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Diversity of Eukaryotes and Their Genomes

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Abstract

My dissertation addresses two aspects of eukaryotic evolution, 1) the organization of eukaryotic diversity and 2) genomic variation in Foraminifera. The bulk of eukaryotic diversity is microbial with plants and animals representing just two of the estimated 75 lineages of eukaryotes. Among these microbial lineages, there are many examples of dynamic genome processes. Elucidating the origin and evolution of genome features requires a robust phylogenetic framework for eukaryotes. Taxon-rich molecular analyses provide a mechanism to test hypothesized evolutionary relationships and enable placement of diverse taxa on the tree of life. These analyses result in a well-resolved eukaryotic tree of life. Relaxed molecular clock analyses of this taxon-rich dataset place the origin on eukaryotes in the Paleoproterozoic, and suggest that all of the major lineages of eukaryotes diverged before the Neoproterozoic. This robust scaffold of the tree of eukaryotes is also used to elucidate common themes in genome evolution across eukaryotes. Mapping dynamic genome features onto this tree demonstrates that they are widespread in eukaryotes, and suggests that a common mechanism underlies genome plasticity. Foraminifera, a diverse lineage of marine amoebae, provide a good model system for investigating genome dynamics because they amplify portions of their genome and go through ploidy cycles during their life cycle. Assessment of nuclear dynamics in one species of Foraminifera, *Allogromia laticollaris* strain CSH, reveals that genome content varies according the life cycle stage and food source, which may differentially impact organismal fitness. The inclusion of diverse microbial eukaryotes enables better resolution of eukaryotic relationships and improves our understanding the dynamic nature of eukaryotic genomes.

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