

BUILDING A LARGE PHYLOGENY OF ARCHAEA. A. J. Coleman¹ and F. U. Battistuzzi^{1,2} Oakland University (Department of Biology, 2200 Squirrel rd, Rochester, MI 48309, ajcolema@oakland.edu; ² battistu@oakland.edu)

Abstract: Evolutionary histories are a powerful tool to reconstruct not only the early stages of life but also to understand the characteristics of Earth as a habitable planet. Of the three domains of life Archaea are among the most ancient ones holding information regarding the earliest steps of life's evolution. Unfortunately, building stable archaeal phylogenies has proven to be an elusive task especially for poorly represented groups (e.g., Nanoarchaeota). This phylogenetic instability has often been attributed to taxon sampling or fast evolutionary rates among genes but little is known about the relative contribution of each of these conditions. We address this issue by using all of the available taxonomic samples to investigate the effect of evolutionary rates on a multi-gene dataset containing 135 species. Fifty individual trees were produced from fully represented orthologous groups but did not result in a consensus phylogeny. We therefore proceeded to evaluate the effect of gene-specific evolutionary rates by creating subsets with slow and fast evolving concatenated genes. A comparison of these two phylogenies shows a discrepancy in the location of the Thaumarchaeota, Nanoarchaeota and Korarchaeota suggesting an effect of evolutionary rates on their uncertain phylogenetic position. These unstable groups also negatively affect the overall accuracy of the trees in closely related clusters and also others that have traditionally been found to be phylogenetically stable. This analysis provides insights into the effect of evolutionary rates on deep phylogenies and suggests guidelines for future tree reconstructions.