

**Phylogenomic resolution of the bacterial genus *Pantoea* and its
relationships with *Erwinia* and *Tatumella***

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Supplementary Table S1. Genome sequencing and assembly statistics

Statistic	<i>Pantoea allii</i> LMG 24248 T	<i>Pantoea breunneri</i> LMG 5343 T	<i>Pantoea calida</i> LMG 25383 T	<i>Pantoea conspicua</i> LMG 24534 T	<i>Pantoea cypripedii</i> LMG 2657 T	<i>Pantoea deleyi</i> LMG 24200 T	<i>Pantoea eucrina</i> LMG 5346 T	<i>Pantoea gaviniae</i> LMG 25382 T	<i>Pantoea rodasii</i> LMG 26273 T	<i>Pantoea rwandensis</i> LMG 26275 T	<i>Pantoea septica</i> LMG 5342 T	<i>Pantoea wallisii</i> LMG 26277 T
NCBI Taxon ID	574096	472694	665913	472705	55209	470932	472693	665914	1076549	1076550	472695	1076551
NCBI BioProject ID	PRJNA252983	PRJNA252984	PRJNA252985	PRJNA252986	PRJNA252995	PRJNA252987	PRJNA252988	PRJNA252989	PRJNA252990	PRJNA252996	PRJNA252991	PRJNA252993
Type strain	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Sequencing Centre	University of Pretoria Ion Torrent Sequencing Facility	University of Pretoria Ion Torrent Sequencing Facility	University of Pretoria Ion Torrent Sequencing Facility	University of Pretoria Ion Torrent Sequencing Facility	Agroscope Wädenswil	University of Pretoria Ion Torrent Sequencing Facility	University of Pretoria Ion Torrent Sequencing Facility	University of Pretoria Ion Torrent Sequencing Facility	University of Pretoria Ion Torrent Sequencing Facility	University of Pretoria Ion Torrent Sequencing Facility	Agroscope Wädenswil	University of Pretoria Ion Torrent Sequencing Facility
Sequencing status	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete
Sequence quality	Draft	Draft	Draft	Draft	Draft	Draft	Draft	Draft	Draft	Draft	Draft	Draft
Library method	316V2 chip single read	316D chip single read	316D chip single read	316D chip single read	454 Sequencing	316D chip single read	316D chip single read	316D chip single read	316D chip single read	316V2 chip single read	454 sequencing	316D chip single read
Number of reads	1,950,718	2,655,168	2,195,506	1,904,440	194,018	1,803,084	2,139,222	2,341,809	1,981,500	2,502,967	263,365	1,519,044
Assembly method	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.7	Newbler 2.5p1	Newbler 2.6
Sequencing depth	113x	44x	123x	88x	13x	79x	126x	126x	81x	155x	21.3x	29x
N50	144,674	50,025	36,326	60,215	292,024	30,022	77,198	14,407	379,375	277,599	103,648	57,032
largest contig size	341,617	145,502	121,085	243,574	994,488	84,071	276,365	70,048	830,902	995,595	229,615	152,472
Average contig size	70,480	24,848	17,056	37,434	107,433	14,287	40,091	7,381	78,729	134,304	48,413	32,752
Contig count	71	198	248	115	61	332	97	602	73	43	112	142
Estimated size (kb)	5,004,101	4,920,006	4,230,118	4,304,984	6,547,166	4,600,463	3,888,871	4,443,500	5,747,282	5,775,072	4,312,672	4,650,880
Accession	MLFE000000.1	MIEI000000.1	MLFO000000.1	MLFN000000.1	MLJI000000.1	MIP000000.1	MIPP000000.1	MLFQ000000.1	MLFP000000.1	MLFR000000.1	MLJJ000000.1	MLFS000000.1

