nov. (7); 7, *P. eucalypti* sp. nov. (2); 8, *P. deleyi* sp. nov. (1); 9, *P. anthophila* sp. nov. (2). +, 90–100% of strains positive in 3–6 days; (+), weakly positive; –, 90–100% of strains negative; ND, not determined. Additional phenotypic data were obtained from Grimont & Grimont (2005).

Characteristic	1	2	3	4	5	6	7	8	9
Indole production	–	+	–	–	+	–	–	–	–
Utilization of:									
D-Arabitol	+	+	+	ND	+	–	–	+	+
Gentiobiose	–	+	+	–	+	(+)	–	+	–
5-Ketogluconate	–	+	+	–	+	(+)	–	–	–
Lactose	–	+	+	–	+	–	+	–	–
Malonic acid	–	–	–	ND	–	+	–	+	+
L-Ornithine	–	–	–	ND	–	+	+	+	+
L-Pyroglutamic acid	–	–	–	ND	–	–	+	+	–
L-Tartrate	–	+	+	–	–	+	+	+	–
Tween 40	–	–	–	ND	+	+	+	+	+
Tween 80	–	–	–	ND	+	+	+	+	+

The type strain is R-21566^T (=LMG 24199^T =BCC 105^T =BD 765^T), isolated from eucalyptus in Uganda. Strains belonging to this species have been isolated from eucalyptus leaves showing symptoms of bacterial blight and die-back in Uganda, Uruguay and Argentina and from maize suffering from brown stalk rot in South Africa.

Description of *Pantoea eucalypti* sp. nov.

Pantoea eucalypti (eu.ca.lyp'ti. N.L. gen. n. *eucalypti* of *Eucalyptus*, referring to the host from which the first strains where isolated).

Cells are Gram-negative, short rods ($0.9 \times 1.5\text{--}3.0\ \mu\text{m}$) occurring singly or in pairs, motile and non-spore-forming. Colonies are beige to yellow with a darker centre, round, convex and smooth with entire margins. Facultatively anaerobic and oxidase-negative. Acetoin and β -galactosidase are produced. Indole, H₂S and urease are not produced. Acid is produced from L-arabinose, D-ribose, D-xylose, L-rhamnose, inositol, D-mannitol, *N*-acetylglucosamine, lactose and sucrose. The following carbon sources are utilized at 28 °C within 3–6 days: L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, maltotriose, L-rhamnose, inositol, aesculin, D-mannitol, maltose, trehalose, cellobiose, lactose, sucrose, glycerol, L-pyrogutamic acid, L-tartrate, succinate, fumarate, L-aspartate, L-glutamate, *cis*- and *trans*-aconitate, L-proline, D- and L-alanine, L-serine, Tweens 40 and 80 and citric acid. The following carbon sources are not utilized at 28 °C within 3–6 days: erythritol, D-adonitol, L-sorbose, dulcitol, D-sorbitol, amygdalin, inulin, raffinose, glycogen, xylitol, turanose, D-tagatose, L-arabitol, 2-ketoglutarate, 5-ketogluconate, L-fucose, 3-*O*-methyl-D-glucopyranose, D-tartrate, L-tryptophan, L-histidine, glutamate, malonate, propionate, L-tyrosine, gentiobiose and malonic acid. The G+C content of the type strain is 54.5 mol%.

The type strain is R-25678^T (=LMG 24197^T =BCC 076^T =BD 769^T), isolated from eucalyptus in Uruguay. Strains belonging to this species have been isolated from eucalyptus leaves showing symptoms of bacterial blight and die-back in Uruguay.

Description of *Pantoea deleyi* sp. nov.

Pantoea deleyi (de.ley'i. N.L. masc. gen. n. *deleyi* of De Ley, named for Jozef De Ley, who contributed to the formation of the genus *Pantoea*).

Cells are Gram-negative, short rods ($0.9 \times 1.5\text{--}3.0\ \mu\text{m}$) occurring singly or in pairs, motile and non-spore-forming. Colonies are beige to yellow, round, convex and smooth with entire margins. Facultatively anaerobic and oxidase-negative. Acetoin and β -galactosidase are produced. Indole, H₂S and urease are not produced. Acid is produced from D- and L-arabinose, D-ribose, D-xylose, L-rhamnose, D-mannitol, *N*-acetylglucosamine, gentiobiose,

sucrose, D-lyxose, D-fucose and D-arabitol. The following carbon sources are utilized at 28 °C within 3–6 days: L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, maltotriose, L-rhamnose, aesculin, D-mannitol, turanose, maltose, trehalose, sucrose, glycerol, L-pyrogutamic acid, inositol, succinate, fumarate, L-aspartate, L-glutamate, L-tartrate, *cis*- and *trans*-aconitate, L-proline, D- and L-alanine, L-serine, malonic acid, Tweens 40 and 80, D-lyxose, D-arabitol, gentiobiose and citric acid. The following carbon sources are not utilized at 28 °C within 3–6 days: erythritol, D-adonitol, cellobiose, lactose, lactulose, L-sorbose, dulcitol, D-sorbitol, amygdalin, inulin, raffinose, glycogen, xylitol, D-tagatose, L-arabitol, gluconate, 2-ketoglutarate, 5-ketogluconate, L-fucose, 3-*O*-methyl-D-glucopyranose, D-tartrate, L-tryptophan, L-histidine, glutamate, malonate, propionate and L-tyrosine. The G+C content of the type strain is 58.6 mol%.

The type strain is R-31523^T (=LMG 24200^T =BCC 109^T =BD 767^T), isolated from eucalyptus leaves showing symptoms of bacterial blight and die-back in Uganda.

Description of *Pantoea anthophila* sp. nov.

Pantoea anthophila (an.tho'phi.la. Gr. n. *anthos* flower; Gr. adj. *philos* loving; N.L. fem. adj. *anthophila* flower-loving, pertaining to the source of isolation of known strains).

Cells are Gram-negative, short rods ($0.9 \times 1.2\text{--}2.5\ \mu\text{m}$) occurring singly or in pairs, motile and non-spore-forming. Colonies are beige to yellow, round, convex and smooth with entire margins. Facultatively anaerobic and oxidase-negative. Acetoin and β -galactosidase are produced. Indole, H₂S and urease are not produced. Acid is produced from L-arabinose, D-ribose, D-xylose, L-rhamnose, inositol, D-mannitol, *N*-acetylglucosamine, sucrose and D-arabitol. The following carbon sources are utilized at 28 °C within 3–6 days: L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, maltotriose, L-rhamnose, inositol, aesculin, glycogen, D-lyxose, D-mannitol, maltose, trehalose, cellobiose, sucrose, glycerol, succinate, fumarate, L-aspartate, L-glutamate, *cis*- and *trans*-aconitate, L-proline, D- and L-alanine, L-serine, malonic acid, Tweens 40 and 80 and citric acid. The following carbon sources are not utilized at 28 °C within 3–6 days: erythritol, D-adonitol, L-sorbose, dulcitol, D-sorbitol, amygdalin, inulin, raffinose, lactose, lactulose, xylitol, turanose, D-tagatose, L-arabitol, L-tartrate, 2-ketoglutarate, 5-ketogluconate, L-fucose, 3-*O*-methyl-D-glucopyranose, D-tartrate, L-tryptophan, L-histidine, glutamate, malonate, propionate, gentiobiose and L-tyrosine. The G+C content of the type strain is 57.5 mol%.

The type strain is LMG 2558^T (=BD 871^T =NCPBP 1682^T), isolated from *Impatiens balsamina* in India. Strains belonging to this species have been isolated from flowering shrubs.

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