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(With significant input from Kelly Dawe, Russell Malmberg, Linda Wordeman, and Joe Howard)

We suggest that the kinesin community adopt the “type specimen” nomenclature scheme shown in Table 1. This naming convention is similar to the one first proposed by Hirokawa (1). In Hirokawa’s published naming convention, families are named for their first cloned member. In the convention we propose here, each family’s namesake is defined as the first kinesin in the family to be both functionally characterized at the protein level and to have its full-length sequence present in GenBank. This yields a standardized naming convention for kinesin wherein all families are named for their first full length, functionally characterized members. In the case of the KIF4 family, mouse KIF4 (4) has been chosen as the family’s type specimen despite the fact that *Drosophila* nod was the first KIF4 family member identified (13). This exception is made because independent phylogenetic analyses do not always group nod with the KIF4 family (1, 14-16).

It is important to note that this naming convention is in the spirit of the model for the naming of organisms proposed by Carl von Linné (Carolus Linnaeus; 17), which was later improved upon and standardized by Thomas A. Sprague (18). This organismal naming convention is one such that any species of organisms has a “type specimen.” The type specimen is based upon priority of publication and is considered to be the ideal for each species, but other species of that genus or family are not expected to be identical to the type specimen. Rather all genera are related phylogenetically and share some evolutionarily key characteristics in common. For instance, the type genus for the Rosaceae or rose family is *Rosa*. While apples don’t look much like roses, they are in the rose family, and bear key characteristics of roses including the presence of many stamens borne on a hypanthium in the flower. In the same way, we should expect members of any single kinesin family to share many things in common with the family’s type specimen, but deviation in function from that of the type specimen also should be expected for some family members.

Finally, there should be an accepted protocol for determining to which family a new kinesin sequence belongs. Our suggestion is to first do a BLAST search (19) using the full-length protein sequence for the kinesin of interest as the query. If all top hits are members of a single kinesin family, the kinesin of interest is probably also a member of that family. If this is not the case, we recommend that the researcher download a published kinesin motor core alignment such as one of the Lawrence et al. alignments* (16), and add their own kinesin’s motor core to that alignment (by hand or using an alignment tool such as Clustal 20). Next use a simple method for building a phylogenetic tree (such as Neighbor Joining 21) to find the family most closely related to the kinesin of interest. These alignment and treebuilding methods are available together on a webserver at <http://www.ebi.ac.uk/clustalw/>. As previously noted by Hirokawa, specific domains or motifs should also be utilized as criteria for classification (1). Although the relatedness of families to one another varies among the recently published phylogenies, the members of each family are relatively consistent among all published trees, making it possible to use any of them for family-level classification.

* Alignments ALIGN_000356, ALIGN_000357, and ALIGN_000358 are available online at <http://srs.ebi.ac.uk> in the SeqRelated library called EMBLALIGN.

Table 1. Standardized names for kinesin families based upon type specimens.

Standardized Name	Reference	Also Known As
MCAK	2	MmKIF2, MCAK, MCAK/KIF2, I-Type, KinI, M
KLP67A	3	Kip3, KinI, N-IIx
KIF4	4	Chromokinesin, Chromokinesin/KIF4, N-V
Unc-104	5	KIF1, N-III
CENP-E	6	N-VII
MKLP1	7	MKLP, N-VI
Kar3	8	DmNCD, C-terminal, C-I, C-II, C-IV
KIFC2	9	C-Terminal, C-I, C-II, C-III
KHC	10	KHC, Kinesin, Kinesin-I, N-I
KRP85/95	11	SpKRP85, Kinesin-II, N-IV
BimC	12	AnBimC, N-II

References:

- Hirokawa N. *Science* 1998; 279: 519-526.
- Wordeman L, Mitchison T. *J Cell Biol* 1995;128: 95-104.
- Pereira A, Dalby B, Stewart R, Doxsey S, Goldstein L. *J Cell Biol* 1997; 136: 1081-1090.
- Sekine Y, Okada Y, Noda Y, Kondo S, Alzawa H, Takemura R, Hirokawa N. *Journal of Cell Biology* 1994; 127: 187-201.
- Otsuka A, Jeyaprasath A, Garcia-Anoveros J, Tang L, Fisk G, Hartshorne T, Franco R, Born T. *Neuron* 1991; 6: 113-122.
- Yen TJ, Compton DA, Wise D, Zinkowski RP, Brinkley BR, Earnshaw WC, Cleveland DW. *EMBO Journal* 1991; 10: 1245-1254.
- Nislow C, Lombillo VA, Kuriyama R, McIntosh JR. *Nature* 1992; 359: 543-547.
- Meluh PB, Rose MD. *Cell* 1990; 60: 1029-1041.
- Saito N, Okada Y, Noda Y, Kinoshita Y, Kondo S, Hirokawa N. *Neuron* 1997: 425-438.
- Vale R, Reese T, Sheetz M. *Cell* 1985; 42: 39-50.
- Cole D, Cande W, Baskin R, Skoufias D, Hogan C, Scholey J. *J Cell Sci* 1992; 101: 291-301.
- Enos AP, R MN. *Cell* 1990; 60: 1019-1027.
- Zhang P, Knowles B, Goldstein L, Hawley R. *Cell* 1990; 62: 1053-1062.
- Moore JD, Endow SA. *BioEssays* 1996; 18: 207-219.
- Kim A, Endow S. *J Cell Sci* 2000; 113: 3681-3682.
- Lawrence CJ, Malmberg RL, Muszynski MG, Dawe RK. *J Mol Evol* 2002; 54: 42-53.
- Linnaeus C. *Species Plantarum*. 1753.
- Sprague T. *Standard-species*. *Kew Bull* 1926: 96-100.
- Altschul S, Gish W, Miller W, Myers E, Lipman D. *J Mol Biol* 1990;215: 403-410.
- Higgins D, Thompson J, Gibson T. *Methods Enzymol* 1996; 266: 383-402.
- Saitou N, Nei M. *Mol Biol Evol* 1987; 6: 406-425.