

Gene Section

Review

MYLK (myosin light chain kinase)

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Published in Atlas Database: June 2012

Online updated version : <http://AtlasGeneticsOncology.org/Genes/MYLKID43364ch3q21.html>
DOI: 10.4267/2042/48362

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Identity

Other names: AAT7, KRP, MLCK, MLCK1, MLCK108, MLCK210, MSTP083, MYLK1, smMLCK

HGNC (Hugo): MYLK

Location: 3q21.1

Note

Strand: Reverse (minus, -); Genomic Size: 272007.

This gene, a member of the immunoglobulin gene superfamily, encodes myosin light chain kinase (MLCK), which is a calcium/calmodulin dependent kinase that phosphorylates myosin regulatory light chains (Potier et al., 1995) to regulate cell contractility (De Lanerolle et al., 1991; Garcia et al., 1995; Garcia et al., 1997b; Katoh et al., 2001) and cytokinesis (Dulyaninova et al., 2004; Fishkind et al., 1991; Matsumura et al., 2011; Poperechnaya et al., 2000).

Multiple transcript variants of this gene have been identified that produce both nonmuscle and smooth muscle isoforms of MLCK (Garcia et al., 1997a; Lazar and Garcia, 1999; Verin et al., 1998b).

In addition, using a separate promoter in an intron in the 3' region, it encodes telokin, a small protein identical in sequence to the C-terminus of MLCK (Gallagher and Herring, 1991; Watterson et al., 1999), which functions to stabilize unphosphorylated myosin filaments in smooth muscle (Kudryashov et al., 2002; Shirinsky et al., 1993).

A pseudogene of MYLK is located on the p arm of chromosome 3 (Brand-Arpon et al., 1999; Giorgi et al.,

2001; Han et al., 2011) (modified from RefSeq, July 2008).

DNA/RNA

Description

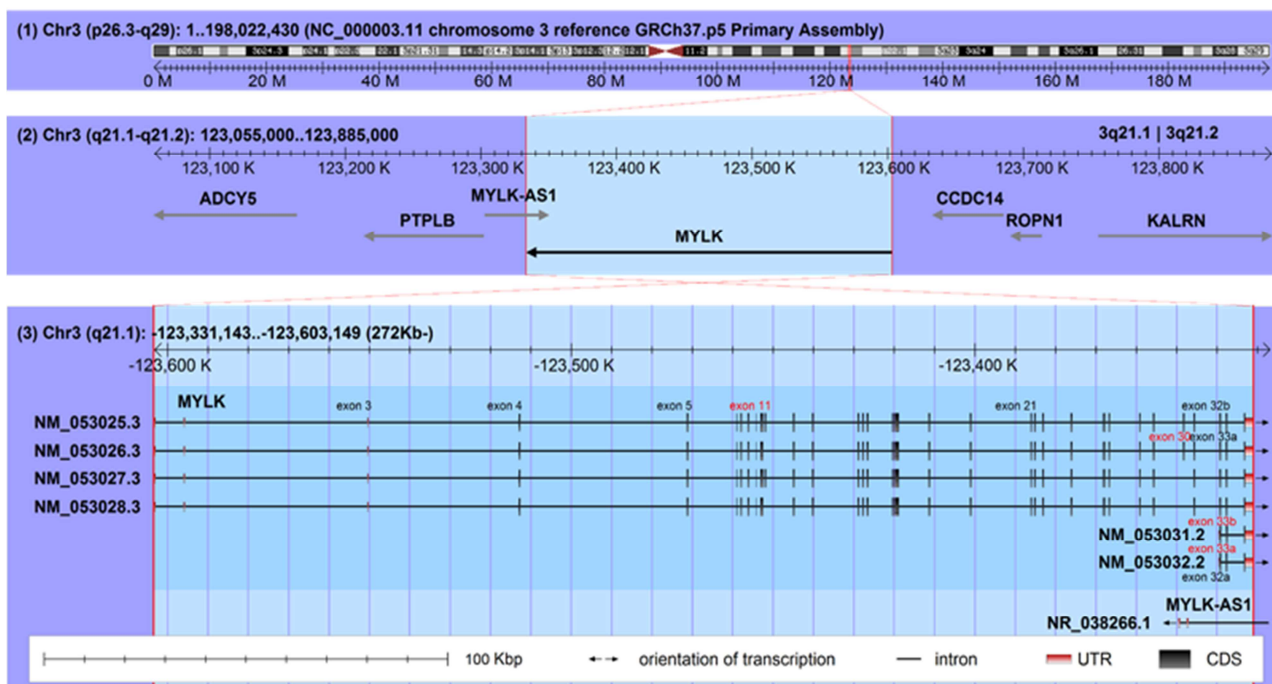
The gene is composed of 34 exons, 31 out of which are coding exons.

