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## Defluviitaleaceae

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1 *Family Defluviitaleaceae*

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8 **Keywords:** thermophilic, fermentative, anaerobic type of metabolism

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11 **Abstract :**

12 The family *Defluviitaleaceae* belongs to the order *Clostridiales*. To date, it is currently  
13 represented by only one genus containing two species and one species not validated. The  
14 genus *Defluviitalea* was phylogenetically distant to the genera *Parasporobacterium*,  
15 *Clostridium* and *Robinsoniella*, pertaining to the family *Lachnospiraceae* with sequence  
16 similarity of the 16S rRNA gene which approximates 87%. The delineation of the novel  
17 family *Defluviitaleaceae* was primarily based on phylogenetic, metabolic and physiological  
18 characteristics, with *Defluviitalea* as the type genus of the family.

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**Defining publication:** *Jabari et al. 2012,*

**Etymology:** De.flu.vi.i.ta.le.a.ce'a.e. N.L. n. *Defluviitalea*, type genus of the family; suff. -aceae, ending to denote a family; N.L. fem. pl. n. *Defluviitaleaceae*, the *Defluviitalea* family.

**Type genus:** *Defluviitalea* Jabari, Gannoun, Cayol, Hamdi, Fauque, Ollivier, Fardeau 2012.

**Description:**

Cells have a **Gram-positive type of cell wall**. They are **non-motile**, terminal spore-forming **thermophilic rods** (length 5-10  $\mu\text{m}$  x 0.5  $\mu\text{m}$ ). **Fermentative. anaerobic**-type of metabolism. Growth is observed only under anaerobic conditions. Optimal growth occurs at 50-55 °C. Major **fatty acids are C16:0 and C14:0**. Respiratory quinones are not detected. Polar lipid profile comprises diphosphatidylglycerol, phosphatidylglycerol, phospholipids, phosphoglycolipid, glycolipid. Belongs to the order *Clostridiales*, phylum *Firmicutes*.

**DNA G+C content (mol %): 35.2**

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50 **Further description:**

51 The family *Defluviitaleaceae* belongs to the order *Clostridiales*. To date, it is currently  
52 represented by only one genus containing two species and one species not validated. The  
53 genus *Defluviitalea* was phylogenetically distant to genera *Parasporobacterium*, *Clostridium*  
54 and *Robinsoniella*, pertaining to the family *Lachnospiraceae* with sequence similarity of the  
55 16S rRNA gene which approximates 87% (Jabari *et al.*, 2012, Ji *et al.*, 2016) while members  
56 of the genus *Vallitalea* (*Vallitalea guaymasensis* and *Vallitalea pronyensis*) represent its  
57 closest phylogenetic relatives with sequence similarity of about 89% (Lakhal *et al.*, 2013, Ben  
58 Aissa *et al.*, 2014). The delineation of the novel family *Defluviitaleaceae* was primarily  
59 based on phylogenetic, metabolic and physiological characteristics, with *Defluviitalea* as the  
60 type genus of the family.

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62 Key to the genera of the family *Defluviitaleaceae*

63 1. The DNA G+C content is around 35 %.

64  
65 **Phylogeny**

66 From the phylogenetic analyses (Figure1), *Defluviitalea* is distantly related to members of the  
67 family *Lachnospiraceae* and the genus *Vallitalea*.

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69 **References**

70  
71 Ben Aissa, F., Postec, A., Erauso, G., Payri, C., Pelletier, B., Hamdi, M., Ollivier, B.  
72 and Fardeau, M. L. 2014. Characterization of *Vallitalea pronyensis* sp. nov., a  
73 novel marine bacterium, isolated from an alkaline hydrothermal chimney in  
74 Prony Bay, New Caledonia. *Int J Syst Evol Microbiol* **64**: 1160-1165.

75 Jabari, L., Gannoun, H., Cayol, J-L., Hamdi, M., Fauque, G., Ollivier, B. and Fardeau,  
76 M-L. 2012. Characterization of *Defluviitalea saccharophila* gen. nov., sp. nov.,  
77 a thermophilic bacterium isolated from an upflow anaerobic filter treating  
78 abattoir wastewaters, and proposal of Defluviitaleaceae fam. nov. *Int J Syst*  
79 *Evol Microbiol* **62**: 550-555.

80 Ji S-Q, Wang B, Lu M & Li F-L (2016) *Defluviitalea phaphyphila* sp. nov., a novel  
81 thermophilic bacterium that degrades brown algae. *Appl Environ Microbiol* **82**, 868-77

82

83 Lakhal, R., Pradel, N., Postec, A., Hamdi, M., Ollivier, B., Godfroy, A. and Fardeau,  
84 M. L. 2013. *Vallitalea guaymasensis* gen. nov., sp. nov., isolated from marine  
85 sediment. *Int J Syst Evol Microbiol* **63**: 3019–3023.

