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Objection to the proposition of the new genus *Abyssivirga*

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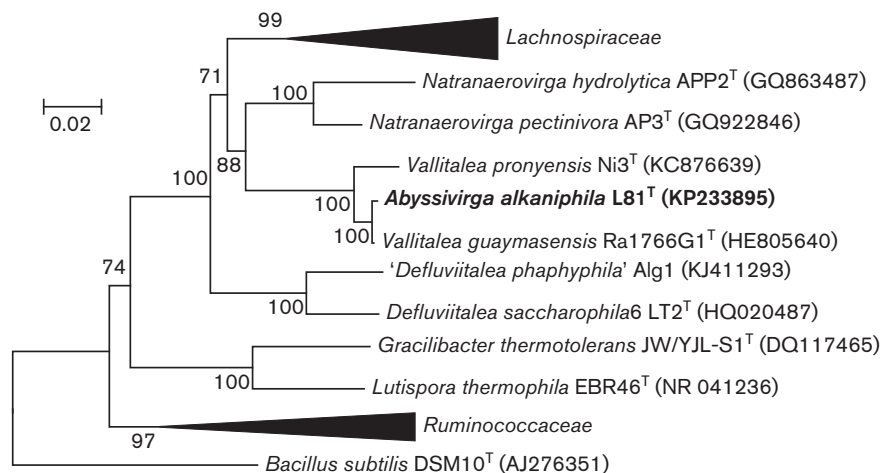


Fig. 1. Phylogenetic tree showing the position of *Abyssivirga alkaniphila* L81^T with the type strains of the closest described species. The neighbour-joining method was used, with Kimura's two-parameter model. Bootstrap values below 70 are not shown (from 1000 replicates). In total, 1211 positions were used in the final dataset. Bar, 0.02 changes per position.

We have read with interest the recent paper published by Schouw *et al.* [1] in IJSEM (Vol 66, pp. 1724–1734) entitled: '*Abyssivirga alkaniphila* gen. nov., sp. nov., an alkane-degrading, anaerobic bacterium from a deep-sea hydrothermal vent system, and emended descriptions of *Natranaerovirga pectinivora* and *Natranaerovirga hydrolytica*'.

We disagree with the proposal of *Abyssivirga* as a new genus due to phylogenetic considerations as shown below. Indeed, we noticed that a BLAST analysis of the *Abyssivirga alkaniphila* 16S rRNA gene sequence indicated 99.4% similarity with *Vallitalea guaymasensis* isolated from sediments of the Guaymas Basin, and 96.1% with *Vallitalea pronyensis* isolated from a hydrothermal chimney in Prony Bay. Both *Vallitalea* species have been fully characterized in IJSEM [2, 3].

Based on phylogenetic analyses, we believe that the proposal of the new genus *Abyssivirga* should be reconsidered. *A. alkaniphila* should be reassigned to the genus *Vallitalea*, and possibly as a novel species, '*Vallitalea alkaniphila*', if demonstrated

by significant DNA–DNA hybridization and phenotypic differences.

With the aim to clearly establish the phylogenetic position of *A. alkaniphila* and its effective affiliation to the genus *Vallitalea*, a phylogenetic tree is reconstructed here (Fig. 1).

References

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