Transcription

Multiple MLCK isoforms are produced from the same MYLK gene by alternative splicing or alternative initiation (Lazar and Garcia, 1999; Verin et al., 1998b; Watterson et al., 1999). Six transcript variants have been identified that produce four kinase domain-encoding isoforms and two isoforms of telokin. Additional variants exist but lack full length transcripts. The longest transcript (nmMLCK1), which encodes the full length nonmuscle isoform (NM_053025), is a 7852 bp mRNA with a 5745 bp open reading frame from base pair 283 to 6027.

Pseudogene

PGOHUM00000250243, PGOHUM00000238157, and PGOHUM00000238160 (Human Pseudogenes, Build 61). Note: Partially duplicated from the original MYLK gene, the MYLKP1 pseudogene (PGOHUM00000250243) is proposed to negatively regulate MYLK gene expression (Han et al., 2011).



The MYLK gene viewed at three different levels of detail (highlighted between two red vertical boundary lines). (1) Overview within chromosome 3. (2) Partial regional view within chromosome 3q21.1-3q21.2. (3) Detailed view within chromosome 3q21.1 showing six of the transcription variants of MLCK, which include nmMLCK1 (NM_053025), 2 (NM_053026), 3A (NM_053027), 3B (NM_053028), and two telokin (NM_053031 and NM_053032). The transcripts are not drawn in exact proportion so that their introns and exons, including CDSs and UTRs, can all be seen at a limited resolution. Abbreviations: Chr, chromosome; CDS, coding sequence; UTR, untranslated region.

Protein

Description

The full length isoform nmMLCK1 is a 1914-aa protein with a molecular weight of 210715 Da.

All isoforms including telokin bind calmodulin (Davis et al., 1996; Gallagher and Herring, 1991; Geguchadze et al., 2004; Katoh et al., 2001). Various MLCK protein isoforms that result from the same MYLK gene (Lazar and Garcia, 1999) by alternative splicing or alternative initiation may be differentially regulated to achieve a tissue-specific spatiotemporal control of the binding (Davis et al., 1996; Dudek et al., 2002; Dudek et al., 2004; Hatch et al., 2001; Kishi et al., 1998) and catalytic activity of MLCK.

The full length isoform nmMLCK1 is activated by post-translational modifications (PTMs) such as phosphorylation on Tyr-464 and Tyr-471 (coded by exon 11) (Birukov et al., 2001; Dudek et al., 2010). These PTMs are catalyzed by c-Abl (Dudek et al., 2010), p60Src (Birukov et al., 2001; Garcia et al., 1999), cAMP-dependent protein kinase (PKA) (Garcia et al., 1997a; Verin et al., 1998a) and p21-activated kinases (Goeckeler et al., 2000; Sanders et al., 1999).

Additional regulatory mechanisms involve acetylation (Shin et al., 2009), carboxyl-terminal deglutamylation (Rogowski et al., 2010), and kinase activation after thrombin, tumor necrosis factor (TNF), sphingosine 1-phosphate, G proteins, and during cell cycle (Garcia et al., 1995; Petrache et al., 2003; Poperechnaya et al., 2000; Somlyo and Somlyo, 2003; Ye et al., 2006; Ye and Ma, 2008).

