

Novel eukaryotes for elucidating the early evolution of eukaryotes

Y. Inagaki

Center for Computational Sciences, University of Tsukuba, Ibaraki, Japan

One of the most fundamental questions in biology is how modern eukaryotic lineages have been diversified from the last eukaryotic common ancestor. Recent large-scale multigene (phylogenomic) studies on diverse eukaryotes clarified local branching patterns in the tree of eukaryotes, but we have yet to resolve the relationship amongst early diverged branches with confidence. There are two major obstacles to reconstruct the deep eukaryotic branches with high confidence, namely limitations on the size and taxon-sampling of data matrices for phylogeny. Firstly, phylogenetic signal in the data matrices analyzed in recent phylogenomic studies is likely insufficient to resolve the deep nodes of the tree. With respect to rapid growth of sequence data, this issue can be overcome in the near future by generating and analyzing data matrices larger than the previously analyzed ones. Secondly, the data matrices analyzed to date may have missed key taxa/lineages that are critical to resolve early eukaryotic evolution. The second issue potentially demands much more effort than the first one, as we need to discover novel eukaryotes in natural environments. I and my colleagues have been surveying, isolating and cultivating potentially novel eukaryotes for years. In this presentation, I introduce a series of novel “deep-branching” eukaryotes, of which we isolated and established laboratory cultures. We also discuss the significance of the mitochondrial or plastid genomes of some of those eukaryotes in the context of organellar genome evolution. Well, I should stop working on this abstract, since I’m currently in an ocean-view hotel room in Langkawi, Malaysia.