

INVESTIGATING THE EFFECTS OF EVOLUTIONARY RATES ON PHYLOGENETIC ACCURACY OF THE ARCHAEA DOMAIN. A. J. Coleman¹, F. U. Battistuzzi^{1,2}, ¹Oakland University (Department of Biological Sciences, 2200 Squirrel rd, Rochester, MI 48309, ajcolema@oakland.edu; battistu@oakland.edu²)

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. Because taxon sampling limitations cannot be easily overcome, we focus on evolutionary rates by analyzing all of the available fully sequenced Archaea species (135) in a multi-gene dataset. Five different analyses were employed to probe the effect evolutionary rates have on the Archaea backbone as well as the relationships for the Class I and Class II Methanogen groups. A set of fifty individual trees were produced from fully represented orthologous genes but did not result in a consensus phylogeny for the Archaea backbone or Methanogen classes. We therefore proceeded to evaluate the effect of gene-specific evolutionary rates by creating subsets with slow and fast evolving concatenated genes. We also created a subset of concatenations by adding individual genes consecutively, moving from the slowest evolving to the fastest evolving genes. A comparison of these phylogenies show a discrepancy in the location of the Thaumarchaeota, Nanoarchaeota and Korarchaeota as well as the positions for the groups within Class I and Class II Methanogens suggesting an effect of evolutionary rates on their uncertain phylogenetic position. The fast evolving genes also negatively affect the overall accuracy of the trees in closely related clusters as well as others that have traditionally been found to be phylogenetically stable. This analysis provides insights into the effect of evolutionary rates on deep phylogenies and suggest guidelines for future tree reconstructions.