

## Supplementary Material

**Table S1.** Similarity values (%) of 16S rRNA gene sequences (*E.coli* positions 33-1467) between type strains of type species of the six most closely related genera (see Fig. 2) to the proposed genus *Limnohabitans* gen. nov. (strain MWH-C5<sup>T</sup>). For strain designations and sequence accession numbers of reference strains see Fig. 2).

	<i>Po. vacu.</i>	<i>Va. para</i>	<i>Ca. kore.</i>	<i>Cu. grac.</i>	<i>Ps. soli</i>	<i>Rh. ferm.</i>	<i>Ra. tata.</i>	MWH-C5 <sup>T</sup>
<i>Polaromonas vacuolata</i>	100	95.3	94.7	95.3	94.0	94.1	93.0	94.4
<i>Variovorax paradoxus</i>		100	96.5	96.4	95.8	95.9	95.6	95.2
<i>Caenimonas koreensis</i>			100	96.5	95.0	94.8	96.0	95.2
<i>Curvibacter gracilis</i>				100	96.5	95.9	96.0	96.2
<i>Pseudorhodoferrax soli</i>					100	96.1	95.2	95.9
<i>Rhodoferrax fermentans</i>						100	94.4	95.3
<i>Ramlibacter tataouinensis</i>							100	95.1
MWH-C5 <sup>T</sup>								100

**Table S2.** Family-wide comparison of chemotaxonomic traits. The presented data were obtained from Mechichi *et al.*, 2003 (*Alicycliphilus*), Takeda *et al.*, 2002 (*Caldimonas*), Ryu *et al.*, 2008 (*Caenimonas* and other genera), Xie and Yokota, 2005 (*Pelomonas*) Gomila *et al.*, 2007 (*Pelomonas*), Pham *et al.*, 2009 (*Diaphorobacter*), Heulin *et al.*, 2003 (*Ramlibacter*), Franca *et al.*, 2006 (*Tepidicella*), Pinel *et al.*, 2008 (*Verminephrobacter*), Elbanna *et al.*, 2003 (*Schlegelella*), Spring *et al.*, 2005 (*Malikia*, *Macromonas*, *Hydrogenophaga*), Blümel *et al.*, 2001 (*Xenophilus* and other genera), Bruland *et al.*, in press (*Pseudorhodoferox*), Spring *et al.*, 2004 (*Ottowia*, *Hylemonella*, *Alicycliphilus*, *Brachymonas*), Lee *et al.*, 2004 (*Lampropedia*), Gomila *et al.*, 2008 (*Roseateles*), Kämpfer *et al.*, 2008 (*Pseudacidovorax*). NA, not available; feat., feature; cy., cyclo; Q, quinone; RQ, rhodoquinone. 1, strain MWH-C5T; 2, *Acidovorax*; 3, *Alicycliphilus*; 4, *Brachymonas*; 5, *Caenimonas*; 6, *Caldimonas*; 7, *Comamonas*; 8, *Curvibacter*; 9, *Delftia*; 10, *Diaphorobacter*; 11, *Giesbergeria*; 12, *Hydrogenophaga*; 13, *Hylemonella*; 14, *Lampropedia*; 15, *Macromonas*; 16, *Malikia*; 17, *Ottowia*; 18, *Pelomonas*; 19, *Polaromonas*; 20, *Pseudacidovorax*; 21, *Pseudorhodoferox*; 22, *Ramlibacter*; 23, *Rhodoferox*; 24, *Roseateles*; 25, *Schlegelella*; 26, *Simplicispira*; 27, *Tepidicella*; 28, *Variovorax*; 29, *Verminephrobacter*; 30, *Xenophilus*.

Characteristics	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	
<b>Quinones</b>	Q-8	Q-8	NA	Q-8 RQ-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	Q-8	NA	NA	Q-8	Q-8	Q-8	Q-8	Q-9	NA	NA	NA	Q-8 RQ-8	Q-8	NA	Q-8	Q-8	Q-8	NA	Q-8
<b>Major fatty acids</b>	16:0 16:1 18:1	16:0 16:1	NA	16:0. 16:1	16:0 18:1 feat. 3	16:0 16:1 18:1	16:0 16:1 18:1	16:0 16:1 18:1	16:0 16:1 18:1	16:0 17:0 cy. feat. 4+7	16:0 16:1 18:1	16:0 16:1 18:0 10:1 17:0	16:0 16:1 18:1	14:0 16:0 18:1	16:1 17:1 18:1	16:0 16:1 18:1	16:0 16:1 18:1	16:0 16:1 18:1	16:0 16:1 18:1	16:0 18:1 feat. 3	NA	16:0 18:1 feat. 3	NA	16:0 16:1 18:1	16:0 16:1 18:1	16:0 17:0 cy.	16:0 16:1 18:1	16:0 18:1 17:0 cy.	16:0 16:1 18:1	16:0 16:1 17:0 cy.	16:0 16:1 18:1
<b>Major 3-OH acid</b>	8:0	10:0 8:0 <sup>s</sup>	10:0	10:0	10:0	10:0	10:0	8:0	10:0	10:0	10:0	8:0 10:0	10:0 12:0	10:0	8:0	8:0	10:0	10:0	8:0	8:0	10:0	NA	8:0	10:0	10:0	10:0	10:0	8:0	10:0	10:0	8:0
<b>DNA G+C content (mol%)</b>	56	62 -	66	63 -	63	66	63	62	67	63 - 65	57	65	65	61	68	66	59	59	52	70	69 - 70	67	59	66	69 - 70	63	65	66	67	70	
		70		65			66	66	69		60	69		67		67			63			70	62			65	69				

\* Present in for *S.*

*psychrophila.*

<sup>s</sup> Present in phytopathogenic species

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**Fig. S1.** Neighbour-joining (NJ) tree (Kimura-2 correction) based on almost complete 16S rRNA gene sequences, showing the phylogenetic relationship of *Limnohabitans curvus* gen. nov, sp. nov. with uncultured bacteria inhabiting various freshwater systems and estuaries. The sequences of uncultured bacteria were retrieved from GenBank by BLAST search with the sequence of strain MWH-C5<sup>T</sup> as query sequence. Only a part of the BLAST hits > 95% sequence similarity are presented in the tree. The so-called “Rhodoferax sp. BAL47” cluster (Zwart et al., 2002) is indicated by the bracket at the right. Bootstrap values  $\geq 60\%$  (1000 iterations) are depicted. The tree was rooted by using archeal sequences (not shown). Bar, 5 nucleotide substitution per 100 nucleotides.