References

Acharya, N. N. and Swain, D. 2003. Hybrid performance in relation to genetic divergence in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. Crop res., 25 (2): 312-315.

Chaudhary, S., Sagar, P. and Hooda, B. K. 2015. Multivariate analysis of Pearl Millet data to delineate genetic variation. Forage Res., 40(4): 201-208.

Hamman, H. K. 1972. Utilization of multivariate statistics for discriminating among flue-cured tobacco varieties. Technical Bulletin Number 212, North Carolina Agricultural Experimental Station (Raleigh, NC).

http://www.religareonline.com /research/Disclaimer/ Disclaimer_rcl.html

Jeffers, J. N. R. 1967. Two case studies in the application of principal component analysis. App. Stat., 16: 225-236.

Kaiser, H. F. 1960. The application of electronic computers to factor analysis, Educ. Psychol. Meas., 20: 141-51.

Neeru, Thakral, N. K., Avtar, R. and Singh, A. 2015. Evaluation and classification of Indian mustard (*Brassica juncea* L.) genotypes using principal component analysis. J. of Oilseed Brasssica. 6(1): 167-174.

Shathi, D. A., Arifuzzaman, M., Biswas, B. K., Hasanuzzaman, M. and Azad, A. K. 2012. Genetic divergence in mustard (Brassica spp. L). African J. of Plant Sci., 6(8): 239-243.

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Role of Molecular Motors in Endosomal Dynamics: A review

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Abstract

Molecular motors are continually agitated by random Brownian motion, which provides both challenges and opportunities for energy conversion mechanisms. Molecular motors, an important class of molecular machines, harness various energy sources to generate unidirectional mechanical motion. In biological systems, molecular motors made of proteins and nucleic acids are ubiquitous, and commonly use the chemical energy of ATP or the electrochemical potential of protons across the cell membrane (the so-called proton-motive force) as an energy source. ATP synthase and V-ATPase also act as energy converters, in which ATP chemical energy and proton electrochemical potential are reversibly converted via mechanical rotation. In the cytoplasm of eukaryotic cells, three different classes of motors that generate linear movement are known to exist – myosin, kinesin and dynein. Most motors studied so far in some detail can generate a force that is sufficient to move even large objects through viscous cytoplasm.

Key words : ATP, brownian, dynein, kinesin, molecular motors, myosin.

Molecular motors are enzymes that transform chemical energy into mechanical work. Cytoskeletal motor proteins that move unidirectionally along an oriented polymer track either towards the plus end or the minus end of the track. These have the ability to use chemical energy to propel them along a linear track, with the direction of sliding dependent on the structural polarity of the track. All of them generate motion by coupling nucleoside

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triphosphate hydrolysis to a large-scale conformational change in a protein. In the cytoplasm of eukaryotic cells, three different classes of motors that generate linear movement are known to exist - myosin, kinesin and dynein.

Myosin : Skeletal muscle myosin, which is responsible for producing force during muscular contraction, was the first motor protein to be discovered. There are at least 24 distinct myosin families in higher species, according to the current boom of genetic information. Myosin II, the second isolating myosin, is a muscle protein that works with actin to generate contraction. The elongated protein known as myosin II (see below) is composed of two heavy chains and two copies of each of the two light chains. The force-generating mechanisms are located in a globular head domain at the N-terminus of each heavy chain, which is followed by a very lengthy amino acid sequence that creates an expanded helix and facilitates heavy chain dimerization.class-2 myosins which encompass the myosins involved in muscle contraction are referred to as 'conventional,' all other myosins as 'unconventional

Unconventional myosins : These unusual myosins are not involved in filament formation or contraction. They play a crucial role in a number of cellular processes, such as the transportation of organelles, organelles, and other cargo along actin filaments. Myosin I proteins are significantly smaller molecules (about 110 kD in mammalian cells) without the lengthy tail of myosin II, but they nonetheless include a globular head group that functions as a molecular motor, similar to that of myosin II. Their tails attach to other structures, including membrane vesicles or organelles, as opposed to dimerizing. The associated cargo can then be transported by the movement of myosin I along an actin filament.

