

# Register list for 16 new names including *Pantoea alvi* sp. nov.

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**Table 1:** Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Pantoea rara</i>	[ra'ra] L. <b>fem. adj.</b> <i>rara</i> , sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species	This species consists of the genomes of strain WMus005, isolated from the oral cavity of a wild house mouse ( <i>Mus musculus</i> ) in the United Kingdom, and the metagenome-assembled genome (MAG) UBA5707 recovered from a metagenomic sample taken from the New York City subway system. Pairwise ANI of the two genomes is over 99% and they thus clearly belong to the same species, with all comparisons to other species below species delineation guidelines. The nomenclatural type for the species is the genome UBA5707 <sup>Ts</sup> , available under the assembly accession number GCA_002419935.1.	<i>Pantoea</i>	NCBI Assembly: GCA_002419935.1 <sup>Ts</sup>	<a href="https://seqco.de/i:31356">seqco.de/i:31356</a>
Species <i>Pantoea astica</i>	[as.ti'ca] N.L. <b>fem. adj.</b> <i>astica</i> , of a city (from Gr. masc. adj. <i>astikós</i> , of a city) referring to the recovery of this organism from New York City, NY, USA	This species consists of a single MAG, UBA6564, which was assembled from a metal surface in New York City. <i>P. conspicua</i> is the most closely related known species, and the ANI between <i>P. astica</i> UBA6564 and the <i>P. conspicua</i> type strain is below 95% confirming that this genome represents a separate species.	<i>Pantoea</i>	NCBI Assembly: GCA_002434205.1 <sup>Ts</sup>	<a href="https://seqco.de/i:31358">seqco.de/i:31358</a>
Species <i>Pantoea borealis</i>	[bo.re.a'lis] L. <b>fem. adj.</b> <i>borealis</i> , pertaining to the North, boreal	At least four genomes are available for this species. One genome is of the strain Russ isolated from an indoor trash can in Stillwater, Oklahoma, USA. The other three genomes are MAGs derived from environmental samples of metallic or plastic surfaces on the New York City subway. Pairwise ANI among the 4 genomes is over 99.25% revealing that they belong to a single clonal lineage. The <i>P. borealis</i> clade shares an most recent common ancestor with <i>P. eucrina</i> , and the ANI between genomes of the <i>P. eucrina</i> and this species is approximately 93%. One publication on a representative genome of this species cluster is available and discusses its potential for being an opportunistic human pathogen (Moghadam et al. 2016), however, evidence for pathogenicity isn't available. The nomenclatural type for the species is the MAG UBA6694 <sup>Ts</sup> , available under the GenBank assembly accession number GCA_002454735.1.	<i>Pantoea</i>	NCBI Assembly: GCA_002454735.1 <sup>Ts</sup>	<a href="https://seqco.de/i:31361">seqco.de/i:31361</a>

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Species <i>Pantoea superficialis</i>	[su.per.fi.ci.a'lis] L. fem. adj. <i>superficialis</i> , of or pertaining to a surface	This species consists of two MAGs, UBA2655 and UBA648, both assembled from a metagenome sampled from a metallic or plastic surface in New York City, USA. It shares an most recent common ancestor with the GTDB taxon " <i>Pantoea mediterraneensis</i> " Marseille-P5165. The ANI between MAG UBA648 and Marseille-P5165 is below 85% showing that they clearly represent two distinct species. The nomenclatural type for this species is the genome UBA648, available under GenBank assembly accession number GCA_002299595.1.	<i>Pantoea</i>	NCBI Assembly: GCA_002299595.1 Ts	<a href="https://seqco.de/i:31371">seqco.de/i:31371</a>
Species <i>Pantoea deserta</i>	[de.ser'ta] L. fem. part. adj. <i>deserta</i> , deserted, or alone, referring to the species being a sole representative at the time of description	This species includes the genome of a single strain, RIT388, isolated from an Ayan tree ( <i>Distemonanthus benthamianus</i> ) known for its antifungal and antibacterial properties (Soutar and Stavrinos 2019), (Gan et al. 2020). This genome is located on the branch splitting off at the most basal node of the clade that includes <i>P. septica</i> , <i>P. alvi</i> , <i>P. piersonii</i> , and " <i>P. latae</i> ".	<i>Pantoea</i>	NCBI Assembly: GCF_003813865.1 Ts	<a href="https://seqco.de/i:31370">seqco.de/i:31370</a>
Species <i>Pantoea varia</i>	[va'ri.a] L. fem. adj. <i>varia</i> , varied, corresponding to the varying sources of isolation for members of this species	This species consists of the genomes of two strains: OV426, isolated during characterization of <i>Populus</i> root and rhizosphere microbial communities in Tennessee, USA, and AF015A5, isolated from an indoor dust sample in Oregon, USA (GCF_004798195.1). The two genomes have a pairwise ANI of approximately 97% and thus clearly belong to the same species. The genome of strain OV426 does not contain the enterobactin biosynthesis cluster, while it does contain the pagRI genes encoding the autoinducer system (Sulja et al. 2022). This strain also contains a Hrp-2a T3SS, but its functionality has not been examined (Moretti et al. 2021). The nomenclatural type for the species is the genome of OV426 <sup>Ts</sup> , available under the NCBI assembly accession number GCF_900115075.1.	<i>Pantoea</i>	NCBI Assembly: GCF_900115075.1 Ts	<a href="https://seqco.de/i:31357">seqco.de/i:31357</a>
Species <i>Pantoea symbiotica</i>	[sym.bi.o'ti.ca] N.L. fem. adj. <i>symbiotica</i> , living together, symbiotic	This species includes nine genomes that belong to <i>P. symbiotica</i> sp. nov. The clade corresponding to this group is a sister clade of the " <i>P. endophytica</i> " clade. Pairwise ANI between the eight genomes is over 97%, while ANI between them and " <i>P. endophytica</i> " genomes, which represent the most closely related known species, is approximately 93%, showing that these strains do in fact represent a separate species. The strains were isolated from poplar ( <i>Populus deltoides</i> ) roots along the Caney Fork River in Tennessee, USA; Eastern cottonwood poplar roots on the Yadkin River in North Carolina, USA (Brown et al. 2012); from fungi in New York State, USA (Wong et al. 2020); and as endophytes of grapevine. Based on these isolation sources, this species appears to be adapted to the rhizosphere. The nomenclatural type for the species is the genome of strain YR512 <sup>Ts</sup> , available under the GenBank assembly accession number GCF_900114175.1.	<i>Pantoea</i>	NCBI Assembly: GCF_900114175.1 Ts	<a href="https://seqco.de/i:31363">seqco.de/i:31363</a>

