A kinesin family tree
Alison J. Kim and Sharyn A. Endow
Dept of Microbiology, Duke University Medical Center, Durham, NC 27710, USA

The kinesin tree was built from a sequence alignment of 144 kinesin motor domains from 31 species using the heuristic search method of PAUP v. 4.0b4a (Swofford, 1998), a maximum parsimony program, and random stepwise addition and ‘tree-bisection-reconnection’ (TBR) branch swapping. The tree is one of six optimal trees that were found in >530 tree-building trials and is arbitrarily rooted, using ScSmy1 as an outgroup protein. ScSmy1 is not known to be the ancestral kinesin but is a highly divergent kinesin protein. The numbers adjacent to nodes are the percentages of 950 bootstrap trials, performed by the heuristic method of PAUP and simple stepwise addition, in which the groups to the right were found. Horizontal branch lengths are proportional to the number of amino acid changes needed to explain the differences in protein sequences, as indicated by the scale. The tree has an overall length of 14,336.

Two kinesin subfamilies (KRP85/95, Unc104/KIF1) had bootstrap values of <90% by maximum parsimony analysis but >90% by neighbor-joining analysis, and are therefore shown as classes. Three subfamilies (Chromokinesin/KIF4, KHC, Kip3) include proteins that were not assigned to the group by parsimony analysis but were included in the classes in a tree built by neighbor joining. Assignment of these proteins to the classes was supported by analysis of sequence identity. Parsimony methods probably failed to assign these proteins to their classes because intermediate taxa are missing from the analysis. A subgroup of three proteins has separated from the main group in the C-terminal motor subfamily, indicating divergence within the class. The C-terminal motor subfamily is unusual in that it may contain only minus-end-directed motors, in contrast to the plus-end-directed kinesins outside the group. One of the proteins in the small group that has separated from the main group is also a minus-end-directed motor (S. A. Endow and A. J. Kim, unpublished). The two groups are therefore both assigned to the C-terminal motor subfamily on the basis

(See poster insert)
of their sequence similarity, domain organization and motility properties. Two *Drosophila* proteins, DmCmeta and DmCana, group together (bootstrap value = 100%), which indicates that they probably arose by gene duplication. These proteins are thought to be related to HsCENP-E (Yucel et al., 2000), but the grouping is not well supported by neighbor-joining or maximum parsimony bootstrap analysis at present, probably because closely related intermediate taxa are missing from the analysis.

The kinesin motor proteins transport vesicles and organelles along microtubules (Hirokawa, 1998) and are essential for chromosome alignment and spindle assembly/elongation (Endow, 1999). These cellular functions appear to segregate with different subfamilies and are color coded in the tree (greens, vesicle/organelle transport; reds, spindle/chromosome motility). Some classes (e.g. MCAK/KIF2) contain proteins that are implicated in both functions. It is therefore possible that this distinction between subfamilies will break down as more information about kinesin protein function is obtained.

The diagrams of representative proteins of various classes are based on atomic structures (Kozierski et al., 1997; Sabin et al., 1998), and information from EM images (Hirokawa, 1998), coiled-coil predictions by PAIRCOIL (Berger et al., 1995) and protein hydrodynamics. The C-terminal motor kinesin depiction contains a ribbon diagram of the crystal structure of homodimeric DmNcd. Another C-terminal motor kinesin, ScKar3, has recently been reported to exist in vivo as a heterodimer with a non-motor protein or as a monomer (Barrett et al., 2000), which indicates that several protein forms may exist within a given class. Similarly, KIF1A has been reported to be monomeric, but other members of the Unc104/KIF1 subfamily have been found to be dimeric – the diagram is based on EM images and the absence of a predicted coiled-coil region in the KIF1A protein. The folded structure of Chromokinesin/KIF4 is inferred from EM images and discontinuities in the predicted coiled coil. The MCAK/KIF2 diagram takes into consideration EM images, protein hydrodynamic data (Maney et al., 1998) and coiled-coil predictions.

Further information about the kinesin proteins, including a table giving alternative names and links to the DNA and protein databases, can be found at the Kinesin Home Page at http://www.blocks.fhcrc.org/~kinesin/ (Greene et al., 1996). Methods used to build the kinesin tree are described in Goodson et al. (1994) and Moore and Endow (1996). The tree search was performed by A. J. Kim and S. A. Endow in July 2000. The tree is not meant to be exhaustive and does not include all the known kinesin proteins, owing to the computational time required to build trees for large data sets and the uncertainty of some of the protein sequences, but includes kinesins identified in organisms as diverse as the protista, protozoa, fungi, vertebrates and higher plants. All the known *S. cerevisiae* kinesins are included in the analysis, together with all the reliable *C. elegans* and *D. melanogaster* kinesins identified to date. The analysis was supported by grants from the NIH and HFSP.


REFERENCES


* REFERENCES


* REFERENCES
A Kinesin Family Tree
Alison J. Kim and Sharyn A. Endow

Key

- Motor
- Coiled coil
- Tail

Abbreviations:
- KHC, Kinesin heavy chain
- LC, Light chain
- KRP85/95, Non-KRP subunit
- Tetramer
- Monomer
- Dimer w/o coiled coil
- C-terminus
- N-terminus

Journal of Cell Science 2000 (113, p. 3681-3682)