Conventional myosins : Traditional myosin molecules are hexamers with two globular heads (each with one active site for ATP processing and one actin binding site), a long coiled-coil tail, and four sets of polypeptide chains: heavy chains (HCs), regulatory light chains (RLCs), and essential light chains (ELCs). At the intersection of the head and tail, the light chains are crucial in controlling the activity of this enzyme. The three cellular myosins, M2A, M2B, and M2C, which are nonsarcomeric, have a variety of roles in vesicle trafficking, endothelial cell migration, cell adhesion, polarity, fusion, and cytokinesis, as well as neuronal dynamics, axon guidance, and synaptic transmission. These three traditional myosins have distinct functional roles that are unique to each cell lineage during development and maturation; the precise roles depend on the developmental stage of the cell, the cellular location, the upstream regulatory controls, and the relative isoform expression (Fig.1).

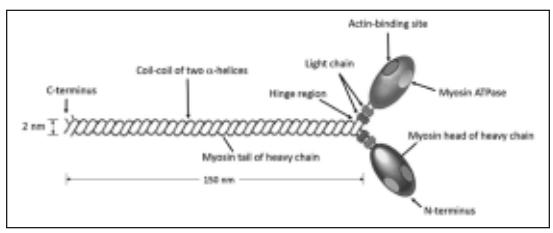

Fig. 1. Structure of myosin

There Are Two Types of Microtubule Motor Proteins:

- Kinesins
- Dyneins

Kinesin : Kinesin is a motor protein that moves along microtubules. Kinesins are ubiquitous in eukaryotic cells, in part because most members of the kinesin family have essential roles in cell division (Clancy and Block, 2012). It was first identified in the giant axon of the squid, where it carries membrane -enclosed organelles away from the neuronal cell body toward the axon terminal by walking toward the plus end of microtubules. Kinesin is similar

structurally to myosin II in having two heavy chains and two light chains per active motor, two globular head motor domains, and an elongated coiled coil responsible for heavy chain dimerization. Like myosin, kinesin is a member of a large protein superfamily, for which the motor domain is the only common element. These are a type of motor proteins that have been preserved throughout evolution. They use the energy produced by ATP hydrolysis to carry out work (Fig. 2). Kinesins interact with microtubules, which are dynamic polar -tubulin filaments that serve a variety of biological purposes. Transport kinesins can move cargo from one area of the cell to another by coupling ATP hydrolysis to translocation along microtubules (Ohi and Wordeman (2013). They are essential for mitosis and the movement of organelles and vesicles. Techniques for measuring the characteristics of certain proteins were created not long after the discovery of kinesin in 1985. These methods have been extensively used to study kinesin over the years, and it is fair to say that kinesin research has coincided with the development of single molecule approaches (Kapitein and Peterman, 2009).

A common, high-homology ATP-binding domain seen in members of the kinesin superfamily is abundant in both and secondary structure. This domain is frequently referred to as the motor domain (MD), sometimes even in the case of non-motor kinesins, because the majority of members of the kinesin superfamily-namely, conventional kinesin or Kinesin-1 as well as many kinesin-related proteins of the other kinesin classes-are involved in active transport and movement. The majority of other domains are class-specific and variable. The same is true of the motor domain's sequential position.

This enables the classification of the kinesin family into N-type kinesins (Kinesin-1 to 12), M-

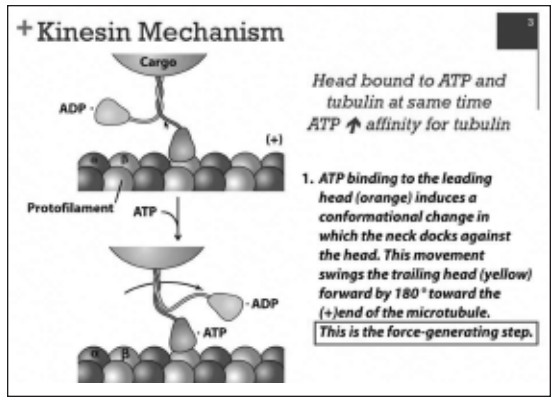

Fig. 2. Kinesin mechanism

type kinesins (Kinesin-13), and C-type kinesins (Kinesin-1 to 12), with the motor domain at or near the N-terminus and flanked on both sides by additional domains (Kinesin-14). Surprisingly, the functional classification of plus-end directed motors (N-type), minus-end directed motors (C-type), and non-motor kinesins matches this domain structure-based classification (I-type).