86 Ma S, Huang Y, Wang C, Fan H, Dai L, Zhou Z, Liu X, Deng Y (2016)  
87 *Defluviitalea raffinosedens* sp. nov., a novel thermophilic, anaerobic, saccharolytic bacterium  
88 isolated from an anaerobic batch digester treating animal manure and rice straw *Int J Syst*  
89 *Evol Microbiol*, doi: [10.1099/ijsem.0.001664](https://doi.org/10.1099/ijsem.0.001664)

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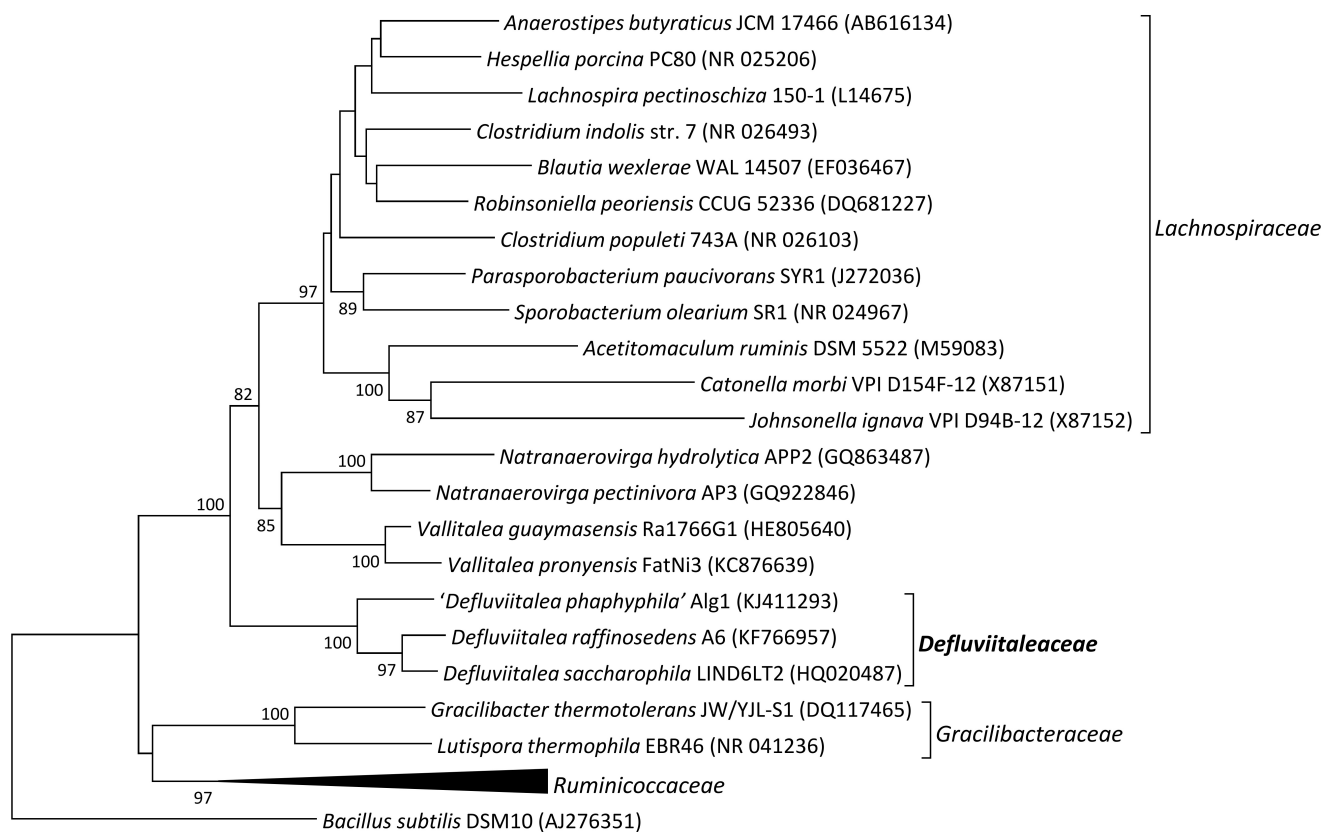
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**Figure 1** Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of *Defluviitalea saccharophila*, *Defluviitalea raffinosedens* and “*Defluviitalea phaphyphila*”.

Bootstrap values higher than 70% (based on 1000 replicates) are shown at branch nodes. Bar: 0.01