

Scott Dawson, UC Berkeley

The evolution and consequent functional diversification of motor proteins such as the kinesins has played an important role in the evolution of the eukaryotic cytoskeleton. Recent phylogenetic analyses have proposed roughly ten major subfamilies of klps, yet the majority of sequences in these phylogenetic analyses derive from a limited sampling of diverse eukaryotic lineages such as protists. A robust molecular phylogeny of known kinesin subfamilies is essential for the future classification of new kinesins into orthologous subgroups. To explore and resolve evolutionary relationships of the kinesins, we have used multiple phylogenetic inference methods (maximum parsimony, minimum evolution, quartet puzzling, Bayesian inference) of more than 500 aligned kinesin motor domains derived from twenty-five publicly available genomic sequences of metazoans, fungi, plants, and microbial eukaryotes. These diverse eukaryotes represent over ten eukaryotic kingdom-level groups, and span the large evolutionary distance from deeply diverging protists (such as *Giardia*, *Leishmania*) to more recently evolved-metazoans. This extensive kinesin phylogeny significantly refines and expands our knowledge of kinesin family evolution. For example, we confirm the presence of at least ten major subfamilies, yet we define several novel subfamilies unique to several lineages of protists. The absence of members of particular kinesin subfamilies in more recently evolved lineages (such as the CENP-E subfamily in yeasts or the novel protist families) is likely due to lineage-specific gene loss. Also our phylogeny indicated that some named subfamilies are phylogenetically shallow (such as the Kip3), whereas others are deeply rooted (such as BimC). Further, Bayesian analysis has allowed us to resolve deep branching structure in the kinesin family which could aid in the classification of new kinesins. The ubiquity of the majority of kinesin subfamilies in diverse and deeply-branching eukaryotes suggests that these subfamilies arose from gene duplications early in eukaryotic history, prior to the divergences of known extant eukaryotes. This revised and expanded kinesin phylogeny has important implications for kinesin nomenclature, and we proposed an interim classification of “candidate” subfamilies to account for phylogenetic groups with no known function.