Myosin and kinesin MD's folds unexpectedly resemble one another, indicating that both motor proteins descended from a single ancestor (Kull *et* al. 1998; Vale and Milligan 2000). This led to theories that myosin and kinesin might share a mechanism. Four motifs seen in myosin, G-proteins, and other P-loop-containing proteins with a Walker fold (Walker *et* al., 1982) make up the ATP binding site in the kinesin motor domain. A phosphate binding loop (P-loop) is formed by the Walker A motif (GxxxxGKT/S) between helix 2 and -strand 3 of the central -sheet. This loop holds the nucleotide's phosphate firmly. The presence or absence of -phosphate affects the conformation and interaction of two additional motifs, the switch-1 (NxxSSR) and switch-2 (DxxGxE) motifs. Adjacent structural elements communicate and magnify these local changes, which ultimately have a large-scale impact.

Dynein : Dyneins are found in many

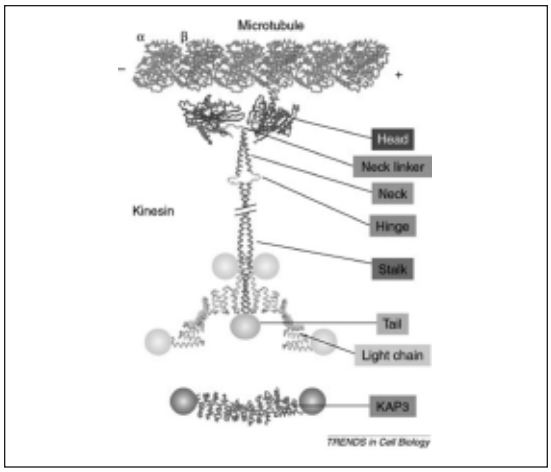

Fig. 3. Microtubule-kinesin interaction (Mandelkow and Mandelkow, 2002)

eukaryotes, including fungi, worms, insects, and vertebrates, but analysis of the Arabidopsis genome shows that they are absent in plants.These are found in many eukaryotes, including fungi, worms, insects, and vertebrates, but analysis of the Arabidopsis genome shows that they are absent in plants..

One, two, or three dynein heavy chains (DHCs) and a number of smaller subunits make up dynein complexes. An N-terminal tail and a

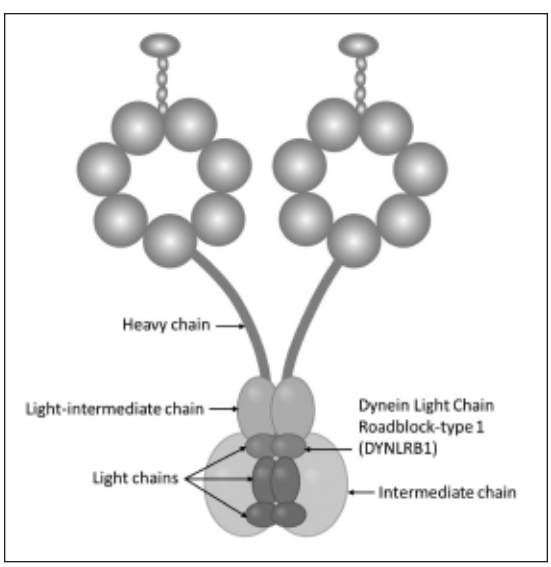

Fig. 4. Dynein structure

C-terminal motor domain make up the two domains of the big DHC, which has between 4,000 and 5,000 amino acids (Fig. 4). The conserved motor domain, which consists of six AAA+ domains and a C domain, transforms the energy of ATP hydrolysis into mechanical work while the tail domain binds the majority of the smaller subunits and promotes anchoring of the dynein complex to other payloads. The DHC motor domain is substantially responsible for each dynein complex's functional characteristics. Most species with motile cilia and flagella possess 15 or more DHC genes, according to recent whole-genome DNA sequencing of a variety of taxa.

