

Dynamin 2 and human diseases

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Abstract Dynamin 2 (DNM2) mutations cause autosomal dominant centronuclear myopathy, a rare form of congenital myopathy, and intermediate and axonal forms of Charcot–Marie–Tooth disease, a peripheral neuropathy. DNM2 is a large GTPase mainly involved in membrane trafficking through its function in the formation and release of nascent vesicles from biological membranes. DNM2 participates in clathrin-dependent and clathrin-independent endocytosis and intracellular membrane trafficking (from endosomes and Golgi apparatus). Recent studies have also implicated DNM2 in exocytosis. DNM2 belongs to the machinery responsible for the formation of vesicles and regulates the cytoskeleton providing intracellular vesicle transport. In addition, DNM2 tightly interacts with and is involved in the regulation of actin and microtubule networks, independent from membrane trafficking processes. We summarize here the molecular, biochemical, and functional data on DNM2 and discuss the possible

pathophysiological mechanisms via which DNM2 mutations can lead to two distinct neuromuscular disorders.

Keywords Dynamin 2 · Centronuclear myopathy · Charcot–Marie–Tooth neuropathy · Endocytosis · Cytoskeleton · Monogenic disease · Biology

Abbreviations

PI4,5P2	phosphatidylinositol 4,5-bisphosphate
PI3,4,5P3	phosphatidylinositol 3,4,5-triphosphate
PI3,4P2	phosphatidylinositol 3,4-bisphosphate
PI4P	phosphatidylinositol 4-monophosphate
PI3P	phosphatidylinositol 3-monophosphate
LPA	lysophosphatidic acid
GLUT4	glucose transporter 4
TGN	trans-Golgi network
BAR	Bin1/Amphiphysin/RVS167

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Dynamin 2 (DNM2) belongs to a superfamily of large GTPases, including three classical dynamins and several dynamin-like proteins, which are involved in a wide range of cell functions [1]. The importance of DNM2 was emphasized in 2005 with the demonstration of *DNM2* gene mutations causing two distinct human diseases [2, 3]. Our purpose is to review the molecular and functional data on DNM2 to highlight the pathophysiological hypotheses in DNM2-related diseases. Knowledge of the dynamins mainly comes from studies of the neuronal dynamin 1 (DNM1). However, we have focused this review on DNM2 since several studies have demonstrated notable differences between DNM1 and DNM2 [4–7].

DNM2 gene organization and isoforms

DNM2, one of three classical dynamins, was identified in rat liver and brain cDNA libraries [4, 8]. A human homologue was thereafter identified by screening of a fibroblast library [9]. The human transcript (3.6 kilobases) is ubiquitously expressed, with higher abundance in heart and skeletal muscle [9]. Human DNM2 is encoded by the *DNM2* gene located on the short arm of chromosome 19 (19p13.2). The gene is composed of 22 exons in a 114-kilobase region. Four major isoforms are expressed by the *DNM2* gene using a combination of two alternative splice

sites (Fig. 1a). Exons 10 and 10bis have the same length (139 base pairs encoding the amino acids 399–445 in the middle domain) and are alternatively spliced. In addition, the exon 13bis (12-base pair length) can be spliced leading to the translation of proteins of 866 or 870 amino acids (Fig. 1) without or with the GEIL sequence at position 516–519 in the C-terminal part of the middle domain (MD). The four major isoforms have been shown to be expressed in a panel of rat tissues including brain, heart, kidney, liver, lung, pancreas, and testis [10]. The human tissue expression pattern is unknown, but we have shown expression of the four isoforms in skeletal muscle and peripheral nerve [11].

