

Functional organization of the nuclear lamina

Research Article

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Abbreviations: NE, nuclear envelope; IF, intermediate filaments; IMPs, integral nuclear membrane proteins; LBR, lamin B receptor; LAP, Lamina Associated Protein; NPC, nuclear pore complex; INM, inner nuclear membrane; ONM, outer nuclear membrane

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Summary

In eukaryotic cells, DNA replication, RNA processing and ribosome assembly all occur in the nucleus, while protein synthesis occurs in the cytoplasm. These activities are physically separated by the nuclear envelope. The inner nuclear membrane and the nuclear lamina are involved in organizing nuclear structure and regulating nuclear events including: nuclear organization, DNA replication, nuclear assembly and disassembly, apoptosis, and correct spacing of nuclear pores. In order to perform these activities the inner nuclear membrane and the nuclear lamina contain a unique set of proteins, including lamin type A and B, otefin, Young Arrest, LAP1, TMPO/LAP2, emerin, LBR and MAN. The proteins of the inner membrane form a complex network of interactions between themselves and with chromatin. Mutations in several of these proteins also result in known diseases. In this paper we review these interactions and discuss their possible roles in normal cell activity and in apoptosis. In addition, we demonstrate that specific regions in lamins can interact with the core histones H2A and H2B. We also show that Thymopoietin (TMPO)/ Lamina Associated Polypeptide 2 (LAP2) gene is alternatively spliced to form a large family of proteins with different size and different distribution within the nucleus. These results are discussed in relationship to the biological roles of the nuclear lamina.

I. Introduction

The main feature of eukaryotic cells is the presence of nuclear and cytoplasmic compartments that are separated by the nuclear envelope (NE). The NE is a large complex structure composed of outer and inner lipid bilayer membranes, nuclear pores, nuclear lamina and perhaps chromatin (**Figure 1**). The outer nuclear membrane is continuous with the endoplasmic reticulum and is covered with ribosomes. The two membranes are separated by a 20-40 nm perinuclear space and are connected at the nuclear pore complexes (reviewed in Burke, 1990a). The nuclear pore complexes are large protein structures that mediate the controlled transport of macromolecules between the cytoplasm and the nucleus (reviewed in Corbett and Silver, 1997; Davis, 1995; Fabre and Hurt, 1997; Gorlich and Mattaj, 1996). The nuclear lamina is a proteinaceous

meshwork of intermediate filaments (IF) that is located underneath the inner nuclear membrane and abuts the peripheral chromatin (reviewed in Harel et al, 1998; Moir et al, 1995; Stuurman et al, 1998). The inner nuclear membrane and nuclear lamina contain unique proteins. Among them are the integral nuclear membrane proteins (IMPs) p58/lamin B receptor (LBR) (Worman et al, 1990; Worman et al, 1988), LAP1 (Martin et al, 1995), TMPO/LAP2 (Berger et al, 1996; Furukawa et al, 1995; Harris et al, 1994), emerin (Manilal et al, 1996), p34 (Simos and Georgatos, 1994) and p18 (Simos et al, 1996). The peripheral nuclear membrane proteins include type A and type B lamins (Fisher et al, 1986; McKeon et al, 1986), otefin (Harel et al, 1989; Padan et al, 1990), and Young Arrest (YA) (Lin et al, 1991; Lin and Wolfner, 1991). It is yet to be determined whether MAN protein(s) are integral or a peripheral proteins (Paulin Levasseur et al, 1996).

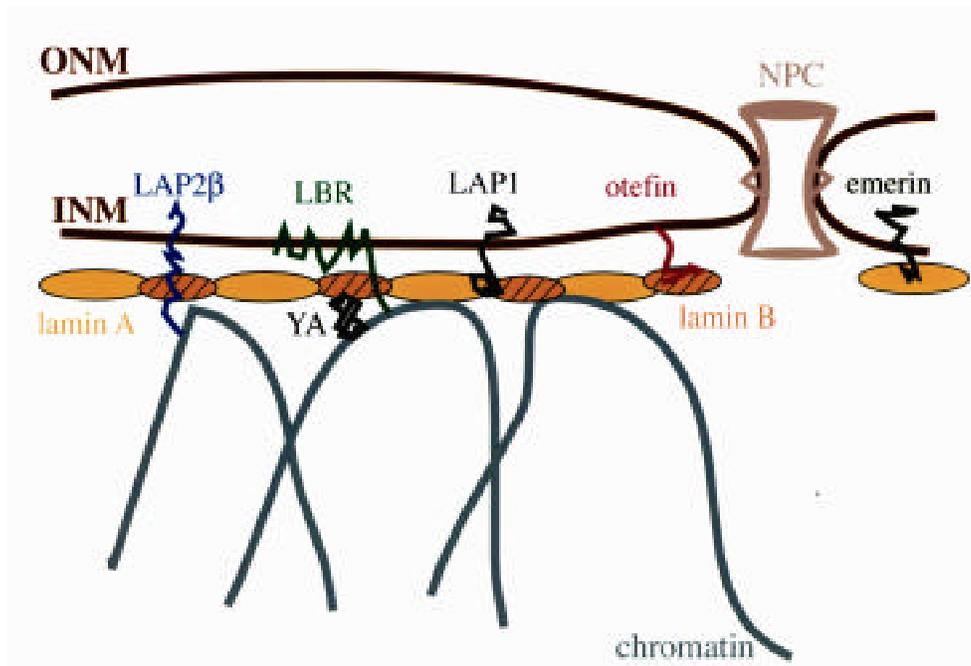


Figure 1. Schematic view of the molecular organisation of the nuclear envelope. ONM, outer nuclear membrane; INM, inner nuclear membrane; NPC, nuclear pore complexes; LAP, Lamina Associated Protein; YA, Young Arrest.

The proteins of the NE form a complex network of interactions (reviewed in Qian et al, 1998). Lamin seems to interact with LBR (Worman et al, 1988), LAP1 (Foisner and Gerace, 1993), p18 (Simos et al, 1996), TMPO/LAP2 (Foisner and Gerace, 1993), p18 (Simos et al, 1996), otefin and YA (Goldberg et al, 1998). p18 and p34 are associated with LBR (Simos and Georgatos, 1992). LBR (Foisner and Gerace, 1993; Pyrpasopoulou et al, 1996), YA (Lopez and Wolfner, 1997), and lamin (Glass et al, 1993; Glass and Gerace, 1990; Goldberg et al, 1999; Hoger et al, 1991; Taniura et al, 1995; Yuan et al, 1991) are all found to interact with chromatin. The inner nuclear membrane and the nuclear lamina are involved in several biological functions, including: (a) regulation of the NE shape and structure (Furukawa and Hotta, 1993; Furukawa et al, 1994; Newport et al, 1990); (b) disassembly, at the beginning of mitosis, and reassembly, at the end of mitosis of the NE (Ashery-Padan et al, 1997b; Burke and Gerace, 1986; Gant et al, 1999; Gant and Wilson, 1997; Heald and McKeon, 1990; Ulitzur et al, 1992, 1997); (c) providing anchoring sites for chromatin and affecting higher order chromatin organization (Belmont et al, 1993; Gerace and Foisner, 1994; Hutchison et al, 1994; Liu et al, 1997); (d) lamins are required for the elongation phase of DNA replication (Ellis et al, 1997; Gant et al, 1999; Goldberg et al, 1995; Moir et al, 1995; Newport et al, 1990); (e) lamins are very early targets for caspases in apoptosis, and inhibition of lamins apoptotic degradation delays apoptosis (Neamati et al, 1995; Oberhammer et al, 1994; Rao et al, 1997; Shimizu et al, 1998); and (f) the abnormal arrangement of nuclear pores in cells mutated in their lamin

gene revealed that lamins have also a central role in spacing the nuclear pores (Lenz-Bohme et al, 1997).