Supplementary Table S2. Average Nucleotide Identity (ANI) values obtained from reciprocal analyses as calculated with blast in JSpecies.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	
1	---	90.31	90.66	86.79	87.96	85.3	84.36	78.79	78.16	78.87	78.73	79.79	77.02	77.82	77.56	78.83	77	76.99	78.06	78.12	78.22	76.3	72.6	72.57	72.28	71.71	75.58	76.47	75.56	74.13	73.53	75.31	74.9	75.02	75.01	75.03	74.53	74.91	75.93	
2	90.32	---	90	86.04	86.89	84.2	83.51	78.66	78.04	78.52	78.45	79.17	76.64	77.52	77.3	78.38	76.81	76.7	77.62	77.58	77.82	75.98	72.12	72.1	72.05	71.65	75.21	75.89	75.18	73.79	73.22	74.79	74.46	74.43	74.58	74.61	74.26	74.74	75.47	
3	90.66	89.86	---	86.44	87.56	84.7	83.92	78.79	78.1	78.81	78.75	79.76	76.87	77.72	77.53	78.75	78.08	77.03	78.01	77.97	78.13	76.2	72.55	72.55	72.16	71.67	75.65	76.31	75.39	74.11	73.49	75.2	74.96	74.89	74.91	74.56	74.83	75.75		
4	87.32	86.2	86.77	---	85.95	83.67	83.01	78.49	77.85	78.51	78.39	80.05	77.2	77.95	77.66	78.87	76.74	76.71	77.75	77.87	77.81	76.09	72.16	72.18	71.97	71.53	75.98	76.47	75.89	73.97	73.11	75.1	74.84	74.88	74.77	74.82	74.6	74.57	75.7	
5	88.03	86.94	87.65	85.84	---	84.38	83.61	78.97	78.19	78.9	78.9	80.72	77.23	78.07	77.83	78.92	76.94	77	77.96	78.02	78.18	76.32	72.53	72.56	72.3	71.66	75.86	76.77	75.85	74.28	73.62	75.33	75.15	75.12	75.06	75.1	74.63	74.88	75.92	
6	85.16	84.15	84.59	83.14	84.31	---	89.29	79.39	79.33	79.2	79.15	80.25	77.32	78.2	77.86	79.24	77.17	77.15	78.33	78.3	78.51	76.38	72.38	72.4	72.44	72.93	71.94	75.08	77.83	75.18	74.57	73.83	75.46	75.07	74.98	74.89	74.93	74.73	74.82	76.03
7	85.25	84.31	84.73	83.62	84.32	90.36	---	79.19	78.75	79.09	78.98	79.94	77.29	77.88	77.97	79.12	77.24	77.47	78.2	78.3	78.48	76.37	72.34	72.42	72.13	71.91	76.09	76.64	76.02	74.33	73.67	75.28	75.1	74.92	74.98	74.99	74.71	74.82	76.15	
8	78.65	78.57	78.71	77.95	78.81	79.16	78.28	---	87.69	83.77	83.62	77.76	75.62	76.23	76.22	77.19	75.92	75.53	76.56	76.7	76.7	75.84	75.3	71.99	71.95	71.71	71.5	74.29	74.97	74.2	73.3	73.03	74.2	73.92	73.78	73.88	73.82	73.82	73.63	74.55
9	78.78	78.6	78.73	77.93	78.66	79.74	78.32	88.21	---	83.93	83.78	77.48	75.47	76.16	76.07	77.16	75.89	75.57	76.54	76.45	76.74	75.16	72.72	72.66	72.56	71.27	74.12	74.69	74.02	73.25	72.86	74.01	73.75	73.66	73.71	73.48	73.44	74.49		
10	79.01	78.79	78.99	78.31	78.05	79.97	83.63	83.87	83.44	---	98.99	77.86	76.76	76.62	76.4	77.54	76.26	76.25	76.82	77.49	77.19	75.38	72.52	72.48	71.98	71.85	74.61	75.27	74.49	73.73	74.1	74.36	74.2	74.09	74.5	73.13	73.75	74.9	74.83	