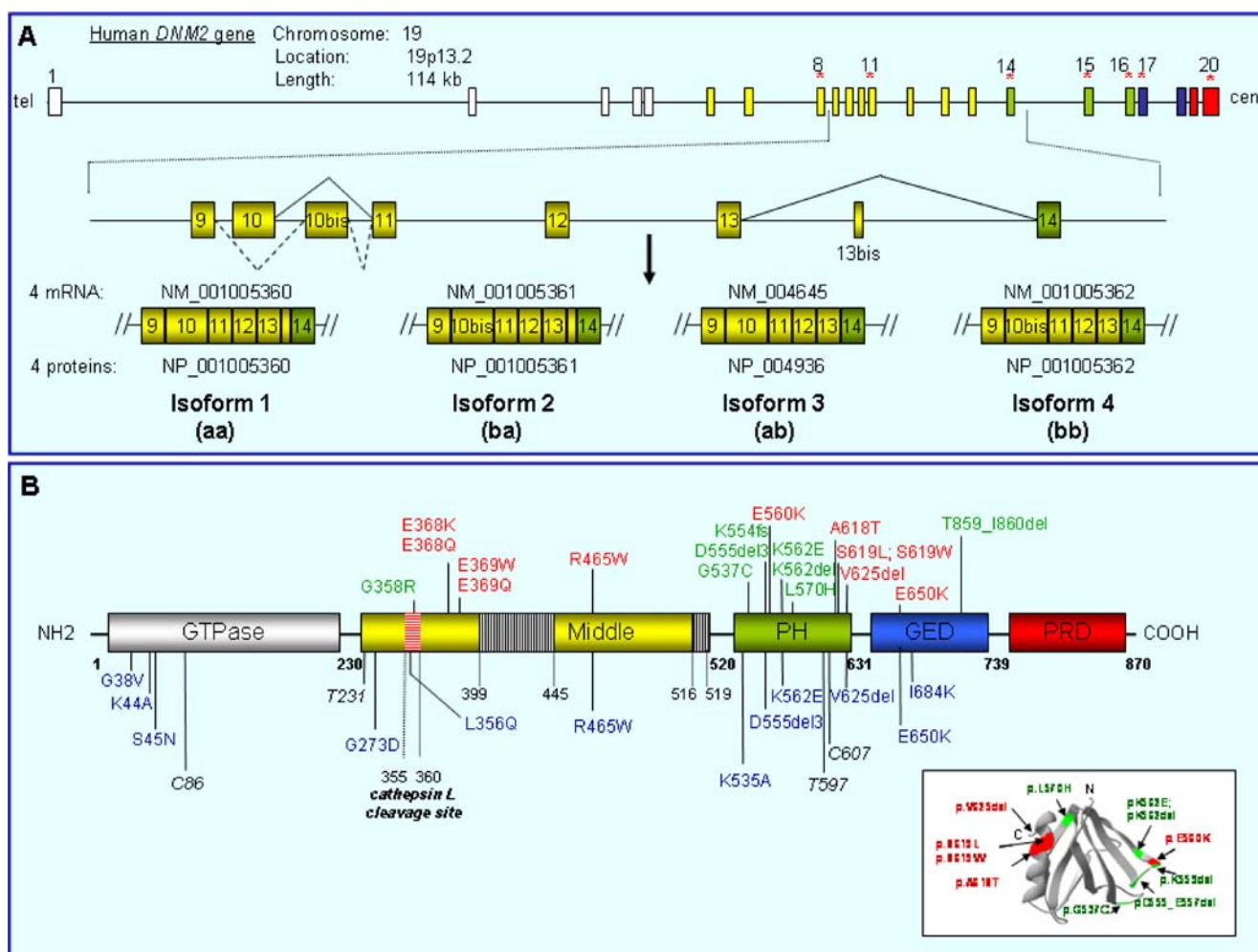


Fig. 1 *DNM2* gene organization and mutations. **a** Schematic organization of the human *DNM2* gene showing alternative splicing. Asterisks indicate the seven exons in which disease-associated mutations have been identified. Exons were colored relative to the encoded protein domain illustrated in **(b)**. The combination of the two alternative splice sites leads to the translation of four *DNM2* isoforms. Isoforms 1, 2, 3, and 4 are also known as isoforms aa, ba, ab, and bb, respectively. **b** Schematic representation of *DNM2* showing the five protein domains and the position of the 19 disease-associated mutations. CMT-mutations are indicated in green and CNM-mutations in red. The two regions of variation (at positions 399–445

and 516–519) between the four isoforms were indicated in the MD by black lines. In black are indicated the sites of post-translational modifications (phosphorylation, nitrosylation, and cathepsin L cleavage). The CMT-mutation G358R is located in the cathepsin L cleavage site. In blue are indicated the *DNM2* constructs with point mutations or small deletions overexpressed in vitro [60]. *Insert in b*: Position of the CNM- and CMT-mutations on the 3D structure of the PH domain (accession number 63660 in the NCBI 3D structure database). The N-terminal part of the domain, bearing CMT-mutations and only one CNM mutation, is composed of β -sheets involved in the interaction with membrane phosphoinositides

Specific functions of these isoforms will be discussed below.

