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Objection to the proposition of the new genus Abyssivirga

Anne Postec,* Bernard Ollivier and Marie-Laure Fardeau

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

Fig. 1. Phylogenetic tree showing the position of Abyssivirga alkaniphila L81T 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.

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