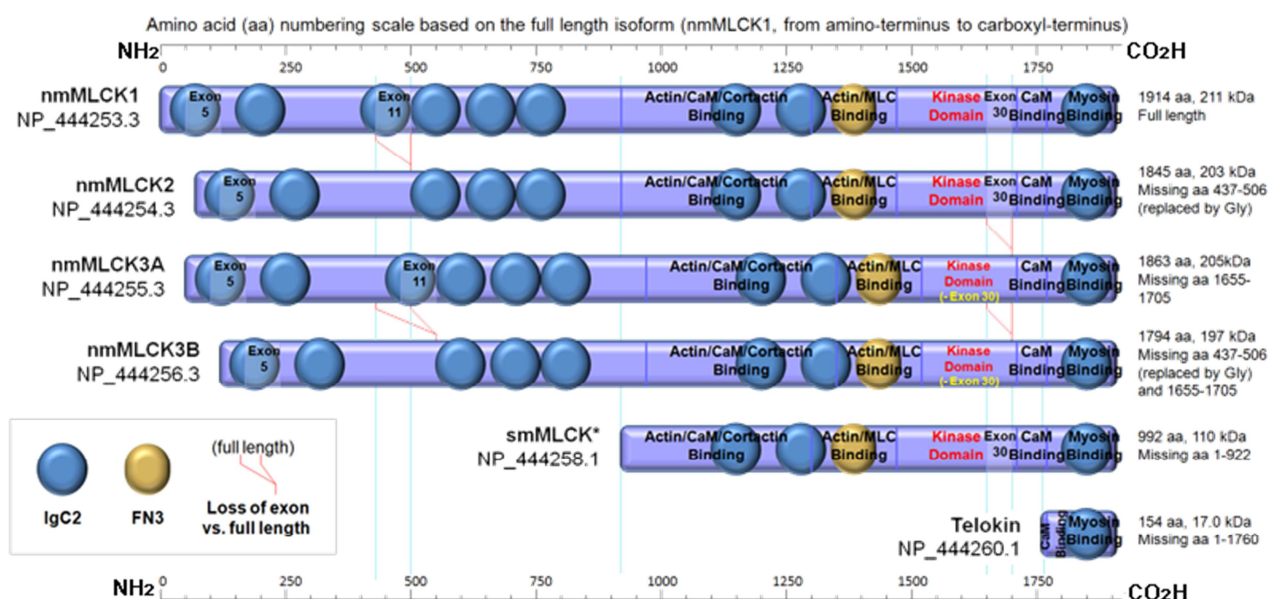
Expression

The nmMLCK or smMLCK isoforms and telokin are ubiquitously expressed in various adult and fetal tissues and in cultured endothelium with qualitative expression appearing to be neither tissue- nor development-specific (Garcia et al., 1997a; Lazar and Garcia, 1999; Potier et al., 1995; Verin et al., 1998b; Watterson et al., 1999).

The nmMLCK 1 and 2 isoforms are dominant isoforms in nonmuscle (endothelial) cells (Brown et al., 2010; Garcia et al., 1997a; Lazar and Garcia, 1999; Verin et al., 1998b).

Localisation

Lamellipodium; cytoplasm; cytoskeleton; stress fiber; cytosol; cleavage furrow.



Representative MLCK protein isoforms shown with select structural/functional information, as compared with the full length isoform (nmMLCK1). The nonmuscle MLCK isoform variants (nmMLCK 1, 2, 3A, 3B) differ in the presence or absence of exons 11 and 30. All nmMLCK variants possess unique amino termini that are absent in the smooth muscle isoform, smMLCK, and two isoforms of telokin. The longer isoform of telokin, differing by one amino acid from its shorter version (with the aa 1790 deletion), is identical to the C-termini of nmMLCK and smMLCK isoforms shown (Watterson et al., 1999). Abbreviations: aa, amino acid; CaM, calmodulin; IgC2, immunoglobulin C-2 type domain; FN3, fibronectin type 3 domain. *Note: NCBI RefSeq NM_053030.2 (NP_444258.1) was permanently suppressed because there was insufficient support for the transcript and the CDS was partial.