A. Lamins: the main components of the nuclear lamina

Lamins are the major and best studied proteins of the nuclear lamina. They are type V intermediate filament (IF) proteins, and, like all IF proteins, contain a helical rod domain flanked by a nonhelical amino terminal “head” and carboxy terminal “tail” domains. The lamin rod domain contains three α -helices, each composed of heptad repeats. These helices form coiled-coil interactions between lamin monomers, resulting in lamin dimers. The lamin dimers form longitudinal polar head-to-tail interaction, leading the formation of higher order structures. The outcome polymers further associate laterally to form 10 nm thick filaments. These 10 nm thick filaments can further associate to form the 50-200 nm thick lamin fibers (reviewed in Krohne, 1998; Stuurman et al, 1998). Lamins are divided into type A and type B lamins, according to their sequence and expression patterns. Type A lamins are essentially expressed in differentiated cells, have a neutral isoelectric point and are soluble during mitosis. Type B lamins are expressed in all somatic cells, have an acidic isoelectric point and remain associated with membrane vesicles during mitosis (reviewed in Moir et al, 1995; Stuurman et al, 1998). Metazoan cells contain between one to six lamin proteins. Mammalian lamin A, C (Fisher et al, 1986; McKeon et al, 1986), A delta10 (Machiels et al, 1996) and C₂ (Furukawa et al, 1994)

are all products of one alternatively spliced gene. Lamin B₁ and B₂ are encoded by two separate genes, and lamin B₃ is a germ cell-specific spliced variant of lamin B₂ (Furukawa and Hotta, 1993). In *Xenopus laevis*, five lamin proteins were identified, lamin B₁, B₂, B₃, B₄ and A (Benavente et al, 1985; Benavente, 1985; Stick, 1992, 1994). In chicken, there are three known lamin genes, termed lamin A, B₂ and B₁ (Peter et al, 1989; Vorburger et al, 1989). *Drosophila melanogaster* has two lamin genes, lamin Dm₀ (Gruenbaum et al, 1988) and C (Bossie and Sanders, 1993). One lamin gene is present in the completely sequenced *Caenorhabditis elegans*, termed lamin CeLam-1 (Riemer et al, 1993). Interestingly, lamins are not present in the yeast *Saccharomyces cerevisiae* genome. All nuclear lamins, except lamin C, contain a CaaX box (C is cysteine, a is an aliphatic amino acid residue and X is any amino acid) at their carboxy terminus. The CaaX box undergoes specific post-translation modifications, which include farnesylation of the cysteine residue, endoproteolysis of the last three amino acids and carboxymethylation of the cysteine residue (reviewed in Moir et al, 1995). These modifications are essential, but not sufficient, for lamin association with the NE (Firmbach Kraft and Stick, 1995; Firmbach-Kraft and Stick, 1993; Krohne et al, 1989; Mical and Monteiro, 1998). Lamins are phosphorylated by several protein kinases in a cell-cycle regulated manner (Ottaviano and Gerace, 1985). Phosphorylation and dephosphorylation of lamins regulate their polymerization disassembly (Heald and McKeon, 1990; Ottaviano and Gerace, 1985; Peter et al, 1991), and their import to the nucleus (Haas and Jost, 1993; Hennekes et al, 1993). In mitotic cells, lamins are probably phosphorylated by cdc2 kinase (Dessev et al, 1991; Eggert et al, 1993; Heald and McKeon, 1990; Peter et al, 1991; Peter et al, 1990; Ward and Kirschner, 1990), the γ isoform of protein kinase C (Fields et al, 1988; Goss et al, 1994; Hocevar et al, 1993; Hocevar and Fields, 1991), and mitogen-activated protein (MAP) kinase (Peter et al, 1992). In interphase cells, lamins are also phosphorylated by protein kinases A and C (Collas and Alestrom, 1997; Eggert et al, 1993; Eggert et al, 1991; Hennekes et al, 1993; Peter et al, 1990), indicating a separate role for lamin phosphorylation during interphase. The rod domain of lamins can bind otefin (Goldberg et al, 1998), LAP2 (Furukawa et al, 1998) and DNA (Baricheva et al, 1996; Christova et al, 1989; Galcheva-Gargova and Dessev, 1987; Luderus et al, 1992; Luderus et al, 1994; Rzepecki et al, 1998; Shoeman and Traub, 1990; Wedrychowski et al, 1989; Zhao et al, 1996), while the tail domain can bind actin (Sasseville and Langelier, 1998) and histones (Goldberg et al, 1999; Taniura et al, 1995).

Lamins are located mainly at the nuclear periphery. However they are also localized internally in the nucleoplasm (Bridger et al, 1993; Goldman et al, 1992; Hozak et al, 1995; Lutz et al, 1992; Moir et al, 1994; Sasseville and Raymond, 1995). The lamin nucleoplasmic foci may represent sites for lamin assembly or modification, prior to their incorporation into the peripheral lamina (Goldman et al, 1992; Lutz et al, 1992; Sasseville and Raymond, 1995) or may be involved in DNA replication (Moir et al, 1994).

B. Lamin-chromatin interaction: implication for NE assembly and disassembly

In higher eukaryotes, the NE disassembles during the prophase stage of mitosis and starts to reassemble around daughter chromosomes at late anaphase. Both lamins and lamin-associated proteins seem to be involved in this process. The NE disassembly is driven by phosphorylation of its major structural components, i.e. lamins (reviewed in Marshall and Wilson, 1997; Moir et al, 1995), proteins of the nuclear pore complex (Favreau et al, 1996; Macaulay et al, 1995), and probably LBR, LAP1 and TMPO/LAP2 (reviewed in Chu et al, 1998; Qian et al, 1998). In *Drosophila* embryos and *Xenopus* oocytes, the NE is fragmented into small vesicles, while the nuclear pore complexes disperse as soluble complexes and the nuclear lamina is depolymerized. NE assembly includes nuclear vesicles binding to chromatin, fusion of these vesicles, flattening onto the chromatin surface and assembly of the nuclear pore complexes (reviewed in Marshall and Wilson, 1997; Wilson and Wiese, 1996). In mammalian cells, the NE loses its identity as a subcompartment of the endoplasmic reticulum (ER) during mitosis. IMPs are probably resorted to the NE during late anaphase by diffusion through the ER and subsequently association with binding sites on the chromosomes. This process requires cooperative assembly of lamins and IMPs of the inner membrane (Gant et al, 1999; Ulitzur et al, 1997; Yang et al, 1997), LAP2 (Dechat et al, 1998) and chromatin. Both in vivo and in vitro studies proved that lamins have a major role in the assembly and disassembly of the NE, probably via their interaction with chromatin. Injection of anti-lamin antibodies to PtK2 cells resulted in cells that were not able to form normal daughter nuclei. The chromatin in the daughter nuclei remained arrested in a telophase-like configuration, and the telophase-like chromatin remained inactive as judged from its condensed state and by the absence of nucleoli (Benavente and Krohne, 1986). Three-dimensional in vivo studies in *Drosophila* and mammalian cells revealed that lamin filaments are closely associated with chromatin (Belmont et al, 1993). Genetic analysis also revealed that lamins are important for an intact NE and that lamins interact with chromatin. Mutations in the *Drosophila* lamin Dm₀ gene revealed that it is an essential gene. Flies homozygous for a strong mutation in the *Drosophila* lamin Dm₀ gene died following 9-16 hours of development. These flies demonstrate aberrant nuclear structure, dissociation of chromatin from the nuclear membranes and accumulation of annulate lamellae-like structures (Harel et al, 1998). Flies that carry a weak mutation in the lamin Dm₀ gene (<20% lamin expression) show retardation in development, reduced viability, sterility, and impaired locomotion. These flies demonstrate enrichment in nuclear pore complexes in cytoplasmic annulate lamellae and in NE clusters and defects in the nuclear envelopes of several types of cells (Lenz-Bohme et al, 1997).