DNM2 structure and regulation

The 98 kDa DNM2 is a large GTPase composed of a N-terminal GTPase domain, an MD, a pleckstrin homology domain (PH), a GTPase effector domain (GED), and a C-terminal proline rich domain (PRD; Fig. 1b). The catalytic GTPase domain is responsible for GTP binding and hydrolysis, whereas the MD is involved in DNM2 self-assembly [12] and in GTP hydrolysis-induced conformational change of the protein [13]. The PH domain interacts with membrane phosphoinositides and therefore is involved in the targeting of dynamin to membranes [14]. The DNM2-PH domain displays phosphoinositide binding affinity following the order: PI4,5P2 \approx PI3,4,5P3 \approx PI3,4P2 $>$ PI4P \approx PI3P, and DNM2 oligomerization appears crucial for high affinity [15]. The GED probably participates in the self-assembly of DNM2 and acts as a GTPase-activating protein [16]. The PRD contains multiple Src homology 3 (SH3) binding motifs and mediates multiple protein–protein interactions (Table 1). A general model of dynamin intramolecular interaction was proposed, in which the GTPase domain, MD and GED interact to drive self-assembly and the PH domain mediates interaction with membrane lipids [1].

In vitro at high ionic strength, DNM2 is in monomer–tetramer equilibrium. At low ionic strength, DNM2 self-assembles into higher-order aggregates leading to a drastic increase in GTPase activity [17, 18]. Microtubules or phospholipid vesicles, especially those containing PI4,5P2, also induce self-assembly and increase DNM2 GTPase activity [5, 17, 19]. Purified from baculovirus, GTP-bound and GDP-bound monomer DNM2 has K_d values of 13.2 and 7.1 μ M, respectively, with GTPase activity of 37 nmol/mg/min. When in an oligomeric state, the GTPase activity of DNM2 markedly increased and K_d values decreased [20]. When compared with small GTPases, DNM2 exhibits a relatively low affinity for GTP (K_m=12 μ M) but high intrinsic rates of GTP hydrolysis.

DNM2 activity is regulated by post-translational modifications. DNM2 becomes phosphorylated on Tyr231 (MD) and Tyr597 (PH domain) through Src-mediated phosphorylation, leading to albumin endocytosis [21]. In contrast, dopamine leads to the dephosphorylation of DNM2 by increasing protein phosphatase 2A activity, necessary for dopamine-induced Na⁺K⁺-ATPase endocytosis [22]. S-nitrosylation of Cys86 (GTPase domain) and Cys607 (PH domain) by nitric oxide (NO) increases GTPase activity and endocytosis [23]. In a mouse model of kidney disease, cathepsin L induction leads to the cleavage of the cytoplas-

mic DNM2 at positions 355–360 (Fig. 1b) [24]. Sever et al. identified a cathepsin L cleavage site at positions 355–360 in the middle domain (Fig. 1b). Actin network is then reorganized in renal podocytes leading to filtration impairment and proteinuria [24]. It remains to be determined whether such proteolytic regulation occurs only in pathological context and in other tissues. Finally, it was demonstrated that Ca²⁺ inhibits DNM2 GTPase activity (IC₅₀=150 μ M) and receptor-mediated endocytosis in HeLa cells [25]. This may have physiological importance in excitable cells like neurons and muscle fibers.

It is still largely unknown how DNM2 expression is regulated. In rat, DNM2 is up-regulated during normal pancreatic development after birth [26] but not in the liver [8] or the brain [27]. In mouse, treatment with opioid agonist results in increased DNM2 protein content in the spinal cord [28] whereas opioid antagonist decreases DNM2 abundance [29]. These changes in the level of DNM2 expression are inversely correlated with opioid receptor density at the plasma membrane, suggestive of feed-back regulation.

DNM2 function

Endocytosis DNM2 has been implicated in the formation of clathrin-coated pits (Fig. 2) [17]. In the cytosol, DNM2 forms a complex with sorting nexin 9 (SNX9) and fructose-1,6-bisphosphate aldolase [30]. Phosphorylation of SNX9 releases aldolase from the SNX9–DNM2 complex which is now competent for membrane targeting [30, 31]. DNM2 anchorage to the membrane occurs via interaction with PI4,5P2 membrane phosphoinositide [32] and BAR domain proteins, amphiphysin 1, amphiphysin 2, and SNX9 (Table 1) in curved sites of the membranes. DNM2 forms an oligomer helical structure around the neck of the nascent vesicles [17], and GTP hydrolysis is associated with the release of the vesicles. Interestingly, DNM2 co-localizes with clathrin before and during the internalization of the coated vesicle [6] suggesting that DNM2 plays also a role during the maturation of clathrin-coated pits [33].