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Species <i>Pantoea floridensis</i>	[flo.ri.den'sis] <b>N.L. fem. adj.</b> <i>floridensis</i> , of or from Florida, referring to where this organism was isolated from	The species consists of the genome of a single strain, JKS000234. Its source of isolation is a fungus-farming ant garden in Wekiwa Springs State Park, Apopka, Florida. This species shares a most recent common ancestor with <i>P. variicola</i> sp. nov. The ANI between the genomes of the two species is below 90%.	<i>Pantoea</i>	NCBI Assembly: GCA_900215435.1 Ts	<a href="https://seqco.de/i:31365">seqco.de/i:31365</a>
Species <i>Pantoea alvi</i>	[al'vi] <b>L. gen. n.</b> <i>alvi</i> , of the bowels, referring to the putative association of this species with the gastrointestinal tract of humans	This species comprises two genomes, PSNIH6 and UMGS54. The corresponding clade is a sister-clade of <i>P. septica</i> . PSNIH6, the strain whose genome serves as nomenclatural type, was isolated from hospital plumbing in the USA, while MAG UMGS54 was assembled from the metagenome of a human gut sample. The two genomes have a pairwise ANI of over 99.75%. Therefore, <i>P. alvi</i> sp. nov. may occupy a similar ecological niche to its sister species <i>P. septica</i> . The genome of PSNIH6 <sup>Ts</sup> is the nomenclatural type for the species.	<i>Pantoea</i>	NCBI Assembly: GCF_002920175.1 Ts	<a href="https://seqco.de/i:31369">seqco.de/i:31369</a>
Species <i>Pantoea gossypiicola</i>	[gos.sy.pi.i.co'la] <b>N.L. neut. n.</b> <i>Gossypium</i> , the scientific botanical genus name for cotton; <b>L. fem. n. suff.</b> <i>-cola</i> , inhabitant, dweller; <b>N.L. fem. n.</b> <i>gossypiicola</i> , inhabitant of <i>Gossypium</i> , referring to the isolation source of the strain for the designated nomenclatural type, from the leaves of cotton plants	Based on the BioSample metadata available for genomes in this group, all strains of this species were recovered as epiphytes from diseased cotton leaves ( <i>Gossypium hirsutum</i> ), from the Punjab province of Pakistan. This species is supported as distinct and exclusive through phylogenomics and is supported by the GTDB. The minimum pairwise ANI of genomes within this species is 99.25% and the ANI to the most similar genomes outside of the species is approximately 94%. Three clonal lineages can be distinguished based on phylogeny and ANI. However, based on reverse ecology analysis using PopCOGenT, all strains of the species cluster belong to the same population suggesting that the clonal lineages have not adapted to separate ecological niches. The nomenclatural type for the species is the genome of strain B-8 <sup>Ts</sup> , available under the GenBank assembly accession number GCA_008632075.1.	<i>Pantoea</i>	NCBI Assembly: GCF_008632075.1 Ts	<a href="https://seqco.de/i:31355">seqco.de/i:31355</a>