Function

Belongs to protein kinase superfamily, non-receptor Ser/Thr protein kinase, EC 2.7.11.18, calcium/calmodulin-dependent protein kinase (CAMK) group, MLCK family.

Regulates smooth muscle and nonmuscle cell contractile processes (De Lanerolle et al., 1991; Garcia et al., 1995; Katoh et al., 2001; Somlyo and Somlyo, 2003), via phosphorylation of myosin light chains (MLC), or through a non-kinase activity (Dudek et al., 2004; Herring et al., 2006; Kudryashov et al., 2002; Nakamura et al., 2008; Shirinsky et al., 1993).

Regulates cyto genesis (Dulyaninova et al., 2004; Fishkind et al., 1991; Matsumura et al., 2011; Poperechnaya et al., 2000).

Regulates other related cellular processes including cell adhesion, migration, morphology, and inflammatory responses (Garcia et al., 1998; Savkovic et al., 2001), e.g., apoptosis (Mills et al., 1998; Petrache et al., 2003; Wright et al., 1993), and vascular permeability (Dudek et al., 2004; Garcia et al., 1995; Garcia et al., 1998; Shen et al., 2010; Vandenbroucke et al., 2008; Yuan et al., 2002), all via the regulation of cytoskeletal rearrangements. Genetic variants in MYLK are implicated in inflammatory disorders such as asthma and acute lung injury (Flores et al., 2007; Gao et al., 2006; Gao et al., 2007).

Implicated in tumor formation and metastasis (see below).

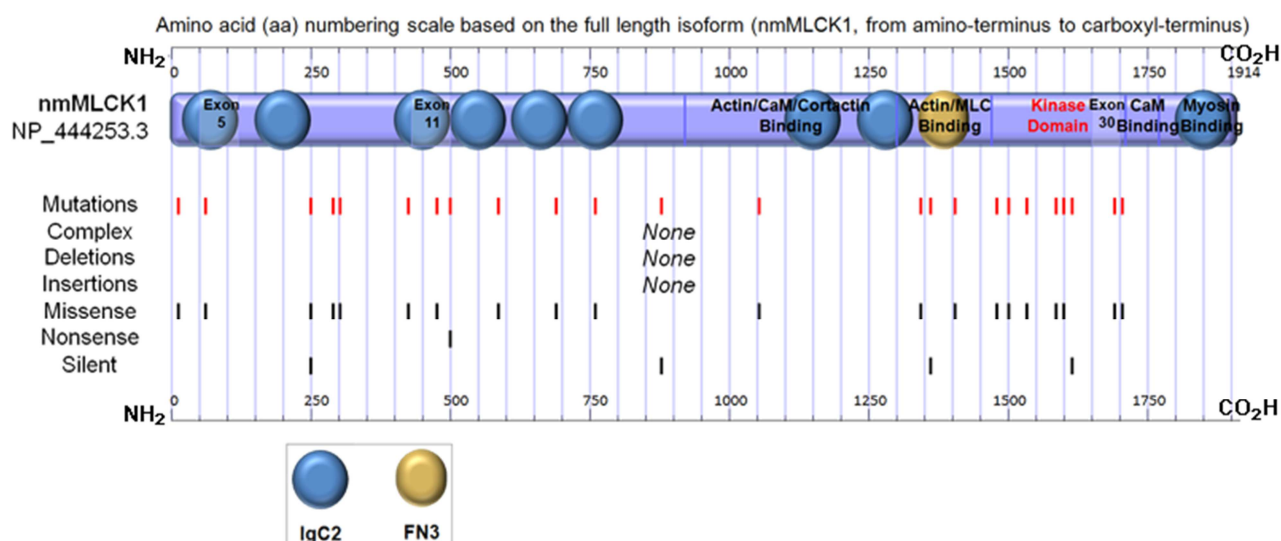
Homology

The human MYLK gene is conserved in Euteleostomi, with a high percentage of identity in the pairwise alignment of protein/DNA vs. chimpanzee (99,1% / 99,4%), monkey (97,3% / 97,0%), dog (89,1% / 89,0%), mouse (85,9% / 85,6%), rat (85,4% / 86,0%), chicken (71,4% / 68,8%), and zebrafish (63,0% / 65,5%) (Homologene). The paralogs of human MYLK gene include MYLK2-4, DAPK1-3, STK17A and STK17B, and SPEG (Ensembl) (Manning et al., 2002).