DNM2 is also involved in clathrin-independent endocytosis by its participation in the formation of the phagosomes and caveolae [34, 35]. Predescu et al. described a protein complex, including DNM2, intersectin, and SNAP-23 that was important for the internalization of caveolae [36]. In caveolae, DNM2 also interacts with endothelial nitric-oxide synthase (eNOS) in bovine aortic endothelial cells [37] where DNM2 may regulate eNOS activation and the NO signaling cascade [37, 38]. DNM2 also participates in coat-independent endocytosis processes, i.e., micropinocytosis and macropinocytosis, by which fluid droplets and specific membrane components are internalized [39, 40].

Table 1 Direct or indirect interactions with DNM2

Name	OMIM	Site of interaction in DNM2	Function	Reference
Abp1	610106	nd	Endocytosis-actin bridge	[52, 95]
Amphiphysin 1	600418	PRD	Membrane trafficking	[14, 96]
Amphiphysin 2	601248	PRD	Membrane trafficking	[14, 97]
Annexin VI	114070	nd	Membrane trafficking	[98]
Aquaporin 2	107777	nd	Aquaporin trafficking	[99]
Arc	612461	PH	AMPA receptor trafficking	[100]
CAP	605264	nd	Actin remodeling during endocytosis	[101]
β -catenin	116806	nd	Blood–testis barrier integrity	[102]
Caveolin-1	601047	nd	Endocytosis	[73, 103, 104]
CBL	165360	nd	Actin remodeling during endocytosis	[105]
CIP4	604504	nd	GLUT4 trafficking	[106]
Complexin I	605032	nd	Acrosome formation and/or exocytosis	[107]
Complexin II	605033	nd	Acrosome formation and/or exocytosis	[107]
cortactin	164765	PRD	Actin assembly–endocytosis	[53, 54, 104]
c-Src	124095	PRD	Cell signaling and membrane trafficking	[108]
eNOS	163729	nd	NO production–cell signaling	[37, 109]
Ese1	602191	PRD	Endocytosis	[110]
FAK	600758	PRD	Focal adhesion disassembly	[58]
FBP17	606191	PRD	Actin reorganization during endocytosis	[111, 112]
Grb2	108355	PRD	Receptor internalization and signaling	[108, 113, 114]
IL-5R α	147851	nd	IL-5 signaling pathway and trafficking	[115]
Jak2	147796	nd	IL-5 signaling pathway	[115]
JAM-A	605721	nd	Blood–testis barrier integrity	[102]
Kalirin 12	604605	GTPase	Membrane trafficking	[116]
KDR	191306	nd	Receptor signaling and expression	[117]
LYN	165120	PRD	IL-5 signaling pathway	[108, 115]
MLK2	600137	PRD	Actin (filipodia and membrane ruffles)	[118]
Myosin 1E	601479	PRD	Receptor-mediated endocytosis	[119]
N-cadherin	114020	nd	Blood–testis barrier integrity	[102]
Nef	–	MD / GED	HIV-1 entry	[120]
Nostrin	607496	PRD	eNOS trafficking	[121]
N-WASp	605056	nd	Actin remodeling	[56]
Occludin	602876	nd	Blood–testis barrier integrity	[102]
p85	171833	PRD		[108]
PDE γ	180073	nd	Cell signaling	[122]
PLC γ	172420	PRD		[108]
PLD2	602384	nd	Cell signaling	[123]
Shank 1	604999	PRD	Postsynaptic membrane turnover	[124]
Pyk2	601212	nd	Podosome dynamics	[125]
Shank 2	603290	PRD	Postsynaptic membrane turnover	[124]
SNX9	605952	PRD	Membrane remodeling–actin dynamics	[126, 127]
SNX18	–	PRD	Endosomal trafficking	[127]
SNX30	–	PRD	Membrane trafficking?	[127]
Syndapin 2	604960	PRD	Vesicle formation from the TGN	[45]
Syndecan-4	600017	PH	Actin-stress fibers and focal adhesion sites	[62]
Tks5/FISH	–	PRD	Cell signaling	[128]
TULA	605736	nd	EGFR trafficking	[129]
Vav1	164875	PRD	T cell activation by actin remodeling	[130]
β -tubulin	191130	PRD		[14]

Table 1 (continued)

Name	OMIM	Site of interaction in DNM2	Function	Reference
γ-adaptin	603533	PRD		[14]
γ-tubulin	191135	MD	Centrosome cohesion	[65]
ZO1	601009	nd	Blood–testis barrier integrity	[102]