The role of lamins in NE assembly was studied in vitro in several ways. Incubation of CHO cell extracts with anti-lamin A/C or anti-lamin B antibodies inhibited NE assembly (Burke and Gerace, 1986). Similarly, addition of anti-lamin

Dm₀ to a *Drosophila* extracts, in a cell-free nuclear assembly system, blocked the binding of nuclear vesicles to chromatin. The NE reformed upon supplementation of purified interphase lamin to the assembly extract (Ulitzur et al, 1992; Ulitzur et al, 1997). In the *Xenopus* nuclear assembly system, antibodies directed against both *Xenopus* lamins B₂ and B₃ inhibited the assembly of the nuclear membranes around chromatin (Dabauvalle et al, 1991). Interestingly, addition of antibodies directed only against *Xenopus* lamin B₃ resulted in nuclei that were smaller and fragile, contained high density of nuclear pore complexes and failed to replicate their DNA (Goldberg et al, 1995; Jenkins et al, 1993; Meier et al, 1991; Newport et al, 1990; Spann et al, 1997). The latter experiments strongly suggest a role for lamins in nuclear organization.

Lamins can bind specific DNA sequences in vitro. These include matrix/scaffold attachment regions (MAR/SARs, Luderus et al, 1992; Luderus et al, 1994), which lamins bind through their rod domain in a way that depends on lamins polymerization (Zhao et al, 1996). Lamins can also bind telomeric sequences (Shoeman and Traub, 1990), as well as, an A+T-rich DNA fragment that is located in the centromeric regions of *Drosophila* chromosomes and is organized similar to a MAR/SAR (Baricheva et al, 1996). Photo-crosslinking of *Drosophila* K_c cells that were grown in the presence of bromodeoxyuridine revealed that interphase lamins, but not mitotic lamins, are associated with both DNA and RNA in vivo (Rzepecki et al, 1998).

Lamins also bind chromatin fragments and interphase chromatin (Goldberg et al, 1999; Hoger et al, 1991; Taniura et al, 1995; Yuan et al, 1991), in vitro assembled chromatin (Ulitzur et al, 1992), mitotic chromosomes (Glass et al, 1993; Glass and Gerace, 1990; Goldberg et al, 1999) and specific chromosomal proteins (Burke, 1990b; Goldberg et al, 1999; Taniura et al, 1995; Yuan et al, 1991). Avian type A lamin binds in vitro to polynucleosomes with a dissociation constant of about 1 nM (Yuan et al, 1991). Mammalian type A and B lamins (Glass et al, 1993; Glass and Gerace, 1990) and *Drosophila* lamin Dm₀ can bind mitotic chromosomes in vitro (Goldberg et al, 1999). The chromatin binding activity of the mammalian lamins is localized at their tail domain, is mediated by core histones and possesses a dissociation constant in the range of 0.12-0.3 μM (Taniura et al, 1995). The binding activity of *Drosophila* lamin Dm₀ is also localized at its tail domain, has a dissociation constant in the range of 1 μM and is mediated by histones H2A and H2B (see below). The actual association of lamins to histones may be stronger since lamins form large polymers in vivo.

The *Drosophila* otefin is also involved in the process of NE assembly (Ashery Padan et al, 1997a). Trypsin treatment of membrane fractions of *Xenopus* and *Drosophila* extracts abolishes the ability of nuclear vesicles to bind demembrated sperm chromatin (Ulitzur et al, 1997; Wilson and Newport, 1988), indicating that NE assembly also depends on the activity of IMPs. IMPs, such as LBR, LAP1 and TMPO/LAP2, are possible targets for this trypsinization. It is likely that protein complexes containing lamin(s), otefin and IMPs mediate this NE assembly activity.

C. The family of Thymopoietin (TMPO)/ Lamina Associated Polypeptide 2 (LAP2) proteins

Thymopoietins (TMPOs) are a family of proteins that are highly conserved in mammals and *Xenopus* and are putatively involved in functional nuclear architecture and cell cycle control. In mammalian cells, six alternatively spliced TMPO isoforms, designated α , β , γ , δ , ϵ , and ζ were isolated and characterized (Berger et al, 1996; Harris et al, 1994). All of them share an identical N-terminal 186 amino acid domain. One member of this family, TMPO is the homologue of the rat Lamina Associated Polypeptide 2 (LAP2) (Berger et al, 1996; Furukawa et al, 1995; Harris et al, 1995). TMPO /LAP2 is a type II integral protein of the inner NE, which binds lamin B1 and chromosomes in a phosphorylation dependent manner (Foisner and Gerace, 1993). It can be divided roughly into four domains: a hydrophilic C-terminus domain, a hydrophobic transmembrane domain, a NE targeting and lamina-binding domain and a chromatin-binding domain (**Figure 2**). As NE disassembly begins at prophase TMPO /LAP2 undergoes phosphorylation by mitotic factors, possibly by p34cdc2 kinase. This has been found to abolish its interphase binding to both lamin B1 and chromosomes. Consistently, during late anaphase, TMPO /LAP2, as well as lamin-associated and non-associated vesicles, associates independently around chromatin to bind the surface of the decondensing chromosomes in order to complete NE reassembly (Foisner and Gerace, 1993; Yang et al, 1997). Thus, it is suggested that TMPO /LAP2 plays a key role in NE disassembly and reassembly during mitosis and linking chromatin to the NE in interphase.

The specific binding of TMPO /LAP2 to lamin was confirmed using the two-hybrid system (Furukawa et al, 1998; Furukawa and Kondo, 1998). Amino acids 78-258 of lamin B₁ rod domain are sufficient for the direct binding of lamin B₁ to TMPO /LAP2 (Furukawa and Kondo, 1998). Interestingly, the lamin binding region of TMPO /LAP2 coincides with TMPO /LAP2 NE targeting domain and includes residues 298-373. The chromosomes binding site of TMPO /LAP2 resides within residues 1-85 (Furukawa et al, 1998; Gant et al, 1999; Yang et al, 1997), a region which is common to all TMPO isoforms. By transfecting truncated clones of TMPO /LAP2, Yang et al (1997), showed that TMPO /LAP2 has a role in regulating the dynamics of the nuclear lamina and the interaction between TMPO /LAP2 and the nuclear lamina is required for nuclear growth after mitosis (Yang et al, 1997).

Three other isoforms of the TMPO family, TMPOs α , β , and γ , are splicing variants of TMPO /LAP2. All four isoforms share a putative hydrophobic transmembrane domain near their C-terminus via which TMPO /LAP2 was suggested to bind to the NE (Berger et al, 1996; Furukawa et al, 1995). However, whereas TMPO /LAP2 contains two putative p34cdc2 kinase phosphorylation sites, TMPOs α and β contain only one such site and TMPO γ lacks both sites (Berger et al, 1996), suggesting alternative regulating roles to these isoforms at the NE.

