

Table S7. Nearest neighbours on the basis of 16S rRNA (*rrs*) gene sequences among validly named bacterial species of all nectar strains characterised in this study, as obtained through the EzTaxon-e server.^a

Nectar group	Isolate	No. of hits showing $\geq 97\%$ similarity ^b	Best hit (accession no., similarity)	Second and third best hits (accession no., similarity)
NG 1	PN703.1	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.59%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.45%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.13%)
NG 1	PN716.2	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.59%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.45%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.13%)
NG 1	PN705.2	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.66%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.52%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.19%)
NG 1	PN708.2	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.45%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.31%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 98.99%)
NG 1	PN707.2	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.66%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.52%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.19%)
NG 1	PN85.3	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.66%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.52%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.19%)
NG 1	PN84.2	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.66%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.52%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.19%)
NG 1	PN96.2	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.66%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.59%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T

				(D84018, 99.26%)
NG 1	PN1008.2	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.66%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.52%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.19%)
NG 1	PN1009.1	3	<i>Pseudomonas psychrotolerans</i> C36 ^T (AJ575816, 99.66%)	<i>Pseudomonas oryzihabitans</i> IAM 1568 ^T (AM262973, 99.59%) <i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> IAM 1508 ^T (D84018, 99.19%)
NG 2	PN195.2	79	<i>Pseudomonas brenneri</i> CFML 97-391 ^T (AF268968, 99.52%)	<i>Pseudomonas migulae</i> CIP 105470 ^T (AF074383, 99.33%) <i>Pseudomonas proteolytica</i> CMS 64 ^T (AJ537603, 99.33%)
NG 2	PN195.3	44	<i>Pseudomonas azotoformans</i> IAM1603 ^T (D84009, 99.66%)	<i>Pseudomonas libanensis</i> CIP 105460 ^T (AF057645, 99.53%) <i>Pseudomonas gessardii</i> CIP 105469 ^T (AF074384, 99.53%)
NG 2	PN289.1	73	<i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.73%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.66%) <i>Pseudomonas extremaustralis</i> 14-3 ^T (AHIP01000073, 99.60%)
NG 2	PN724.1	74	<i>Pseudomonas extremaustralis</i> 14-3 ^T (AHIP01000073, 99.87%)	<i>Pseudomonas antarctica</i> CMS 35 ^T (AJ537601, 99.73%) <i>Pseudomonas grimontii</i> CFML 97-514 ^T (AF268029, 99.73%)
NG 2	PN725.1	44	<i>Pseudomonas brenneri</i> CFML 97-391 ^T (AF268968, 99.66%)	<i>Pseudomonas trivialis</i> DSM 14937 ^T (AJ492831, 99.40%) <i>Pseudomonas proteolytica</i> CMS 64 ^T (AJ537603, 99.39%)
NG 2	PN770.2	76	<i>Pseudomonas simiae</i> OLi ^T (AF936933, 99.85%)	<i>Pseudomonas poae</i> DSM 14936 ^T (AJ492829, 99.80%) <i>Pseudomonas trivialis</i> DSM 14937 ^T (AJ492831, 99.73%)
NG 2	PN829.3	55	<i>Pseudomonas lutea</i> OK2 ^T (AY364537, 99.87%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 99.26%) <i>Pseudomonas umsongensis</i> Ps 3-10 ^T (AF468450, 98.90%)
NG 2	PN1059.2	59	<i>Pseudomonas syringae</i> ATCC 19310 ^T (AJ308316, 98.68%)	<i>Pseudomonas chlororaphis</i> subsp. <i>chlororaphis</i> DSM 50083 ^T (Z76673, 98.51%) <i>Pseudomonas kilonensis</i> 520-20 ^T (AJ292426, 98.39%)
NG 2	PN34.1	62	<i>Pseudomonas koreensis</i> Ps9-14 ^T (AF468452, 100%)	<i>Pseudomonas reinekei</i> Mt-1 ^T (AM293565, 99.59%) <i>Pseudomonas jessenii</i> CIP 105274 ^T (AF068259, 99.46%)
NG 2	PN49.1	50	<i>Pseudomonas extremorientalis</i> KMM 3447 ^T (AF405328, 99.93%)	<i>Pseudomonas simiae</i> OLi ^T (AJ936933, 99.78%) <i>Pseudomonas poae</i> DSM 14936 ^T (AJ492829, 99.65%)