Abp1 actin-binding protein, *CAP* CBL-associated protein, *CBL* Cas–Br–M murine ecotropic retroviral transforming sequence homolog, *CIP4* cdc42 interacting protein-4, *eNOS* endothelial nitric-oxide synthase, *Ese1* EH domain and SH3 regulator of endocytosis 1, *FAK* focal adhesion kinase, *FBP17* formin-binding protein 17, *Grb2* growth factor receptor-bound protein 2, *IL-5Rα* α subunit of the interleukin 5 receptor, *Jak2* Janus kinase 2, *JAM-A* junctional adhesion molecule A, *KDR* kinase insert domain receptor also known as: vascular endothelial growth factor receptor-2, *MLK2* mixed-lineage kinase 2, *Nef* accessory protein of the HIV-1, *N-WASp* Wiskott Aldrich syndrome protein, *PDEγ* inhibitory γ subunits of the retinal cGMP phosphodiesterase, *PLCγ* phospholipase C gamma 1, *PLD2* phospholipase D2, *SNX9* sorting nexin 9, *Tks5/FISH* tyrosine kinase substrate 5/five SH3 domains, *TULA* Cbl- and ubiquitin-interacting protein T-cell ubiquitin ligand, *Vav1* Rho family guanine nucleotide exchange factor Vav1, *ZO1* Zonula occludens 1

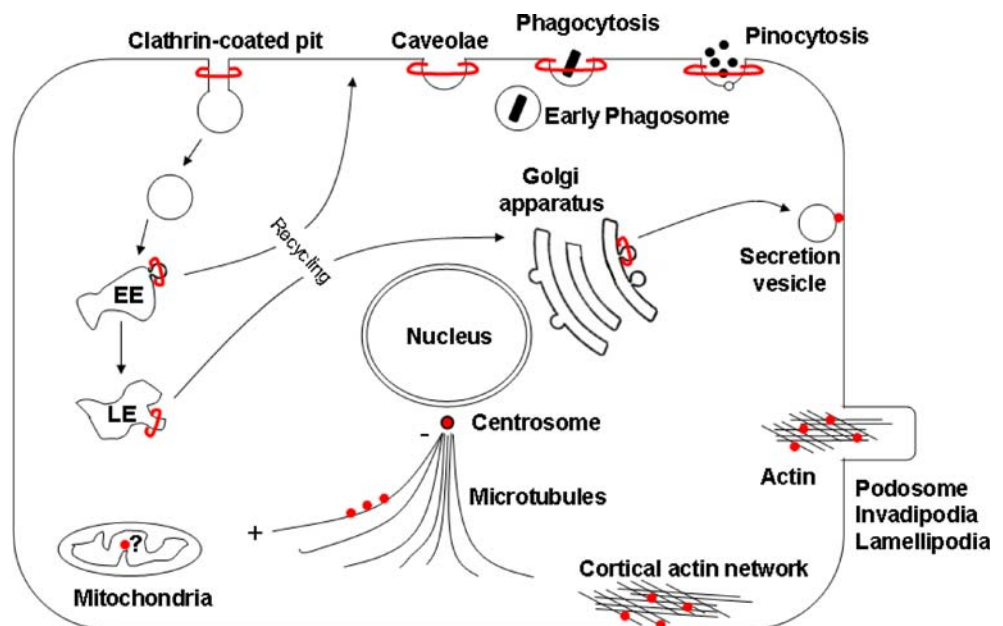
Intracellular membrane trafficking DNM2 is targeted to the Golgi apparatus where it is predominantly localized in the trans-Golgi network (TGN) [41]. Anti-DNM2 antibody injection and over-expression of DNM2 mutants impair vesicle formation from the TGN [42, 43]. Association of DNM2 with cortactin and syndapin 2 is required for trafficking of nascent vesicles from the TGN [44, 45]. DNM2 is also found at the clathrin-coated buds of early endosomes [46] and in late endosomes in Hela cells, located to the tubulo-vesicular appendices [47]. In these two cases, interfering DNM2 mutant impairs the recycling of components from the endosomal system towards the plasma membrane or TGN [46, 47]. These data highlight the role of DNM2 in the secretory pathway and in the sorting of cell components from the Golgi apparatus and endosomal compartment.

Exocytosis DNM2 may participate in endocytosis–exocytosis coupling as suggested in mouse pancreatic β-cells [48].

However, a role for DNM2 in exocytosis alone has been reported. During cell-mediated killing by natural killer (NK) cells, DNM2 co-localizes with lytic granules after NK cell activation and is required for fusion of the granules with the plasma membrane [49]. Similarly in macrophages, focal exocytosis is blocked after anti-DNM2 antibody microinjection [50], and DNM2 GTPase activity regulates the fusion of secretory vesicles at the plasma membrane [51]. Further studies will be necessary to precisely identify the molecular role played by DNM2 in the exocytosis machinery.