Dynein is thought to be the main motor for microtubule-based retrograde axonal transport, and dynein has been shown to be associated with mitochondria. Cytoplasmic dynein 1 moves membrane organelles, kinetochores, and viruses along microtubules. It is also a motor for retrograde axonal transport and is involved in the assembly and function of the mitotic spindle. A second type of cytoplasmic dynein, cytoplasmic dynein 2, is responsible for a component of intraflagellar transport (IFT), namely the transport of protein complexes from the tips of cilia and flagella to their base, which occurs between axonemal microtubules and the flagellar membrane.

References

Asai, D. J. 1995. Multi-dynein hypothesis. Cell Motil. Cytoskeleton 32, 129-132.

Clancy, B. E. and Block, S. M. 2012. In: Comprehensive Biophysics.

Glater, E. E. Schwarz, T. L. 2009. In: Encyclopedia of Neuroscience.

Gibbons. Dynein family of motor proteins: Present status and future questions. Cell Motil. Cytoskeleton 32, 136-144.

Pfister, K. K. 2021. In Encyclopedia of Biological Chemistry (Third Edition).

Pfister, K. K. 2013. in Encyclopedia of Biological Chemistry (Second Edition).

Kamiya, R. 2002. Functional diversity of axonemal dyneins as studied in Chlamydomonas mutants. Int. Rev. Cytol. 219, 115-155.

Pfister, K. K. 2004. In Encyclopedia of Biological Chemistry.

Kull, F. J., Vale, R. D., Fletterick, R. J. 1998. The case for a common ancestor: kinesin and myosin motor proteins and G proteins. Journal of Muscle Research and Cell Motility. 19:877-886.

Lukas, C., Kapitein, Erwin J. G. Peterman. 2009. In Single Molecule Biology.

Mandelkow, E. and Mandelkow, E. M. 2002. Kinesin motors and disease. Trends in cell biology, 12(12), 585-591.

Marx, A., Hoenger, A. and Mandelkow, E. 2009. Structures of kinesin motor proteins. Cell motility and the cytoskeleton, 66(11), 958-966.

Morris, R. L., Hoffman, M. P., Obar, R. A., McCafferty, S. S., Gibbons, I. R., Leone, A. D., Cool, J., Allgood, E. L., Musante, A. M., Judkins, K. M., Rossetti, B. J., Rawson, A. P., *et al*. 2006. Analysis of cytoskeletal and motility proteins in the sea urchin genome assembly. Dev. Biol. 300, 219-237.

Gilbert, P. Sardar, H. S. 2012. In Comprehensive Biophysics.

Ohi, R. Wordeman, L. 2009. In Encyclopedia of Biological Chemistry (Second Edition).

Toshiki, Y. 2009. In Methods in Cell Biology.

Vale, R. D. and Milligan, R. A. The way things move: looking under the hood of molecular motor proteins. Science. 2000; 288(5463): 88-95.

Walker, J. E., Saraste, M., Runswick, M. J., Gay, N. J. Distantly related sequences in the alpha-and beta-subunits of ATP synthase, myosin, kinases and other ATP-requiring enzymes and a common nucleotide binding fold. Embo J. 1982; 1(8): 945-51.

Wickstead, B. and Gull, K. 2007. Dyneins across eukaryotes: A comparative genomic analysis. Traffic 8, 1708-1721.

Wilkes, D. E., Watson, H. E., Mitchell, D. R., and Asai, D. J. 2008. Twenty-five dyneins in Tetrahymena: A re-examination of the multidynein hypothesis. Cell Motil. Cytoskeleton 65, 342-351.