Mitochondria branch within alphaproteobacteria

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The endosymbiotic origin of mitochondria was a key event in the origin of eukaryotic cells. Most studies by far suggest that mitochondria originated from an alphaproteobacterial-like ancestry [1]. Recently, it has been proposed that mitochondria evolved from a proteobacterial lineage that branched off before the divergence of all sampled alphaproteobacteria [2]. In this study, we found that site removal did not efficiently lower the compositional heterogeneity between the mitochondrial group and the non-fast-evolving alphaproteobacterial groups. The Alphaproteobacteria-sister tree topology could be the result of losing phylogenetic information in the removed sites. Furthermore, we used GC-rich mitochondria to efficiently reduce compositional heterogeneity between taxonomic groups and conducted multiple tree comparisons and proved the strong connection between mitochondria and alphaproteobacteria as in almost all cases, the former robustly branched within the latter. Our study provides strong evidence in support of the canonical view that mitochondria's closest relatives are among sampled alphaproteobacteria.
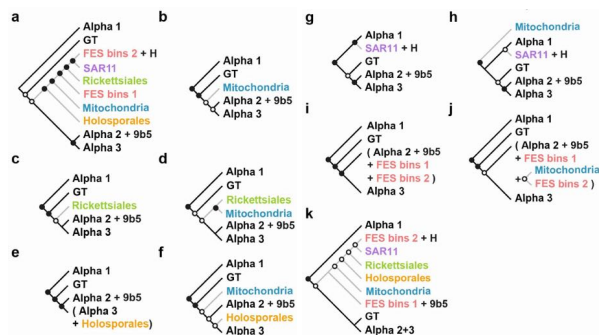
Figure 1: Schematic phylogenetic trees of alphaproteobacteria and mitochondria.

[1] Roger (2017) *Curr. Biol* **27**, R1177-R1192. [2] Martijn (2018) *Nature* **557**, 101-105.