NG 2	PN52.2	51	<i>Pseudomonas extremorientalis</i> KMM 3447 ^T (AF405328, 100%)	<i>Pseudomonas simiae</i> OLi ^T (AJ936933, 99.78%) <i>Pseudomonas poae</i> DSM 14936 ^T (AJ492829, 99.65%)
NG 2	PN2.2	79	<i>Pseudomonas extremorientalis</i> KMM 3447 ^T (AF405328, 99.93%)	<i>Pseudomonas simiae</i> OLi ^T (AJ936933, 99.78%) <i>Pseudomonas poae</i> DSM 14936 ^T (AJ492829, 99.67%)
NG 2	PN34.2	52	<i>Pseudomonas extremorientalis</i> KMM 3447 ^T (AF405328, 100%)	<i>Pseudomonas simiae</i> OLi ^T (AJ936933, 99.78%) <i>Pseudomonas poae</i> DSM 14936 ^T (AJ492829, 99.65%)
NG 2	PN8.1	54	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.78%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.57%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.51%)
NG 2	PN21.1	54	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.78%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.57%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.51%)
NG 2	PN31.1	54	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.78%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.57%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.51%)
NG 2	PN50.1	52	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.79%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.59%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.53%)
NG 2	PN48.1	54	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.78%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.57%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.51%)
NG 2	PN71.1	54	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.70%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.49%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.42%)
NG 2	PN20.1	54	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.78%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.57%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.51%)
NG 2	PN21.3	55	<i>Pseudomonas palleroniana</i> CFBP 4389 ^T (AY091527, 99.79%)	<i>Pseudomonas costantinii</i> CFBP 5705 ^T (AF374472, 99.58%) <i>Pseudomonas lurida</i> DSM 15835 ^T (AJ581999, 99.52%)
NG 3	PN704.1	53	<i>Pseudomonas rhizosphaerae</i> IH5 ^T (AY152673, 99.60%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 98.72%) <i>Pseudomonas lutea</i> OK2 ^T (AY364537, 98.59%)
NG 3	PN716.3	50	<i>Pseudomonas rhizosphaerae</i> IH5 ^T (AY152673, 99.66%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 98.86%) <i>Pseudomonas lutea</i> OK2 ^T (AY364537, 98.73%)
NG 3	PN705.1	49	<i>Pseudomonas rhizosphaerae</i> IH5 ^T (AY152673, 99.67%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 98.80%)

				<i>Pseudomonas lutea</i> OK2 ^T (AY364537, 98.60%)
NG 3	PN706.2	51	<i>Pseudomonas rhizosphaerae</i> IH5 ^T (AY152673, 99.60%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 98.73%) <i>Pseudomonas lutea</i> OK2 ^T (AY364537, 98.59%)
NG 3	PN708.1	57	<i>Pseudomonas rhizosphaerae</i> IH5 ^T (AY152673, 99.66%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 98.79%) <i>Pseudomonas lutea</i> OK2 ^T (AY364537, 98.66%)
NG 3	PN1008.1	57	<i>Pseudomonas rhizosphaerae</i> IH5 ^T (AY152673, 99.66%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 98.86%) <i>Pseudomonas lutea</i> OK2 ^T (AY364537, 98.73%)
NG 3	PN1059.1	59	<i>Pseudomonas rhizosphaerae</i> IH5 ^T (AY152673, 99.60%)	<i>Pseudomonas graminis</i> DSM 11363 ^T (Y11150, 98.73%) <i>Pseudomonas lutea</i> OK2 ^T (AY364537, 98.59%)

^a <http://eztaxon-e.ezbiocloud.net/> (Kim *et al.*, 2012; *Int J Syst Evol Microbiol*, 62: 716–721) [last accessed 28 Mar. 2013].

^b Number of reference sequences in the database showing ≥ 97% DNA similarity with the query sequence.