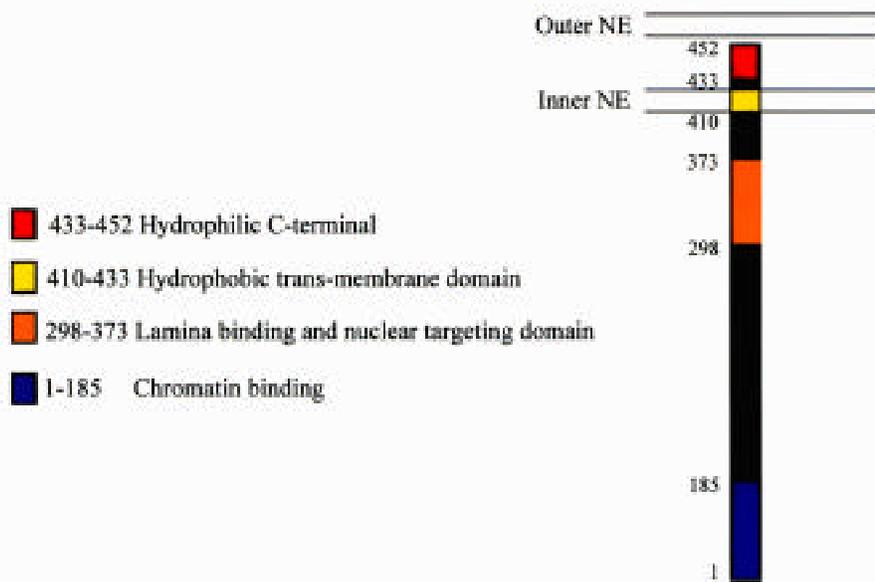


Figure 2. The molecular organisation of TMPO /LAP2 protein. The positions of the different domains are marked.

Another isoform, TMPO₂ has a completely different C-terminus, lacking a trans-membrane domain but containing a putative nuclear localization signal (NLS) and a putative tyrosine and cdc2-specific phosphorylation sites. It is localized throughout the nuclear interior in interphase cells. During metaphase it dissociates from chromosomes and becomes concentrated around the spindle poles, probably due to specific phosphorylation. The protein is relocated to chromosomes at early stages of nuclear reassembly during telophase (Dechat et al, 1998; this study-see results). It is therefore suggested that, similar to the TMPO /LAP2-type isoforms, TMPO₂ has a major role in the process of NE reassembly but in a different manner. For example, it will be interesting to reveal whether TMPO₂ is a true LAP that binds one of the lamins either in interphase or during mitosis like its TMPO /LAP2 family member. TMPO₁, the shortest isoform, lacks both the trans-membrane domain of the TMPO /LAP2-type isoforms and the NLS of TMPO₂. The expression of the various TMPO isoforms is ubiquitous, with higher levels in proliferative tissues (Berger et al, 1996; Harris et al, 1994; Ishijima et al, 1996; Theodor et al, 1997; Zevin-Sonkin et al, 1992).

D. Interactions between lamins and other nuclear lamina and inner nuclear membrane proteins.

1. Lamin interaction with IMPs

The interactions between lamins and IMPs are discussed below. These interactions are required for lamins to exert their biological roles. The interaction between lamins and TMPO /LAP2 is discussed above. The abnormal arrangement of nuclear pores in cells mutated in their lamin

gene indicates an additional interaction between lamins and nuclear pore proteins, possibly gp210.

a. Lamin-LBR/p58 interaction: LBR/p58 is an IMP that binds lamin B in a saturable and specific fashion, with a dissociation constant of about 200 nM (Worman et al, 1988). LBR is composed of a nucleoplasmic amino terminal domain followed by a hydrophobic domain that contains eight putative transmembrane segments (Worman et al, 1990). LBR's hydrophobic region has high sequence homology to the yeast sterol c-14 reductase (Gerace and Foisner, 1994; Shimanuki et al, 1992), and it was shown to possess c-14 reductase activity in *Saccharomyces cerevisiae* (Silve et al, 1998). The amino terminal domain of LBR has three DNA-binding motifs (Worman et al, 1990) and was suggested to bind DNA (Ye and Worman, 1994). LBR is phosphorylated in a cell cycle dependent manner, on serine residues in interphase and on serine and threonine residues in mitosis (Courvalin et al, 1992; Nikolakaki et al, 1997; Nikolakaki et al, 1996; Papoutsopoulou et al, 1999; Simos and Georgatos, 1992; Worman et al, 1990). It is degraded at late stages of apoptosis, interacts with chromatin (Pyrpasopoulou et al, 1996), and with several nuclear proteins including lamin B (Worman et al, 1988), p34, p18 (Simos and Georgatos, 1992) and the human protein homologous to the *Drosophila* heterochromatin associated protein, HP1 (Ye and Worman, 1996; Ye et al, 1997). Though its name, there is a recent work, utilizing biochemical fractionation analysis, that suggests that LBR and lamin B do not bind directly to each other in vivo (Mical and Monteiro, 1998). By using in vitro reconstituted vesicles assay it was shown that LBR can provide chromatin docking sites for nuclear vesicles (Pyrpasopoulou et al, 1996). An LBR-related protein from sea urchin can be

involved in providing chromatin docking sites for nuclear vesicles and can bind to the nuclear lamina (Collas et al, 1996).

b. Lamin-LAP1A-C interaction: LAP1A-C are related IMPs, which are presumably alternatively spliced transcripts of the same gene (Foisner and Gerace, 1993; Martin et al, 1995). LAP1A and LAP1B, but not LAP1C, can bind to both lamin A and lamin B in vitro. However, LAP1C associates with type B lamin in vivo as a component of a protein complex, albeit a direct LAP1C-lamin interaction has not been demonstrated (Maison et al, 1997). Cloning of LAP1C revealed that it is a type II IMP with a single membrane spanning region and a hydrophilic amino terminal domain that is exposed to the nucleoplasm. LAP1 isotypes are differentially expressed during development. LAP1C protein is present both in non-differentiated and differentiated cells whereas LAP1A and LAP1B proteins are abundant only in differentiated cells (Martin et al, 1995).

c. Lamin-emerin interaction: Mutations in the emerlin gene result in the X-linked Emery-Dreifuss muscular dystrophy (Bione et al, 1994). Emerlin is a ubiquitous IMP of the inner nuclear membrane (Manilal et al, 1996; Nagano et al, 1996) with sequence and structural homology to TMPO /LAP2 (Manilal et al, 1998). It is reasonable to speculate that emerlin and lamin A/C interact with each other, directly or indirectly, since mutations in the gene encoding the human lamin A/C cause the autosomal dominant Emery-Dreifuss muscular dystrophy (Bonne et al, 1999) and both proteins are associated with the inner nuclear membrane.

2. Lamin interaction with peripheral proteins

a. Lamin-YA interaction: YA is a *Drosophila* NE protein that is present in the nuclear lamina during the first two hours of zygotic divisions and whose function is essential for initial embryonic development (Lin et al, 1991; Lin and Wolfner, 1991; Lopez et al, 1994). YA molecules are present in complexes with each other (Goldberg et al, 1998; Liu and Wolfner, 1998), and embryonic YA can associate with decondensed chromatin in vitro (Lopez and Wolfner, 1997). The carboxy terminal 179 amino acids of YA are necessary to target and retain YA in the NE. The condensation state of the chromosomes in YA-deficient eggs and embryos is abnormal (Liu et al, 1995) and ectopically expressed YA associates with polytene chromosomes in vivo (Lopez and Wolfner, 1997). YA interacts with *Drosophila* lamin Dm₀ in the yeast two-hybrid system. This interaction requires the rod and tail domains and part of the head domain of lamin Dm₀ and the C-terminal domain of YA (Goldberg et al, 1998).

b. Lamin-otefin interaction: Otefin is a peripheral nuclear membrane protein, characterized in *Drosophila*, which has no apparent homology to other known proteins (Padan et al, 1990). In *Drosophila*, otefin is present in the NE of essentially all cells examined during *Drosophila*

development, except for sperm cells. In eggs and young embryos, otefin is also associated with the maternal fraction of membrane vesicles (Ashery Padan et al, 1997a). Otefin is a phosphoprotein in vivo and is phosphorylated by cdc2 protein kinase and cAMP-dependent protein kinase in vitro (Ashery Padan et al, 1997a). The otefin protein contains a large hydrophilic domain and a C-terminal hydrophobic domain of 17 amino acids. The C-terminal domain of otefin is essential but not sufficient for the targeting of otefin to the nuclear periphery. Sequences at the hydrophilic domain of otefin are required for both the localization and stabilization of otefin in the NE (Ashery Padan et al, 1997b), and for interaction with lamins. Otefin and lamin interact with each other in the yeast two-hybrid system and are present in vivo in the same protein complex (Goldberg et al, 1998). This interaction requires the rod domain of lamin Dm₀ and two hydrophilic regions in otefin (Goldberg et al, 1998).