Actin network Actin-based dynamic processes are crucial for late-stage endocytosis and vesicle formation, and DNM2 interacts with the actin-binding proteins Abp1 (actin-binding protein 1) [52] and cortactin [53, 54]. Abp1 is an Src kinase which provides a physical bridge between the endocytosis machinery and the cortical actin network, and cortactin is a component of the clathrin-mediated

Fig. 2 DNM2 cellular functions. Representation of the multiple cellular localizations reported for DNM2 (in red) EE early endosome, LE late endosome



endocytosis machinery. However, interaction between DNM2 and the actin cytoskeleton may have another cytoskeletal role such as in the formation of membrane tubules and protrusions. Furthermore, a recent study showed the crucial function played by the DNM2-cortactin complex in the global organization and remodeling of the actomyosin cytoskeleton [55]. In addition, DNM2 is present in cortical ruffles and lamellipodia, both important in cell migration [10, 53]. The supramolecular complex including DNM2, cortactin, and Arp2/3 mediates the reorganization of actin allowing lamellipodia formation at the leading edge of migrating cells [56]. Disruption of DNM2 functions by DNM2-K44A mutant or small interfering RNA (siRNA) inhibits the formation of lamellipodia [57]. Similarly, under PDGF stimulation, DNM2 is concentrated within the leading ruffles of migrating fibroblasts where it co-localizes with cortactin [53]. To allow cell migration, DNM2 participates in disassembly of focal adhesions, as well as β -integrin internalization at the rear of the cell [58, 59]. Additionally, DNM2 is enriched in specialized membrane protrusions such as podosomes and invadopodia. Podosomes represent attachment sites between cells and substratum [60], and invadopodia are focalized matrix degradation sites [61]. Inhibition of DNM2 diminishes the amount of such structures [61]. It has also been shown that DNM2 regulates the formation of actin-stress fibers by interaction with the cell surface heparin sulfate proteoglycan syndecan-4 [62]. Expression of DNM2-mutant, truncated for the PRD domain mediating interaction with cortactin, increases the number of actin-stress fibers, which is associated with abnormal cell shape [53].

Microtubule network and MTOC DNM2 interacts with microtubules [17, 63], and the binding region was located to the PRD [5, 64]. It was shown that down-regulation of DNM2 by siRNA increases the amount of acetylated tubulin, a more stable form of tubulin in microtubules and reduces their growing capacity [63], suggesting that DNM2 may regulate the polymerization–depolymerization equilibrium of microtubules. Through its interaction with microtubules, DNM2 appears involved in Golgi apparatus cohesion [63]. Moreover, DNM2 has been identified as a component of the centrosome, the main microtubule organizing center (MTOC), where it binds to γ -tubulin [65]. The centrosome consists of a pair of centrioles embedded in a filamentous pericentriolar matrix, where γ -tubulin is essential for microtubule nucleation. The function played by DNM2 at the centrosome is still unknown, but DNM2 silencing by siRNA suggests a role in centrosome splitting [65]. Likewise, participation of DNM2 in all the phases of mitosis has also been reported. DNM2 is detected in the two MTOC during early prophase, along the mitotic spindle during metaphase and in the spindle midzone

region during anaphase and early telophase [66]. Thereafter, DNM2 is accumulated at the intracellular bridge where the final separation occurs. The time required for separation of the two daughter cells is longer in DNM2 knock-out cells [40]. Taken together, these data suggest that DNM2 may regulate microtubule-dependent processes by acting on microtubule dynamics and organization.

Apoptosis In order to establish a stable HeLa cell line over-expressing DNM2 isoform 2, Fish et al. have reported a significant cell toxicity in dividing cells [67]. The cytotoxicity occurred via induction of apoptosis by a p53-dependent mechanism. Similar results were gained in vascular smooth muscle cells [68]. The capacity to trigger apoptosis appears DNM2-specific as DNM1 over-expression does not induce apoptosis [67]. The GTPase domain of DNM2 is crucial to induce apoptosis [69]. In addition, a point mutation (p. I684K) in the DNM2 GED enhances the apoptosis induction by the wild-type DNM2 suggesting that GED negatively regulates this DNM2 function [69]. Mitochondria are key players in apoptosis and, interestingly, DNM2 has been detected in isolated mitochondria from bovine lymphoblastoid BL-3 cells [70]. However, to our knowledge, such localization has not been reported in other cell lines or tissues. DNM2 also regulates the apoptosis-inducing Fas–Fas ligand pathway by facilitating the transport of Fas from the trans-Golgi network to the plasma membrane [71].