Mutations

Note

Some protein-coding somatic mutations in MYLK are associated with cancers (Catalogue of Somatic Mutations in Cancer-COSMIC) (Greenman et al., 2007). Several variants of MYLK are associated with familial aortic dissections (Wang et al., 2010). A few race-specific single nucleotide polymorphism (SNP) variants of MYLK, both in coding and noncoding regions, are associated with the susceptibility to acute lung injury, sepsis and severe asthma (Flores et al., 2007; Gao et al., 2006; Gao et al., 2007).



Cancer-associated somatic mutations in MYLK in the protein coding region (Catalogue of Somatic Mutations in Cancer-COSMIC). Abbreviations: CaM, calmodulin; IgC2, immunoglobulin C-2 type domain; FN3, fibronectin type 3 domain; Complex, complex substitutions; Missense, missense substitutions; Nonsense, nonsense substitutions; Silent, silent substitutions.

Implicated in

Cancers

Note

Myosin light chain kinase (MLCK) plays a crucial role in the cell migration and tumor metastasis. Some somatic mutations in MYLK are associated with cancers (Greenman et al., 2007). MLCK is critical for adhesion turnover at the cell front, a process central to migration (Webb et al., 2004) and it is involved in membrane blebbing (Godin and Ferguson, 2010). Deficiency in MLC phosphorylation causes cytokinesis failure and multipolarity (hence genomic instability) in cancer cells (Wu et al., 2010).

Breast cancer

Note

MLCK activity correlates the recruitment of nonmuscle myosin IIA and myosin IIB into the spreading margin of MDA-MB-231 breast cancer cells, with both myosin isoforms required for cell migration but only myosin IIB critical to lamellar protrusion (Betapudi et al., 2006).

MLC phosphorylation by MLCK through $\beta 1$ -integrin is required for actin stress fiber formation and the dormancy-to-proliferation metastatic switch for latent breast cancer cells (Barkan et al., 2008; Barkan et al., 2011). MLCK functions downstream of Ras, MAP kinase kinase (MEK) and extracellular signal regulated kinase (ERK) to promote invasive migration of breast cancer cells in an integrin-selective manner, i.e., mediated by a $\beta 1$ -integrin (probably $\alpha 5\beta 1$) and $\alpha 5\beta 5$, but not by $\alpha 5\beta 3$ (Mierke, 2011; Mierke et al., 2011b; Nguyen et al., 1999; Zhou et al., 2008).

Endothelial nmMLCK is activated by invasive breast cancer cells at the invasion site, leading to regional MLC diphosphorylation and myosin contraction.

Blocking endothelial MLC diphosphorylation blunts tumor transcellular (i.e., through individual endothelial cells), but not paracellular (i.e., through cell-cell junctions) invasion (Khoun et al., 2010). Human mammary tumor cells exhibit at least two modes of invasive migration, including the extracellular proteolysis-dependent mesenchymal mode (invadopodia-associated extracellular matrix degradation) (Alexander et al., 2008) and the proteolysis-independent amoeboid mode, with both modes mediated by MLCK and Rho kinase ROCK (Alexander et al., 2008; Torika et al., 2006).

TNF induction of apoptosis and DNA fragmentation requires MLCK activation in mammary carcinoma and other cancer cell lines (Wright et al., 1993).

MLCK is responsible for high proliferative ability of breast cancer cells via anti-apoptosis (Cui et al., 2010). The increase in MLC phosphorylation correlates with apoptotic blebbing (Mills et al., 1998).

Subsequent MLC dephosphorylation that results from a proapoptotic agent or MLCK inhibition (inhibitor or antibody) precedes caspase activation (Fazal et al., 2005), which further induces apoptosis *in vitro* and *in vivo*, and retards the growth of mammary cancer cells in mice (Fazal et al., 2005; Gu et al., 2006).