11	78.58	78.41	78.59	77.72	78.57	79.07	78.05	83.6	83.37	98.72	---	77.52	75.58	76.17	75.92	77.13	75.78	75.46	76.51	76.59	76.74	75.27	72.02	72.98	71.57	71.48	74.24	74.9	74.09	73.43	72.88	74.07	73.88	73.69	73.84	73.88	73.7	73.67	74.56	
12	79.73	79.12	79.65	79.47	79.98	80.2	79.35	77.81	76.76	77.67	77.52	---	78.03	78.75	78.71	80.11	77.24	77.55	78.64	78.46	78.57	76.35	72.2	72.23	71.86	71.34	77.45	78.27	77.47	74.06	73.23	75.54	75.91	75.35	75.19	75.17	74.9	75.13	76.31	
13	77.94	77.55	77.76	77.72	78.05	78.34	77.53	76.48	75.76	76.59	76.49	78.97	---	98.38	80.80	81.85	78.77	78.91	79.71	78.81	79.07	75.72	72.32	72.3	72.05	71.69	76.76	76.5	76.05	74.14	73.57	74.91	75.15	74.83	74.77	74.54	74.68	75.74		
14	78.03	77.73	77.98	77.74	78.34	78.61	77.79	76.69	75.85	76.61	76.51	79.05	97.66	---	80.79	81.87	79.01	79.06	79.85	79.95	79.34	75.83	72.47	72.62	72.15	71.64	76.43	80.51	76.32	74.01	73.67	75.01	75.28	75.12	74.99	74.97	74.49	74.88	75.84	
15	78.38	78.05	78.34	77.76	78.47	78.71	77.72	77.08	76.14	76.88	76.8	79.29	80.22	81.05	---	84.37	81.43	81.42	82.44	80.78	81.01	76.38	72.19	72.26	72.03	71.65	75.64	76.43	75.41	74.05	73.39	75.1	75.01	74.73	74.89	74.9	74.65	74.74	75.78	
16	78.68	78.4	78.69	78.27	78.85	79.24	78.15	77.3	76.34	77.37	77.27	80.11	80.59	81.56	83.57	---	81.66	81.82	82.89	81.43	81.66	76.75	72.43	72.38	72.24	71.64	76.05	77.13	76.09	74.43	73.63	75.52	75.55	75.2	75.57	75.35	75.33	75.21	76.35	
17	76.53	76.36	76.55	75.59	76.41	76.75	75.63	75.64	75.74	75.76	75.57	76.75	77.87	78.37	79.57	81.22	---	83.78	81.91	79.51	79.84	75.48	71.46	71.46	71.41	71.06	73.73	74.4	73.44	72.83	72.73	73.83	73.24	73.3	73.63	73.66	73.47	73.4	74.37	
18	77.25	77.05	77.18	76.18	77.17	77.59	76.6	76.18	75.18	76.18	76.79	77.77	79.08	80.52	82.21	84.94	---	83.2	80.42	80.78	76.05	71.6	71.68	71.53	71.29	74.15	75.37	74.74	73.25	72.68	74.64	73.98	73.86	74.11	74.17	73.93	73.91	75.2		
19	77.68	77.41	77.68	76.47	77.65	78.15	76.9	76.47	75.32	76.56	76.44	78.43	78.08	79.4	81.04	82.59	82.21	82.35	---	80.8	81.12	76.12	71.58	71.66	71.65	71.27	74.72	75.79	74.57	73.54	72.94	74.9	74.43	74.06	74.44	74.43	74.18	74.43	75.52	
20	77.7	77.37	77.73	76.34	77.65	78.03	76.72	76.62	75.28	76.64	76.52	78.24	76.87	78.46	81.85	79.02	79.74	80.14	80.78	---	85.48	76.11	72.15	72.33	71.75	71.34	74.56	75.68	74.62	73.8	73.3	74.78	74.41	74.18	74.65	74.67	74.1	74.49	75.61	