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Species <i>Pantoea communis</i>	[com.mu'nis] L. <b>fem. adj.</b> <i>communis</i> , common or widespread, referring to the broad global distribution of members of this species	This species consists of seven genome-sequenced strains. The genomes are monophyletic with phylogenomic analyses. This clade shares an ancestor with the genomes of the GTDB species " <i>Pantoea rwandensis_B</i> ". The minimal pairwise ANI among the seven genomes is as low as 97%. ANI between the seven genomes and the closest relative is approximately 94%, showing that the two clades represent two different, but closely related, species. Isolation sources include insects, like stink bugs ( <i>Plautia stali</i> , <i>Sibaria englemani</i> , <i>Taurocerus</i> sp.), and an ant ( <i>Atta laevigata</i> ) fungus garden, as well as plants ( <i>Garcinia morella</i> ) and other environmental sources. Overall, this species shares plants and insects as isolation sources with many other <i>Pantoea</i> species, and no adaptation to any specific environment is evident.	<i>Pantoea</i>	NCBI Assembly: GCF_011752685.1 Ts	<a href="https://seqco.de/i:31366">seqco.de/i:31366</a>
Species <i>Pantoea formicae</i>	[for'mi.cae] N.L. <b>gen. n.</b> <i>formicae</i> , of an ant	This species is represented by the genome of a single strain, Acro-805, isolated from the fungal garden of an ant belonging to the genus <i>Acromyrmex</i> , in Brazil. It shares an MRCA with the type strain of <i>P. rwandensis</i> LMG 26275 <sup>T</sup> . The pairwise ANI between the two strains is approximately 92% supporting the designation of this species as distinct and novel.	<i>Pantoea</i>	NCBI Assembly: GCF_011752625.1 Ts	<a href="https://seqco.de/i:31367">seqco.de/i:31367</a>
Species <i>Pantoea multigeneris</i>	[mul.ti.ge.ne'ris] L. <b>fem. adj.</b> <i>multigeneris</i> , multifarious, of different kinds or varied, referring to the varied sources of isolation of this organism	This species consists of the genomes of two strains, A4 and Acro-835, which have a pairwise ANI of approximately 96%, likely indicating higher genomic diversity within this species. Strain A4 was isolated from a decaying flower bud in Malaysia while strain Acro-835 was isolated from an ant ( <i>Acromyrmex</i> ) fungus garden in Brazil. This species splits off at a basal node within the <i>Pantoea</i> phylogeny, with lower than 80% ANI to the genomes of the closest known relatives. The nomenclatural type for the species is the genome of Acro-835 <sup>Ts</sup> , available under the GenBank assembly accession number GCF_011752615.1.	<i>Pantoea</i>	NCBI Assembly: GCF_011752615.1 Ts	<a href="https://seqco.de/i:31368">seqco.de/i:31368</a>
Species <i>Pantoea haifensis</i>	[hai.fen'sis] N.L. <b>fem. adj.</b> <i>haifensis</i> , of Haifa, Israel, where this organism was isolated from	This species currently consists of the genome of a single strain, EnvH, which was isolated from asphalt in Haifa, Israel. The pairwise ANI values between this species and the two closest relatives, GCF_018842675.1 and GCF_014946725.1, are below 80% confirming that this species is distinct from those with which it shares a most recent common ancestor.	<i>Pantoea</i>	NCBI Assembly: GCA_018842655.1 Ts	<a href="https://seqco.de/i:31360">seqco.de/i:31360</a>
Species <i>Pantoea bituminis</i>	[bi.tu.mi'nis] N.L. <b>gen. n.</b> <i>bituminis</i> , of bitumen, asphalt	This species currently consists of the genome of a single strain, EnvD, which was isolated from asphalt in Jerusalem, Israel. The most closely related species, named <i>Pantoea mediterraneensis_A</i> in GTDB (GCF_014946725.1) share an ANI value with EnvD below species delineation guidelines, revealing that the two genomes represent two distinct species.	<i>Pantoea</i>	NCBI Assembly: GCF_018842675.1 Ts	<a href="https://seqco.de/i:31359">seqco.de/i:31359</a>

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Species <i>Pantoea soli</i>	[so'li] L. <b>gen. n.</b> <i>soli</i> , of soil	The genome of a single strain, DSM 32899 was isolated from soil in Singapore. It splits off at a node that is basal to the <i>P. eucrina</i> / <i>P. borealis</i> group. The ANI between the genome of DSM 32899 and the <i>P. eucrina</i> / <i>P. borealis</i> genomes is below 85%, indicating that this represents a distinct species.	<i>Pantoea</i>	NCBI Assembly: GCF_007833795.1 <small>Ts</small>	<a href="https://seqco.de/i:31362">seqco.de/i:31362</a>