Lung cancer

Note

The invasiveness of tumor cells depends in part on their motility, which in turn depends on cytoskeletal function (Minamiya et al., 2005). The expression level

of MLCK, the cytoskeletal regulator, correlates with disease recurrence and distant metastasis in non-small cell lung cancer (NSCLC) (Minamiya et al., 2005). E1AF, an Ets family transcription factor frequently overexpressed in NSCLCs, induces motility and invasion as well as tumorigenesis and metastasis in NSCLC cells in a MLCK-dependent pathway (Hakuma et al., 2005). A few anti-cancer drug candidates, including glabridin, 7-chloro-6-piperidin-1-yl-quinoline-5,8-dione (PT-262), and all-trans-retinoic acid (ATRA), inhibit cell metastasis by decreasing cancer cell migration and invasion of human lung adenocarcinoma A549 cells via modulation of expression (Gui et al., 2011) or activity (Tsai et al., 2011a; Tsai et al., 2011b) of MLCK. Glycosylphosphatidylinositol-anchored receptor CD24 is found to enhance invasion of A125 human lung cancer cells through increased generation or transmission of contractile forces which is dependent on MLCK activity (Mierke et al., 2011a).

Colon cancer

Note

MLCK is differentially expressed in microsatellite stable (MSS) sporadic colon cancer and hereditary nonpolyposis colorectal cancer (HNPCC) (Lee et al., 2008). It is suggested to be a potential colon tumor marker. MLCK regulates transendothelial migration of colon cancer cells in E-selectin-mediated activation of p38 MAPK (Tremblay et al., 2006), and possibly via changing cellular contractility by regulation of adhesion sites and stress fibers (Krdija et al., 2010). Inhibition of MLCK suppresses peripheral accumulation of phospho-MLC and Src-induced formation of integrin-dependent adhesions in KM12C colon cancer cells, whereas at the same time restoring E-cadherin redistribution to regions of cell-cell contact (Avizienyte et al., 2004; Avizienyte et al., 2005; Nguyen et al., 2002).

Prostate cancer

Note

Inhibitors of MLCK markedly reduce the invasiveness of prostate cancer cells due to impaired cellular motility (Tohtong et al., 2003). These inhibitors also retard the growth of established prostate tumor in vivo (Gu et al., 2006). MLCK is considered as a central mediator of migration, proliferation and invasion of prostatic adenocarcinoma cell line (Tohtong et al., 2003) downstream of PKC delta (Kharait et al., 2007), boric acid, and phenylboronic acid (McAuley et al., 2011) in DU145 cell line (metastatic prostate cancer cell line). The MYLK gene is one of the top seven most informative genes that discriminate between normal and tumoral prostate conditions by analyzing cDNA microarrays of approximately 25000 genes (Fujita et al., 2008). MLCK is down-regulated by androgens in human prostate cancer cells (Leveille et al., 2009).

Other cancers

Note

MLC phosphorylation or MLCK activation is directly involved in the activation of membrane-associated actomyosin required for the collection of surface proteins into a cap structure in mouse T-lymphoma cells (analogous to muscle cell sliding filament contraction) (Bourguignon et al., 1981; Kerrick and Bourguignon., 1984). Inhibitors of MLCK (ML-7 and ML-9) induce differentiation of human monoblastic leukemia U937 cells (Makishima et al., 1991; Makishima et al., 1993; Yamamoto-Yamaguchi et al., 1996). Apoptotic membrane blebbing is accompanied by increased MLC phosphorylation and regulated by MLCK in PC12, a neuroendocrine tumor cell line (Mills et al., 1998). MLCK regulates the activation of volume-sensitive organic osmolyte/anion channels (VSOAC) by mediating hypotonicity-induced Ca^{2+} entry (not correlating with MLC phosphorylation) in cervical cancer cells (Shen et al., 2002).

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This article should be referenced as such:

Shen K, Wang T, Garcia JGN. MYLK (myosin light chain kinase). *Atlas Genet Cytogenet Oncol Haematol*. 2012; 16(12):901-908.