Supplementary Table S2. Average Nucleotide Identity (ANI) values obtained from reciprocal analyses as calculated with blast in JSpecies.

21	77.85	77.43	77.67	76.2	77.79	78.1	76.71	76.57	75.17	76.56	76.43	78.3	76.96	78.68	78.94	81.18	79.9	79.15	80.79	85.3	---	76.04	72	72.16	71.63	71.36	74.61	75.76	74.25	73.93	73.21	74.59	74.2	74.13	74.63	74.72	74.37	74.31	75.59		
22	75.93	75.8	75.86	75.07	75.92	76.19	75.11	75.09	74.12	75.2	75	76.13	74.53	75.43	75.07	76.44	75.68	75.2	75.96	76.04	76.26	---	71.37	71.41	71.36	70.91	73.57	74.38	73.46	72.81	72.37	73.67	73.32	73.28	73.54	73.57	73.27	73.39	74.17		
23	72.53	72.36	72.44	72.44	72.59	72.62	72.35	72.12	71.68	72.24	72.11	72.17	72.12	72.36	72.08	72.52	71.72	71.82	71.75	72.3	72.49	71.71	---	99.07	76.2	76.17	71.95	72.26	71.9	71.53	71.19	71.75	71.31	71.7	71.74	71.73	71.5	71.56	71.18		
24	72.28	72.24	72.26	72.14	72.34	72.5	72.1	72.72	71.33	72.21	72.04	72.17	71.81	72.28	71.85	72.41	71.7	71.55	71.8	72.26	72.56	71.7	99.2	---	76.16	76.07	71.67	72.13	71.66	71.39	71.23	71.7	71.29	71.69	71.54	71.62	71.45	71.46	71.98		
25	72.24	72.27	72.23	71.92	72.36	72.6	72.04	71.83	71.43	72.02	71.72	72.08	6	72.03	71.71	72.45	71.71	71.39	72.72	72.23	72.72	71.76	---	74.69	71.68	72.03	71.74	71.32	70.99	71.66	71.29	71.55	71.71	71.62	71.65	71.4	71.53	71.72			
26	71.72	71.69	71.63	71.17	71.72	71.83	71.29	71.41	70.81	71.7	71.54	71.3	71.06	71.6	71.1	71.59	71.36	71.8	70.36	71.48	71.69	71.06	76.05	75.99	74.57	---	70.9	71.38	70.94	71.23	71.09	71.12	70.75	71.24	71.06	71.13	70.97	71.91	71.41		
27	76.23	75.86	76.36	76.15	76.45	76.67	76	74.88	74.28	74.94	74.96	78.1	75.79	76.42	75.69	77.1	74.78	74.94	75.88	75.82	76.1	74.57	72.1	72.05	71.94	71.49	---	98.77	88.74	73.75	76.9	76.02	76.14	76.09	75.61	75.63	75.43	75.63	77.37		
28	76.55	76.22	76.53	76.32	76.81	77.41	76.64	75.25	74.72	75.27	75.75	78.49	76.33	80.58	76.03	77.44	75.07	75.17	76.12	76.18	76.4	74.8	72.38	72.42	72.17	71.32	---	88.7	74.75	74.05	76.3	76.48	76.08	76.06	76.08	75.6	76.96	75.95	77.59		
29	76.62	76.16	76.55	76.03	76.76	77.11	75.85	75.18	74.05	75.24	75.06	78.48	75.74	76.82	75.57	77.6	75.06	74.67	76.19	76.27	76.25	74.83	72.42	72.43	72.17	71.7	88.79	89.55	---	75.1	74.2	76.27	76.58	76.29	75.88	75.8	75.88	75.95	77.54		
30	74.22	74.02	74.24	73.71	74.29	74.36	73.93	73.51	73.11	73.65	73.6	74.24	73.6	74.16	73.66	74.64	73.39	73.39	73.92	74.22	74.42	73.24	71.46	71.47	71.16	71.19	74.4	74.81	74.2	---	78.79	77.86	76.66	76.86	75.58	75.57	75.38	75.46	75.62		
31	73.46	73.41	73.57	73.05	73.54	73.78	73.36	73.13	73.74	73.16	73.08	73.38	73.27	73.6	73.16	73.78	72.95	72.76	73.62	73.68	72.72	71.25	71.21	70.97	71.07	73.69	73.98	73.59	73.76	78.4	---	76.71	75.1	76.79	74.84	74.58	74.66	74.74	74.74		
32	75.24	75.01	75.3	74.36	75.25	75.55	74.49	74.31	73.43	74.21	74.2	75.61	73.85	74.84	74.28	75.51	74.36	74.31	75.24	75.19	75.14	74.05	71.8	71.81	71.59	70.97	75.01	76.17	74.85	77.56	76.44	---	78.14	78.7	76.94	76.98	76.47	76.86	77.22		
33	75.07	74.8	75.08	74.67	75.23	75.37	74.76	74.3	73.62	74.29	74.21	76.15	74.84	75.31	74.69	75.77	73.89	74.14	74.85	74.74	74.75	73.85	71.52	71.71	71.27	70.7	75.94	76.55	75.9	76.82	75.92	75.6	78.92	78.6	---	78.5	76.69	76.7	76.18	76.59	76.41
34	75.12	74.97	75.08	74.94	75.35	75.26	74.87	74.22	73.77	74.23	74.22	75.74	74.71	75.17	74.74	75.56	73.99	74.05	74.63	74.8	74.87	73.95	72.01	72.02	71.66	71.21	76.03	76.42	75.84	77.09	76.26	78.93	78.54	---	76.74	76.75	76.18	76.69	76.65		
35	75.03	74.83	75.13	74.87	75.19	75.32	74.92	74.19	73.91	74.15	74.06	75.49	74.81	75.08	74.95	75.69	74.25	74.47	74.88	75.16	75.75	73.87	71.87	71.85	71.77	70.06	75.11	76.45	75.66	75.01	75.26	77.59	76.61	---	98.01	90.27	85.47	76.77			
36	74.96	74.78	75.02	74.75	75.1	75.28	74.9	74.15	73.82	74.06	73.99	75.38	74.59	74.9	74.82	75.71	74.07	74.37	74.85	74.96	75.06	73.81	71.72	71.75	71.71	70.93	75.61	75.97	75.52	75.42	74.91	77.17	76.41	97.49	---	90.29	85.36	76.59			
37	74.57	74.4	74.68	74.39	74.8	74.98	74.41	73.92	73.42	73.7	75.75	74.11	74.27	74.48	74.42	75.35	73.8	73.84	74.44	74.58	74.74	73.51	71.41	71.44	71.33	71.03	75.33	75.71	75.35	75.43	74.52	76.76	76.21	76.11	90.27	90.35	---	84.31	76.44		
38	75.05	74.85	75.11	74.81	75.23	75.34	74.84	74.14	73.6	73.99	74.02	75.57	74.66	75.03	74.71	75.64	74.19	74.13	74.93	74.95	74.95	73.94	71.86	71.92	71.7	71.15	75.63	76.16	75.46	75.67	74.88	77.27	76.71	76.67	85.58	85.55	84.49	---	76.67		
39	75.71	75.31	75.6	74.83	75.58	75.92	75.22	74.41	73.68	74.47	74.34	76.23	74.58	75.4	74.86	76.24	74.75	74.63	75.66	75.71	75.84	74.16	71.73	71.78	71.64	71.32	76.16	77.22	75.88	75.4	74.77	77.17	76.1	76.12	76.2	76.24	76.04	76.06	---		