Otefin was shown to be involved in NE assembly as the inhibition of otefin activity in *Drosophila* cell-free system, with anti-otefin antibodies, blocked the attachment of the nuclear vesicles to chromatin (Ashery Padan et al, 1997a). The similar phenotype observed in the inhibition studies of both lamin Dm₀ (see above) and otefin is probably due to their co-localization to nuclear vesicles in the same protein complex (Goldberg et al, 1998).

E. Lamin and apoptosis

During apoptosis, lamins are major targets for the caspase family of proteases, which trigger nuclear lamina breakdown. Lamin degradation has been reported in different cell types and in response to different apoptosis-inducing stimuli (Anjum and Khar, 1997; Antoku et al, 1997; Fraser et al, 1997; Kaufmann, 1989; Kawahara et al, 1998; Kluck et al, 1997; Lazebnik et al, 1993; Neamati et al, 1995; Oberhammer et al, 1994; Orth et al, 1996; Rao et al, 1996; Shimizu et al, 1998; Shimizu and Pommier, 1997; Takahashi et al, 1996a; Takahashi et al, 1996b; Ucker et al, 1992; Zhivotovsky et al, 1997). Lamin B is phosphorylated by PKC during apoptosis before its degradation (Shimizu et al, 1998). The degradation of lamin B₁ precedes DNA fragmentation in apoptotic thymocytes (Neamati et al, 1995), HeLa cells (Mandal et al, 1996) and HL60 cells (Shimizu et al, 1998).

Lamins may be involved directly in the regulation of apoptosis since ectopic expression of uncleavable mutant lamin A or B caused a 12 hours delay in the onset of apoptosis. The cells expressing the mutant lamins failed to undergo chromatin condensation and nuclear shrinking, which is a hallmark of apoptotic cell death. However, in these cells the NE collapsed and the nuclear lamina remained intact. However, the late stages of apoptosis were not affected (Rao et al, 1996). Thus, the proteolysis of lamin facilitates the nuclear events of apoptosis, perhaps by facilitating nuclear breakdown. A possible role for lamin cleavage during apoptosis is to enable the dissociation of the chromatin from the nuclear lamina and thereby to affect nuclear condensation.

II. Results and discussion

A. Lamin Dm0 binds chromosomes through two separate regions within its tail domain.

Lamin Dm0 can bind specifically to decondensed sperm chromatin in *Drosophila* in vitro nuclei assembly assay, as well as to mitotic chromosomes (Goldberg et al, 1999; Ulitzur et al, 1992). The binding assay of lamin Dm0 to mitotic chromosomes includes incubation of purified lamin Dm0 protein with isolated CHO mitotic chromosomes for 30-60 min at 22°C in the presence of excess amount of non-relevant proteins. Lamin binding to the surface of the chromosomes was observed following immunofluorescence analysis with either monoclonal anti-lamin Dm0 antibody or monoclonal anti-RGSHis antibody (Qiagen, Germany) that recognises a RGS(H)4 epitope, as primary antibodies, and Cy3-conjugated goat-anti-mouse antibodies, as secondary antibodies. Alternatively, it was detected directly by a fusion between lamin Dm0 and the green fluorescence protein (GFP) (Figure 3).

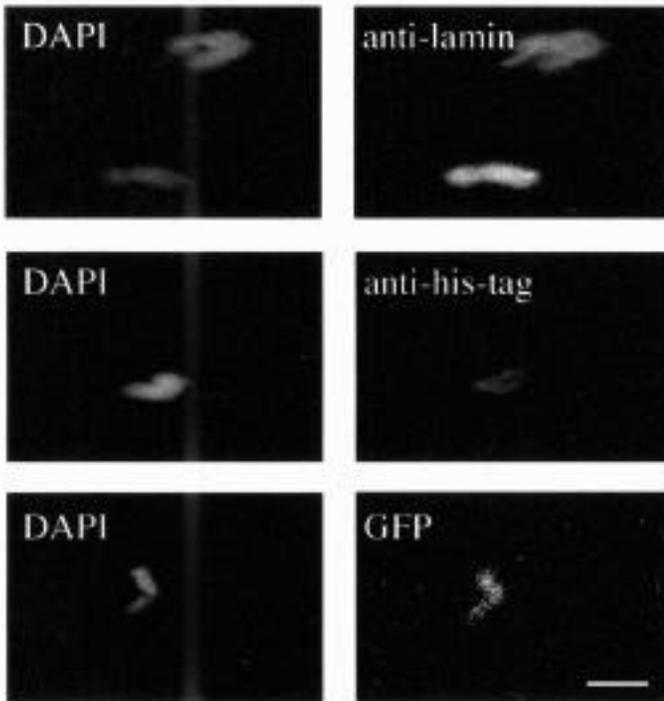


Figure 3. The binding of the tail domain of lamin Dm₀ to mitotic chromosomes can be observed with different detection systems. Upper panel – Detection was with monoclonal anti-lamin Dm₀ antibody, as primary antibody, and Cy3-conjugated goat-anti-mouse antibodies, as secondary antibodies. Middle panel – Detection was with monoclonal anti-RGSHis antibody (Qiagen, Germany), as primary antibody, and Cy3-conjugated goat-anti-mouse antibodies, as secondary antibodies. Lower panel – The tail domain of lamin Dm₀ was fused in frame to the Green Fluorescent Protein (GFP). Chromatin was stained with the DNA-specific dye DAPI. In all three cases, viewing was with a Leitz microscope equipped with epifluorescence. (Bar = 5µ).

The binding of lamin Dm0 to chromosomes did not require lamin polymerization, since lamin Dm0 mutated in Arginine 64 (R64>H), which is unable to polymerize (Zhao et al, 1996), still bound chromosomes in a similar way to that of wild type lamin Dm0 (Figure 4). Further mapping of the regions that are involved in lamin Dm0 binding to mitotic chromosomes, using deletion mutants of lamin Dm0 protein, revealed that the lamin Dm0 tail domain (amino acids 425-622) mediates this binding (Figures 3, 4). The isolated lamin Dm0 tail domain bound to the periphery of mitotic chromosomes with similar intensity to that of wild type lamin Dm0 (Figure 4). The dissociation constant of lamin tail domain binding to chromatin is approximately 1 µM (Goldberg et al, 1999). The existence of a chromatin binding site in the lamin tail domain was also reported for *Xenopus* type A and B₂ lamins (Hoger et al, 1991) and for mammalian type A and B lamins (Taniura et al, 1995).

Deletion mutants of the lamin Dm0 tail domain were designed in order to map the region in this domain that mediates the binding of lamin Dm0 to chromosomes. Each deletion mutant was expressed in bacteria, purified to near homogeneity and subjected to the binding assay. The ability of the different protein constructs to bind mitotic chromosomes is summarized in Figure 4. The T425-522 protein bound chromosomes with lower immunofluorescence intensity as compared to the complete lamin tail domain, but with significantly higher intensity as compared to the T473-622, T523-622 and T473-572 proteins. In addition, the intensity of T473-572 binding to chromosomes was close to background levels (Figure 4). Taken together, these data indicate that there are two regions that are required for efficient binding of lamin Dm0 to chromosomes. The major binding region includes amino acids 425-473 of lamin Dm0 and the minor binding region includes amino acids 572-622 of lamin Dm0. T425-572 protein that contains the first binding region binds to chromosomes with similar efficiency to the complete tail domain, while T523-622 and T473-622 proteins that contain the second binding region bind to chromosomes with significantly weaker intensity. The lower signal obtained with T425-522, as compared to T425-572, can be explained by a difference in protein folding or requirement of additional residues.