Specific functions of DNM2 isoforms In a cultured rat epithelial cell line (clone 9), both DNM2 isoforms 1 and 3 show punctuate labeling of clathrin heavy chain-positive or heavy chain-negative structures, but only isoform 1, with the GEIL sequence in the MD, appears located to the Golgi apparatus [10]. These data suggest a role for the GEIL sequence in targeting to the Golgi apparatus. However, cell-type specificity probably exists, as isoforms without the GEIL sequence were also shown to be targeted to the Golgi apparatus in MDCK cells [43], 3T3L1 adipocytes [72], and fibroblastoid-like cells derived from mouse embryonic stem cells [40]. Nevertheless, this possible differential localization argues for distinct functions. Indeed, in clone 9 cells, the K44A mutants of isoforms 2 and 4 are able to inhibit fluid-phase endocytosis, whereas the mutant forms of isoforms 1 and 3 do not [39] and are also more potent inhibitors of clathrin-mediated endocytosis. Similarly, in a hepatocyte cell line, the K44A-isoform 1 inhibits caveolae-dependent internalization, but not the other K44A mutant isoforms [73]. In fibroblastoid-like cells derived from mouse embryonic stem cells, isoforms 2 and 4 are the most efficient at rescuing export from the Golgi in DNM2 knock-out cells [40]. Altogether, these data suggest a preferential involvement of isoforms 1 and 3 in clathrin- and caveolae-dependent endocytosis, whereas isoforms 2

and 4 participate in uncoated endocytosis and trafficking from the Golgi apparatus. However, cell-type specificity also occurs as the four isoforms exhibit a similar subcellular distribution in 3T3L1 adipocytes, and dominant negative mutants of each isoform similarly affect basal and insulin-stimulated GLUT4 trafficking [72].

DNM2 and human diseases

Mutations in the *DNM2* gene cause rare forms of the Charcot–Marie–Tooth peripheral neuropathy (CMT) [2, 74–77] and autosomal dominant centronuclear myopathy (CNM) [3, 11, 78–80]. The 19 reported heterozygous mutations affect only the MD, the PH domain, and the GED (Fig. 1b). DNM2-related CNM is a slowly progressive congenital myopathy characterized by frequent centrally located nuclei in muscle fibers. The most common clinical features are delayed motor milestones, facial and generalized muscle weakness, ptosis, and ophthalmoplegia [81]. Nevertheless, the severity of DNM2-CNM is variable, ranging from severe neonatal to mild late-onset forms. DNM2-CMT is a peripheral neuropathy characterized by progressive muscle weakness and atrophy. *DNM2* mutations can cause axonal CMT (CMT2) and dominant intermediate CMT (DI-CMT-B). In some CMT patients, neuropathy is associated with neutropenia [2, 75, 77] but this association has not been described in DNM2-CNM patients. Clinical overlap could exist in some patients [81], but the majority of patients are affected by a tissue-specific disorder. No clear genotype–phenotype relationship can be generated, except for the de novo mutations located in the C-terminal part of the PH domain, which are all associated with a severe neonatal CNM phenotype [98]. In these patients, the phenotype progressively improves, suggesting compensatory mechanisms.

More recently, the *DNM2* gene has been described as a susceptibility gene for late-onset Alzheimer disease [82], and DNM2 expression was found to be decreased in the brains of these patients [83]. Cognitive impairments have been reported in some CNM patients harboring the p.E368Q [78], p.R465W [84; Family 1], and p.R369Q [84; Families 2 and 3] DNM2 mutations. Future studies will be necessary to determine the prevalence of central nervous system involvement in DNM2-related diseases.

Pathophysiological hypotheses

The DNM2 mutations identified so far in CNM and CMT are heterozygous missense mutations or small deletions (Fig. 1). We have shown that DNM2 transcript, protein

expression, and localization are normal in fibroblasts from CNM patients [3, 11]. These data are in agreement with DNM2 mutants having a dominant negative effect, resulting in a loss of function of DNM2 in endocytosis [11] or in microtubule-related functions [63] (see below).