Supplementary Table S2. Average Nucleotide Identity (ANI) values obtained from reciprocal analyses as calculated with blast in JSpecies.

1. *P. agglomerans*
2. *Pantoea eucalypti*
3. *P. vagans*
4. *P. deleyi*
5. *P. anthophila*
6. *P. brenneri*
7. *P. conspicua*
8. *P. ananatis*
9. *P. allii*
10. *P. stewartii* ssp. *stewartii*
11. *P. stewartii* ssp. *indologenes*
12. *P. septica*
13. *P. eucrina*
14. *Pantoea* sp. PSNIH1
15. *P. wallisii*
16. *P. dispersa*
17. *P. rwandensis*
18. *P. rodasii*
19. *Pantoea* sp. GM01
20. *Pantoea* sp. At-9b
21. *P. cyripedii*
22. *Pantoea* sp. A4
23. *Tatumella* sp. UCD-suzukii
24. *T. tyseos*
25. *T. saanichensis*
26. *T. morbirosei*
27. *P. calida*
28. *Pantoea* sp. PSNIH2
29. *P. gaviniae*
30. *E. mallotivora*
31. *E. tracheiphila*
32. *E. billingiae*
33. *Erwinia* sp. 9145
34. *Pantoea* sp. IMH
35. *E. pyrifoliae*
36. *Erwinia* sp. Ejp617
37. *E. amylovora*
38. *E. tasmaniensis*
39. *E. toletana*

Supplementary Table S3Results from the Tajima's test for *P. agglomerans*, *E. amylovora* and *S. marcescens*

Configuration	Count
Identical sites in all three sequences	171,255
Divergent sites in all three sequences	11,594
Unique differences in Sequence A	11,410
Unique differences in Sequence B	11,485
Unique differences in Sequence C	18,963

NOTE: The equality of evolutionary rate between sequences **A** (*P_agglomerans*) and **B** (*E_amylovora*), with sequence **C** (*S_marcescens*) used as an outgroup in Tajima's relative rate test (Tajima, 1993). The χ^2 test statistic was 0.25 ($P = 0.62013$ with 1 degree[s] of freedom). A p -value < 0.05 is often used to reject the null hypothesis of equal rates between lineages, thus there is an equal rate of evolution between these three sequences. The analysis involved 3 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 224707 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 (Tamura et al., 2013).

Supplementary Table S4Results from the Tajima's test for *P. agglomerans*, *T. morbirosei* and *E. amylovora*

Configuration	Count
Identical sites in all three sequences	170,682
Divergent sites in all three sequences	12,194
Unique differences in Sequence A	8,612
Unique differences in Sequence B	19,536
Unique differences in Sequence C	13,683

NOTE: The equality of evolutionary rate between sequences **A** (*P_agglomerans*) and **B** (*T_morbirosei*), with sequence **C** (*E_amylovora*) used as an outgroup in Tajima's relative rate test (Tajima, 1993). The χ^2 test statistic was 4239.51 ($P = 0.00000$ with 1 degree[s] of freedom). A p -value < 0.05 is often used to reject the null hypothesis of equal rates between lineages, thus there is not an equal rate between lineages. The analysis involved 3 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 224707 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 (Tamura et al., 2013).

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