B. Lamin Dm0 tail domain binding to chromosomes can be displaced with histones H2A and H2B

In order to detect the molecules that are required for the binding of lamin Dm0 to chromosomes, we analyzed the ability of various chromosomal components to displace the binding of the lamin Dm0 tail domain to mitotic chromosomes. MAR/SAR DNA sequences were previously found to bind lamin Dm0 in vitro (Baricheva et al, 1996; Luderus et al, 1992; Luderus et al, 1994), through the rod domain of lamin Dm0 (Zhao et al, 1996). MAR/SAR DNA sequences, as well as yeast ARS sequences and plasmid DNA, are not the target of lamin tail binding, since they could not displace the binding of the lamin Dm0 tail domain

to chromosomes (Goldberg et al, 1999). This is expected since it is the tail domain that mediates the binding of lamin Dm0 to chromosomes. In contrast, isolated nucleosome core particles and commercially crude preparation of core histones and histone H1 displaced lamin tail domain binding to chromosomes (Goldberg et al, 1999).

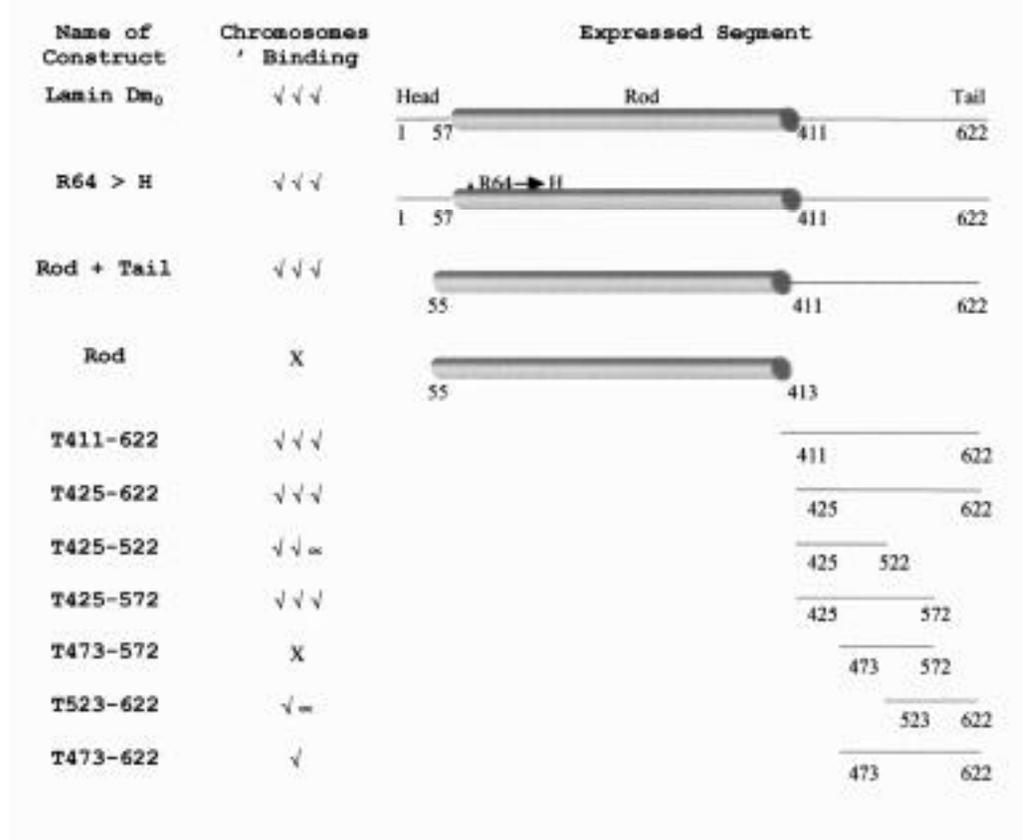
To identify specific histone(s) that interact with the lamin Dm0 tail domain, the individual core histones (Figure 5) or histone H1 (Goldberg et al, 1999) were tested for their ability to displace the binding of the lamin Dm0 tail domain to chromosomes. A 30-120-fold molar excess of purified histones H2A or H2B could each displace the binding of lamin Dm0 tail domain to chromosomes (Figure 5). In contrast, a 30-120-fold molar excess of individual histones H3 or H4 did not displace the lamin Dm0 tail domain binding to chromosomes (Figure 5). Similarly, a 32-fold molar excess of purified histone H1 (amino acids 1-142) did not displace the binding of lamin Dm0 tail domain to chromosomes (Goldberg et al, 1999). It is, therefore, likely that the interaction between lamin Dm0 and chromosomes is mediated by histones H2A and H2B. The biological significance of this lamin-histones interaction is probably in the processes of nuclear envelope assembly and nuclear organization. The significance of this interaction in vivo is currently under investigation..

C. Analysis of the mouse TMPO , , ' , , and isoforms.

The first mouse TMPO isoforms that was cloned was TMPO (Berger et al, 1996; Theodor et al, 1997). Its cDNA clone was isolated from thymus cDNA library and characterized, using a 126 bp fragment, encoding thymopoietin amino acids 1-42, from the bovine TMPO cDNA (Zevin-Sonkin et al, 1992), as a probe. The same library was subsequently screened with a 790 bp probe, derived from the N-terminus of the TMPO cDNA. Repeated screenings and restriction enzyme analysis revealed at least six distinct TMPO transcripts (Figure 6).

Examination of the mouse TMPO sequence revealed a short region of basic amino acids (amino acid 188-194) suggestive of a NLS (Kalderon et al, 1984), and a possible tyrosine phosphorylation site (amino acids 618-625) (Patschinsky et al, 1982). The sequence S/T-P-X-X, a potential recognition sequence for cdc2-related kinases (Nigg, 1993), is found 10 times throughout the TMPO sequence. Hydropathy analysis revealed that similar to the human isoforms, all mouse TMPOs lack an N-terminal hydrophobic signal sequence typical of secreted polypeptides (not shown). However, this analysis revealed that TMPOs , , and contain, like the human TMPO and , a hydrophobic transmembrane domain near their C-terminus (amino acid 409-432 of TMPO), suggesting their association with cellular membranes such as the nuclear envelope.

Figure 4. Binding of different lamin Dm₀ constructs to mitotic chromosomes derived from Chinese Hamster Ovaries (CHO) requires specific sequences in their tail domain. R64>H is a point mutation in lamin Dm₀ in Arginine 64 that inhibits its ability to form filaments. The numbers in the name of the construct represent the amino acids of lamin Dm₀ that are included in the construct and their position is shown below the map of the construct. √√√ indicates strong binding; √√ indicates medium binding, √ indicates weak binding and X indicates lack of detectable binding. √ indicates detection with the monoclonal anti-R^{GS}His antibody or with GFP.



