

between classes as shown by the branching order at the centre of the tree is unreliable, but evolutionary information can be derived within a class. Each class is defined by the first node represented in >90% of bootstrap trials starting from the centre of the tree. The inclusion of myosin sequence data recently added to the public databases has resulted in the clustering together at such a node of some of the more disparate examples based on their motor domains (Classes III, XII, XVI and the chitin synthase containing myosins). While this would normally be taken to define a class, the low sequence similarity (long branches), lack of significance for this grouping obtained by maximum parsimony algorithms and general

dissimilarity between complete molecules argue against such a classification. Analysis of the sequence identity of the two chitin synthase myosins (Pg csm1 and En csmA) shows they are orthologues; they also group together by distance matrix analysis with >90% confidence. This evidence allows us to define a new class (XVII), and the branches have been coloured accordingly.

The molecular cartoons serve to indicate possible molecular structure, especially the expected single- or double-headed nature of the myosins. Regarding the myosin XIII cartoon, the '?' denotes one of the sequences (Acl myo1) having a

surprisingly short tail, which may reflect a sequence truncation.

The complete alignment, the bootstrapping data, references and links for the software packages and hyperlinks to database entries for all the myosins included in the analysis, along with other myosin-related information, can be found at the Myosin Homepage: www.mrc-lmb.cam.ac.uk/myosin/

Cell Science at a Glance on the Web

Electronic copies of the full-size poster insert are available in the online version of this article (see www.biologists.com/jcs). Files in several formats are provided and may be downloaded for use as slides.