

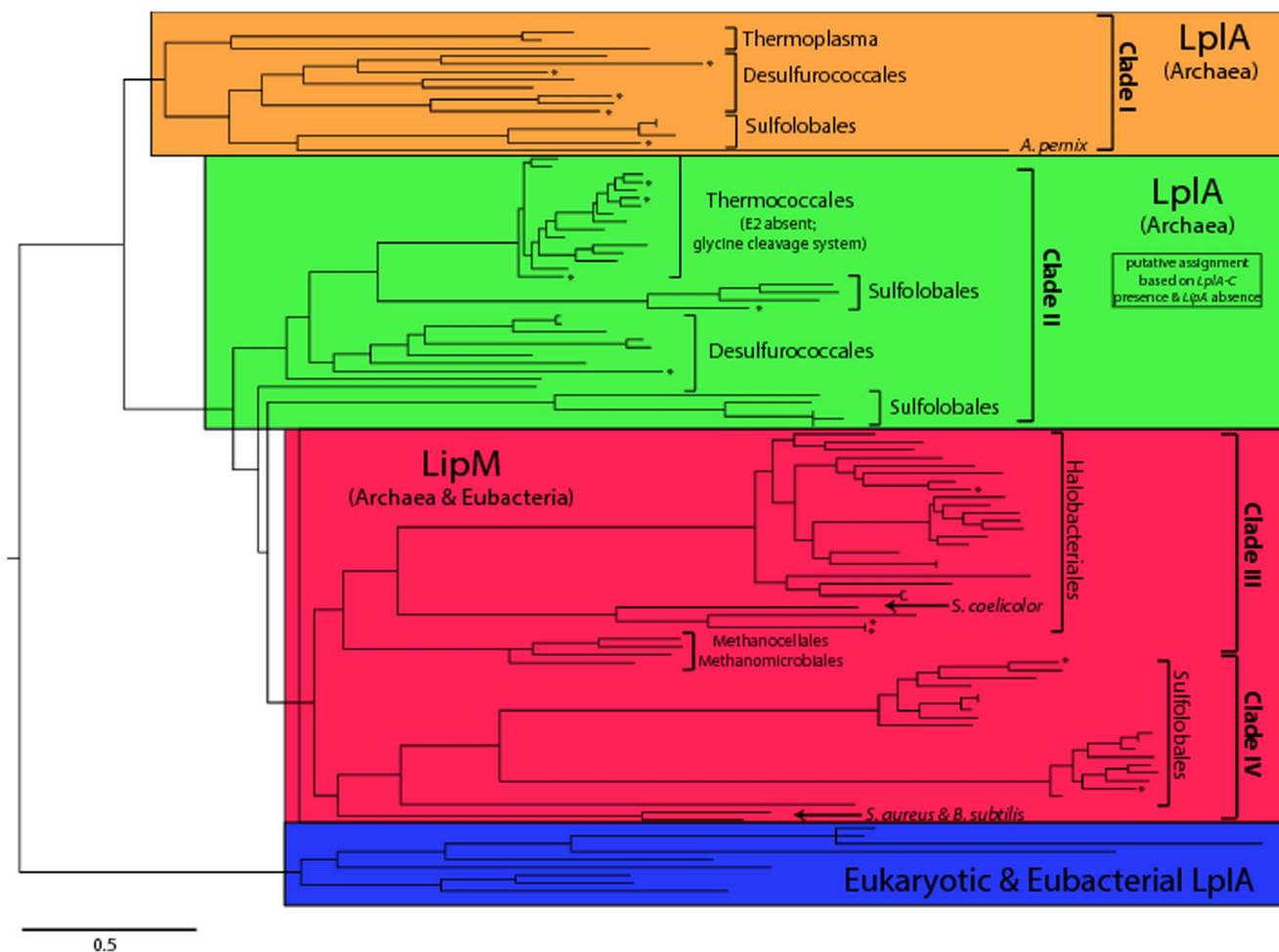


Correction

# Correction: Comparative Genomic Analysis Reveals 2-Oxoacid Dehydrogenase Complex Lipoylation Correlation with Aerobiosis in Archaea

The PLOS ONE Staff

There are errors in Figure 2. The authors have provided a corrected version here.



**Figure 2. Phylogenetic analysis of LipM and LplA.** Maximum likelihood phylogenetic tree including 131 LipM and LplA sequences from archaea, LplA sequences from major eukaryotic species (*S. cerevisiae*, *D. melanogaster*, *M. musculus* and *H. sapiens*) and LplA and LipM sequences from eubacteria representing Actinobacteria (*S. coelicolor*), Bacteroidetes (*B. thetaiotaomicron*), Firmicutes (*B. subtilis* and *S. aureus*) and Proteobacteria (*E. coli* and *B. pseudomallei*). Putative cases of horizontal gene transfer are indicated (asterisk) and major phylogenetic clades are highlighted: archaeal LplA (Clade I - orange; Clade II - green), LipM (red), and eukaryotic and eubacterial LplA (blue). The full phylogenetic tree including species names and bootstrap values is provided Figure S2.  
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## Reference

1. Borziak K, Posner MG, Upadhyay A, Danson MJ, Bagby S, et al. (2014) Comparative Genomic Analysis Reveals 2-Oxoacid Dehydrogenase Complex Lipoylation Correlation with Aerobiosis in Archaea. *PLoS ONE* 9(1): e87063. doi:10.1371/journal.pone.0087063.