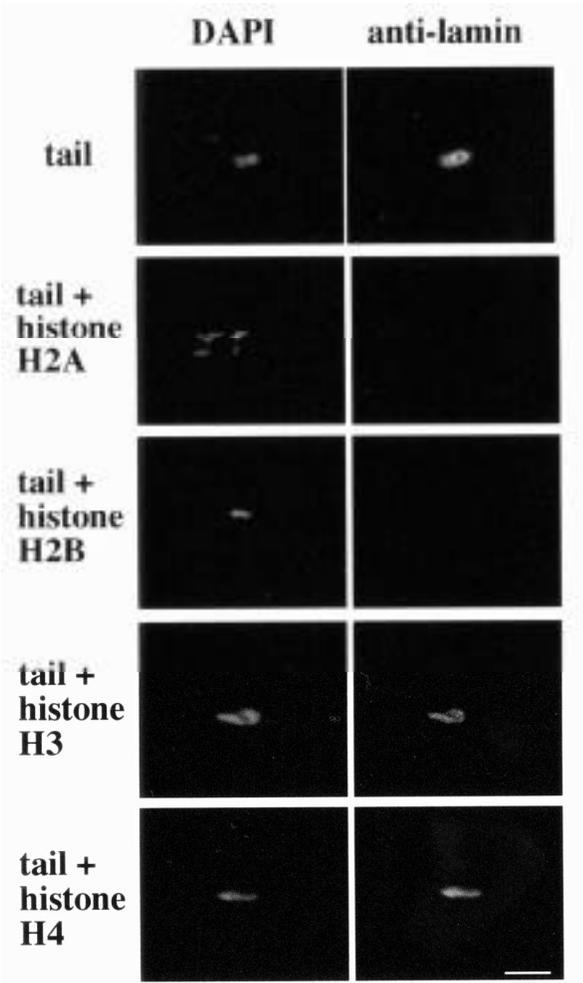


Figure 5. The binding of lamin Dm₀ to mitotic chromosomes can be displaced with histones H2A and H2B. The tail domain of lamin Dm₀ was used to bind the mitotic chromosomes in the presence or absent of histones. DAPI staining – left panels; MAb anti-lamin Dm₀ antibody as primary antibody and Cy3-conjugated goat-anti-mouse antibodies as secondary antibodies – right panels. (Bar=5μ).

Mouse TMPO α , β , ϵ , δ , and ζ share an identical N-terminal 186 amino acids domain (**Figure 6**). Like the human and the bovine TMPOs, amino acids 1-49 are highly homologous to the originally purified 49-amino acid bovine TP (Schlesinger and Goldstein, 1975). After Glu186, TMPO diverges from the other TMPOs. TMPO differs from TMPO β only in lacking the β -specific residues 220-259. TMPO δ lacks both the β and the ϵ -specific domains, which is contained within residues 220-291 of TMPO β . TMPO γ is missing the β , ϵ and δ -specific domains contained within amino acids 220-328 of TMPO β . Interestingly, two TMPO ζ 3'-UTR versions were isolated in mouse and designated TMPO ζ and TMPO ζ' . The two clones are identical in their ORF sequence, but differ in an additional 3'-UTR sequence starting at A1715 of the ζ' clone, probably due to an alternative polyadenylation signal.

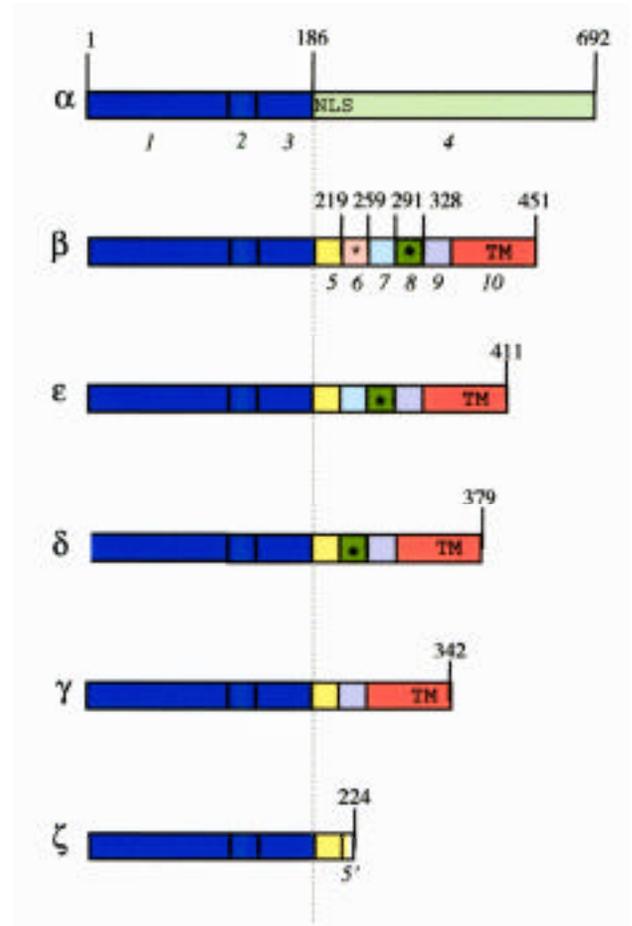


Figure 6. TMPO/LAP2 is a growing family of nuclear envelope proteins derived from a single alternatively spliced gene. The numbers above each isoform represent the corresponding amino acid. The numbers below the β and ϵ isoforms represent the corresponding exons in the TMPO gene. The exons that are common to all TMPOs are colored in blue and the alternatively spliced exons have different colors. NLS-nuclear localization signal; TM-transmembrane domain; 5'- the last 5 amino acids of the ζ isoform that are included in intron 5 of the TMPO gene. Asterisk in β and ϵ isoforms show the location of putative sites for the cdc2-kinase.

D. Monoclonal antibodies identify alternatively spliced forms of TMPOs

Three monoclonal antibodies (mAbs) were generated in order to characterize the expression and localization of the different TMPO isoforms (Dr. Gideon Goldstein, generous gift). The 6E10 mAb was raised against a synthetic peptide common to the N-terminus of all TMPOs. Indeed, Western blot analysis revealed that the 6E10 antibody recognized both recombinant and native TMPOs α , β , and ϵ as well as native TMPOs δ and ζ (**Figure 7a**). Although all TMPOs are present in both the hematopoietic K562 and the epithelial HeLa cell lines, TMPO α is clearly more abundant than all

other TMPOs and the relative amounts of the different TMPOs vary between these cell lines. Thus, it would be interesting to investigate if the different levels of expression of the various TMPOs in specific cells have a role in the biological functions that these cells have to exert. The 4G10 mAb was raised against recombinant TMPO α and the 6G11 mAb was raised against a synthetic peptide, derived from TMPO β /LAP2 specific region (amino acids 313-330). These antibodies recognized both recombinant and native TMPO α and TMPO β , respectively (Figure 7b and c). Interestingly, the 6G11 antibody cross-reacted with two close bands in both cell lines, suggesting two forms of TMPO β that differ in their phosphorylation pattern (Figure 7c).

E. TMPO α is localized both to the nucleus and centrosomes, while the TMPO β /LAP2 type isoforms are localized to the nuclear envelope.

TMPO α is the largest member of the TMPO family. It shares the first 187 amino acids of all TMPOs but has a unique long C-terminus. This region lacks a transmembrane domain but contains a NLS, a putative tyrosine phosphorylation site and two perfect p34cdc2 kinase phosphorylation sites (Nigg, 1993). This unique region suggests a different intra-cellular localization than that of the

TMPO β /LAP2-type isoforms.

The localization of TMPO α was studied by immunofluorescence microscopy during the different cell cycle stages of HeLa cells, using the 4G10 anti TMPO α mAb. In interphase, TMPO α was diffusely distributed throughout the nucleoplasm but was excluded from the nucleoli (Figure 8a). In addition, it was found in the centrosomal region (the bright spots in Figure 8a). In early prophase, prior to its complete disintegration of the nuclear envelope, a large fraction of TMPO α was observed at the nuclear periphery (Figure 8a). In metaphase and early anaphase, TMPO α was disseminated throughout the cell. In addition, the two centrosomes at the spindle poles were stained brightly (Figure 8b). In telophase a bulk of the TMPO α protein re-localized to the two newly forming nuclear envelopes. At this stage, the nucleus itself was negatively stained (Figure 8c). Upon completion of mitosis and reentry of the cells to G1, TMPO α regained its typical interphase intranuclear and centrosomal localization, while the nuclear envelope was not stained. This staining pattern of TMPO α throughout the cell cycle was exemplified in other cell lines such as PTK, K562 and HL-60 (not shown). The presence of TMPO α at the nuclear periphery during prophase indicates a possible association of TMPO α with NE components during this stage. The association of TMPO α with the chromatin periphery during telophase strongly suggests a role for this isoform in nuclear assembly.