Membrane trafficking and signaling pathway hypothesis In addition to the *DNM2* mutations in autosomal dominant CNM, mutations in the *BIN1* gene encoding amphiphysin 2, a partner of DNM2 in the endocytic process, cause the autosomal recessive form of the disease [85]. This suggests that endocytic impairment is a potential pathomechanism of autosomal CNM. Indeed, impairment of clathrin-mediated endocytosis was reported in cultured cells expressing CNM- or CMT-DNM2 mutants [2, 11, 63]. Among these studies, one CMT-mutant was unable to block the uptake of transferrin, a marker of clathrin-mediated receptor endocytosis [63]. Nevertheless, the transferrin-containing compartment was not located to the perinuclear region after 30 min of incubation showing that its intracellular trafficking was impaired by the CMT-mutant. The crucial question which remains to be explored is how a defect in endocytosis can alter the cell function, especially in a tissue-specific manner. On one hand, inhibition of DNM2-dependent trafficking may lead to a decrease in receptor stimulated signaling as shown for the MAPK ERK1/2 pathway [11]. On the other hand, DNM2 mutations may lead to a prolonged half-life of various proteins at the cell surface due to a defect in protein removal, as shown for the GLUT4 glucose transporter [72]. A deregulation of glucose transport in patients with DNM2 mutations could have a strong impact on muscle fibers given their high glucose consumption.

To date, the impact of disease-associated DNM2 mutants on other DNM2-dependent membrane trafficking processes, especially in endosomal and Golgi pathways, has not been studied. We cannot exclude a participation of these pathways in the pathomechanisms of DNM2-related disorders.

Cytoskeleton impairment and its putative role on nuclear positioning In DNM2-CNM, the majority of patients harbor a mutation in the MD, which is essential for the centrosomal localization of DNM2 and for its interaction with γ -tubulin [65]. Previous results in skin fibroblasts indicate that transfected GFP-DNM2-mutants fail to correctly target to the centrosome, suggesting that DNM2 mutations might cause CNM by interfering with centrosomal functions [3]. In addition, CMT-related DNM2 mutants can disorganize the microtubule cytoskeleton [2], and one particular CMT-mutant was shown to impair microtubule-dependent membrane transport [63]. In addition to their roles in intracellular trafficking, the microtubule and actin networks regulate cellular architecture including nuclear positioning [86, 87]. Thus, cytoskeletal impairment may

play a role in the abnormal central location of the nuclei in the muscle fibers in CNM. In CMT, DNM2 mutations could also induce a destabilization of the microtubule network leading to abnormal axonal transport and protein trafficking, a pathophysiological mechanism described previously in various forms of CMT [88].

T-tubule hypothesis in CNM The X-linked recessive form of CNM (also called XLMTM for X-linked myotubular myopathy) is due to mutations in the *MTM1* gene encoding the myotubularin, and the autosomal recessive and dominant CNMs result from mutations of amphiphysin 2 and DNM2, respectively [89]. The muscle specific isoform of amphiphysin 2 is concentrated at T-tubules in mouse and drosophila and is involved in the organization of this plasma membrane invagination acting in excitation–contraction coupling [90, 91]. Myotubularin is also located to the T-tubules in mouse [92] and zebrafish [93], and knock-down of myotubularin in these species leads to disorganization of the T-tubule system, reduction in Ca^{2+} release from the sarcoplasmic reticulum, and defect in excitation–contraction coupling [93, 94]. In addition, abnormal localization of T-tubule markers was shown in muscle biopsies from *BINI*-CNM and *MTM1*-CNM patients [85, 93], suggesting that an excitation–contraction coupling impairment due to T-tubule dysfunction could be a common pathomechanism leading to muscle weakness in CNMs. Future studies are necessary to explore this hypothesis in the *DNM2*-CNM in which no morphological abnormalities of the T-tubule system have been reported to date.

Concluding remarks and open questions

Given the numerous distinct functions in which the ubiquitously expressed DNM2 is involved, the identification of pathophysiological mechanisms will be a challenge. The phenotypes encountered in CNM and CMT patients could be due to impairment of the various functions of the protein. To date, there is no explanation for the tissue-specific impact of the DNM2-mutations in human diseases. DNM2 is engaged in numerous protein–protein interactions (Table 1), but these interactions in muscles and nerves are largely unexplored. Another unresolved question is whether each particular mutation can similarly affect the functions of the four DNM2 isoforms. Finally, whereas some data emerge on the impact of disease-related DNM2 mutations on the microtubule network, their impact on the actin cytoskeleton is totally unknown. Future developments of animal models will certainly be useful to better determine the main functions of DNM2 in vivo, especially in skeletal muscle

and nerves where membrane trafficking displays unique cell length dependent characteristics.

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