Marine amoebae with cytoplasmic and perinuclear symbionts deeply branching in the *Gammaproteobacteria*

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Supplementary Material

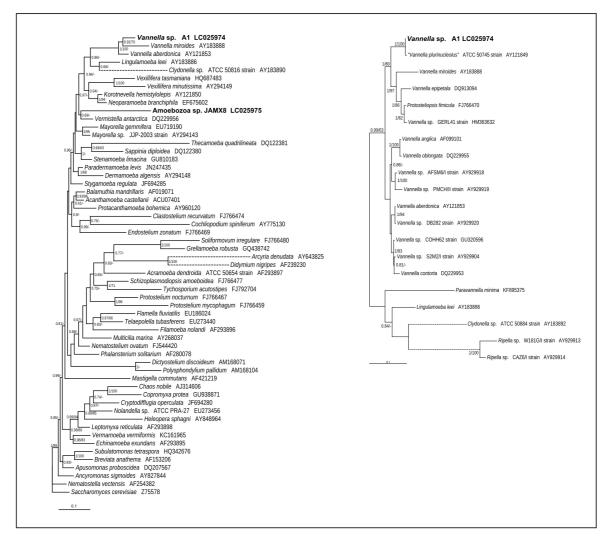


Figure S1. Phylogenetic relationships of *Vannella* sp. A1 and amoeba isolate **JAMX8** within the Amoebozoa. Phylogenetic 18S rRNA-based trees of the Amoebozoa (left panel) and Vannellidae (right panel) constructed using the Bayesian inference method. Bayesian posterior probabilities 8 (> 0.6) and RaxML bootstrap support values (> 60%) are indicated at the nodes; the dashed line indicates a branch shortened by 50% to enhance clarity.

HM467180, Rickettsiella sp. 5-186-2
AY447040, Rickettsiella symbiont of Asellus aquaticus
0.71 AB522697, Rickettsiella endosymbiont of Acyrthosiphon pisum
0.99 GQ857549, Diplorickettsia massiliensis
AF327558, endosymbiont of Folsomia candida
AQJ02000001, Rickettsiella grylli
0.84 HQ287535, bacterium symbiont of Haemaphysalis shimoga
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0.79 FJ516765, uncultured Legionellales bacterium 0.63 JN438482, uncultured organism
0.99 JN441708, uncultured organism
0.99 JN446160, uncultured organism
0.61 LC025959, Occultobacter vannellae A1
d.99 FJ719055, uncultured bacterium
0.98 DQ223216, uncultured bacterium
0.95 FN553442, uncultured sediment bacterium
0.52 FJ516829, uncultured Legionellales bacterium
0.92 JN533140, uncultured organism
0.99 JN537232, uncultured organism
0.85 JN535805, uncultured organism
0.93 LC025958, Nucleophilum amoebae JAMX8
1 JF 30159, uncultured bacterium
AF418944, uncultured bacterium
0.7 GQ264261, uncultured bacterium
0.7 EF492067, Legionella-like amoebal pathogen CC99
0.58 JQ684380, uncultured bacterium
0.99 JN445744, uncultured organism
JQ770048, uncultured bacterium
0.96 HQ403243, uncultured bacterium
0.95 ¹ AY741401, Legionella-like amoebal pathogen HT99
1 AM997640, uncultured deep-sea bacterium
0,99 L JF344063, uncultured gamma proteobacterium
0.75 EU221518, Trachelomonas scabra
0.51 - AY491597, uncultured bacterium
0.99 AY102612, Caedibacter taeniospiralis
AB176554, Fangia hongkongensis
Z21931, Francisella tularensis
AY444740, Legionella longbeachae
6.99 AE017354, Legionella pneumophila subsp. pneumophila str. Phi
0.93 AF424887, Legionella busanensis
0.95 D78004, Photorhabdus luminescens
AF366383, Yersinia pestis
0.63 GU394001, Serratia symbiotica
M35019, Haemophilus influenzae
0.95 M75083, Pasteurella pneumotropica 1 X80725, Escherichia coli
0.99 X56575, Vibrio campbellii 0.7 X74720, Vibrio parahaemolyticus
0.83 Z76654, Pseudomonas amygdali
1 Z76669, Pseudomonas syringae
AY152673, Pseudomonas rhizosphaerae
0.78 JX986961, Xanthomonas citri subsp. citri
0.99 AB558557, Xanthomonas theicola
AF192343, Xylella fastidiosa
0.82 AF533354, Azospirillum brasilense
0.72 AB071665, Tistrella mobilis
1 Y10110, Magnetospirillum magnetotacticum
AY738130, Rhizobium lusitanum
1

Figure S2. Phylogenetic relationship of '*Candidatus* Occultobacter vannellae' and '*Candidatus* Nucleophilum amoebae' with the *Gammaproteobacteria*. The phylogenetic tree (Phylobayes, CAT+GTR) is based on the 16S rRNA sequences, Bayesian posterior probabilities are indicated at the nodes.