Figure 7. Different monoclonal anti-TMPO antibodies detect the various of TMPO isoforms and show variability in their relative expression in human cells. (a) Detection was with the 6E10 monoclonal anti-all TMPO antibody. The left lane was loaded with recombinant proteins. Although all TMPO proteins are expressed in both HeLa and K562 cells, their relative abundance is different. (b) Detection was with 4G10 monoclonal anti-TMPO α antibody. (c) Detection was with 6G11 monoclonal anti-TMPO β antibody.

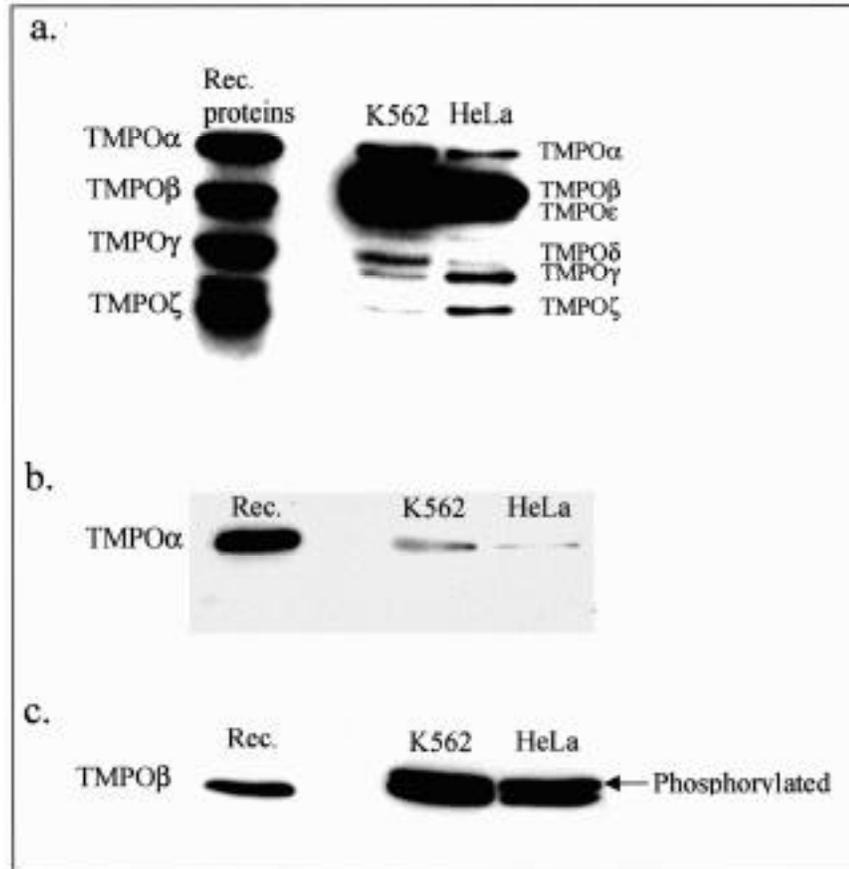
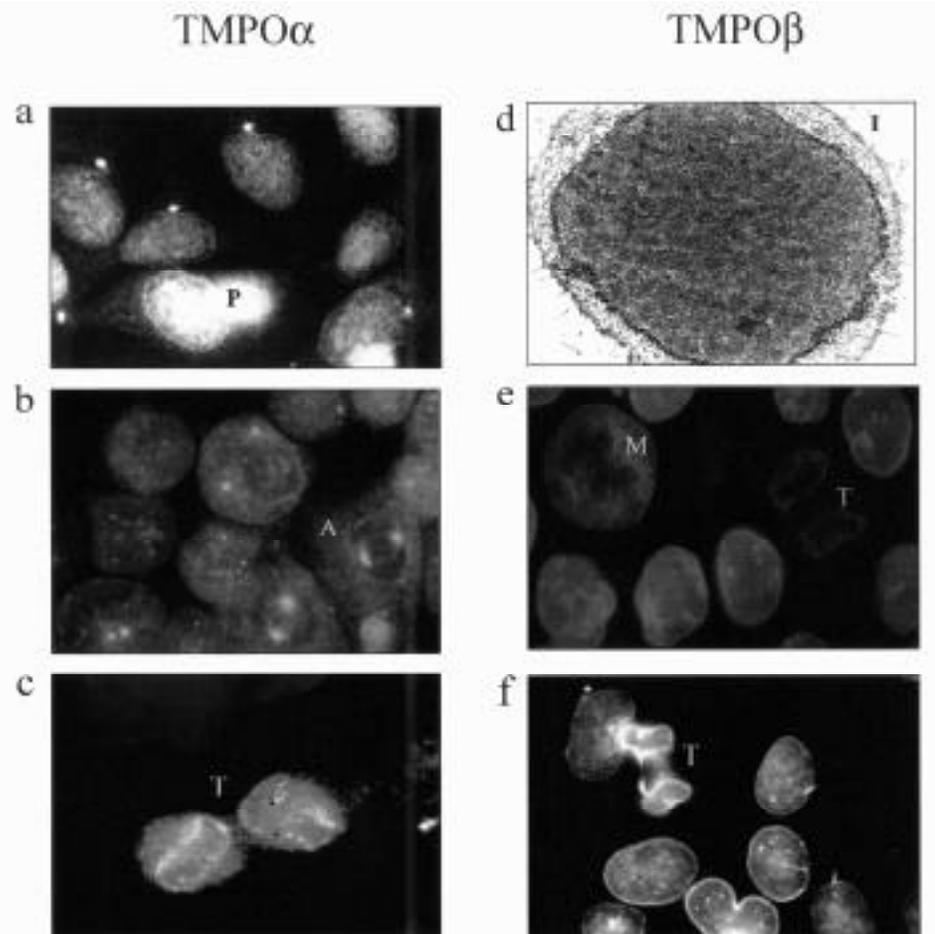


Figure 8. TMPO α and TMPO β have different localisation in human cells. TMPO α localisation was detected with the 4G10 monoclonal anti-TMPO antibody (a-c) and TMPO β localisation was detected with the 6G11 monoclonal anti-TMPO β antibody (d-f). P, a cell in prophase; M, metaphase; T, telophase. Panel d shows immunogold electron microscope detection of TMPO β ; all other panels show indirect immunofluorescence analysis.



Previous studies have shown that TMPO β /LAP2 is an integral protein of the inner nuclear membrane (Foisner and Gerace, 1993). Its NE targeting and binding are probably mediated by its carboxy terminus-located lamin binding region and trans-membrane domain (Furukawa et al, 1995). Since TMPO α , and also share this carboxy-terminus and parts of the lamin binding domain, and transfected TMPO α was localized to the NE (data not shown), we suggest that these isoforms are also nuclear membrane proteins.

The localization of TMPO β /LAP2 to the nuclear envelope during the cell cycle was studied in Hela cells, by immunofluorescence and immuno-electron microscopy. In interphase, immuno-gold analysis demonstrated the localization of TMPO β /LAP2 to the NE (Figure 8d). The immuno-fluorescence staining was confined to the NE, as well as to intra nuclear speckles (Figure 8f). These speckles possibly represent replication origins (Gant et al, 1999; Moir et al, 1994). In metaphase, TMPO β was dispersed in the cytoplasm (Figure 8e). In telophase, TMPO β re-localized to the two newly forming nuclear envelopes. However, the staining of TMPO β during telophase is more continuous than that of TMPO α .

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