

Nogo and its paRTNers

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Reticulons (RTNs) are a relatively new eukaryotic gene family with unknown functions but broad expression and peculiar topological features. RTNs are widely distributed in plants, yeast and animals and are characterized by a ~200-amino-acid C-terminal domain, including two long hydrophobic sequences. Nogo/RTN4 can inhibit neurite growth from the cell surface via specific receptors, whereas more general, 'ancestral', RTN functions might relate to those of the endoplasmic reticulum - for example, intracellular trafficking, cell division and apoptosis. Here, we review the taxonomic distribution and tissue expression of RTNs, summarize recent discoveries about RTN localization and membrane topology, and discuss the possible functions of RTNs.

The Reticulon/Nogo family of proteins has attracted more and more interest during the past two years, although the functions of most members still remain largely elusive. Over a decade ago, RTN1 was the first member identified, as a cDNA (called C1-13) specific for neural tissue [1]. Shortly thereafter, it was found to be the antigen recognized by two lung-cancer monoclonal antibodies that are specific for small-cell lung carcinoma (SCLC) cell lines and neuroendocrine cells [2]. Owing to its neuroendocrine-specific expression, the gene was called NSP (for neuroendocrine-specific protein). Immunocytochemical studies revealed that the protein is a membraneanchored component of the endoplasmic reticulum (ER), and it was renamed reticulon (RTN) [3].

Nine years later, >300 family members sharing homologies within the C-terminal region of ~200 amino acids, called the reticulon-homology domain (RHD), are known in a variety of organisms (T. Oertle, unpublished). One member, Nogo-A/RTN4-A, has recently been the focus of intense investigation because of its function as an inhibitor of neurite outgrowth and its involvement in restricting the plasticity of the central nervous system (CNS) [4-6]. Another member, Nogo-B/RTN4-B1 has been implicated in the induction of apoptosis, specifically in cancer cells [7]. Several reviews in the past three years have concentrated on Nogo and its possible clinical implications [8-10], but the rest of the RTN family has received little attention. Here, we highlight the shared features of the RTN family. Our purpose is to summarize the relatively few existing data about the RTN proteins, to project possible functions and hence to indicate new directions for future research.

Taxonomic distribution and evolution of the RTN family

Genes for RTN-like proteins have been identified in most eukaryotic taxa and have evolved from an intron-rich ancestor (T. Oertle, unpublished). In prokaryotes, no homologues have been identified so far, suggesting that RTNs emerged relatively recently in eukaryotes, potentially in parallel with the evolution of the endomembrane system (T. Oertle, unpublished). There are four mammalian reticulon genes (RTN1, RTN2, RTN3 and Nogo/RTN4), each of which can give rise to a range of alternative transcripts (Fig. 1). The four paralogues have a similar gene structure and probably arose during the putative genome-duplication events that occurred after the urochordata-craniata split. There is no homology between the N-terminal regions of paralogues, and the divergence of these segments compared with the C-terminal RHD within orthologues is significant (T. Oertle, unpublished). Nogo-A, which is

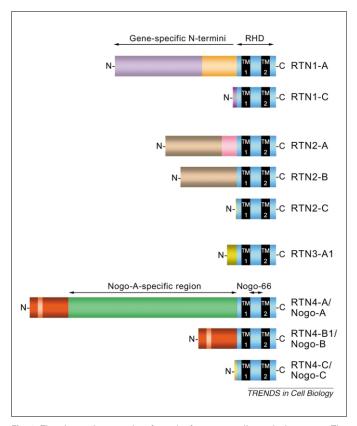


Fig. 1. The nine main transcripts from the four mammalian reticulon genes. The common C-terminus encodes the reticulon-homology domain (RHD), whereas the N-termini are specific for each paralogue and have no obvious sequence homologies to other proteins. The 66-amino-acid loop region between the two putative transmembrane (TM) domains (called Nogo-66) and stretches within the Nogo-Aspecific N-terminal region have been found to inhibit neurite outgrowth.

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the largest of these RTN proteins, has sequences essential for neurite growth inhibition encoded by N-terminal exons that occur in amphibians but not in fish. They probably emerged during the transition from fish to land vertebrates (T. Oertle, unpublished).

Tissue expression of mammalian RTN genes

The four mammalian RTN genes have a broad tissue expression pattern (Table 1) Most transcripts are enriched in nervous tissues (RTN1-A, RTN1-C, RTN2-A, RTN2-B, Nogo-A/RTN4-A). The RTN1 transcripts are almost exclusively expressed in neurons and neuroendocrine cells. Nogo-A/RTN4-A is expressed by oligodendrocytes, the myelin-forming cells of the adult CNS, and some neuronal subpopulations, heart and testis (Table 1). Two RTN transcripts (RTN2-C, Nogo-C/RTN4-C) are particularly enriched in skeletal muscle and both have E-boxes in their promoters to which muscle-specific transcription factors of the basic-helix-loop-helix family could bind [11,12]. By contrast, RTN3 and Nogo-B/RTN4-B1 have a widespread expression pattern (Table 1), as is the case for housekeeping genes. Their promoters lack a canonical TATA box and are GC rich [11,13]. Interestingly, the expression levels of both RTN2 and RTN3 seem to cycle in the suprachiasmatic nucleus, with a cycling phase of 22 h and 14 h, respectively [14].

There is evidence from expressed sequence tags that some *RTN* genes are expressed very early in development. It is currently unknown whether there are cells that do not express any *RTN* family members.

Subcellular localization

The shared feature of RTN proteins is their association with membranes of the endoplasmic reticulum (ER) [3] (Fig. 2b). This has been shown for mammalian RTN1 [3,15], RTN3 [16] and Nogo/RTN4 ([4,6,]; T. Oertle, unpublished) as well as for *Drosophila* Rtnl1 [17] and *Caenorhabditis* RTNL [18]. Because all RTNs lack a canonical leader peptide at their N-termini, translocation into the ER is assumed to be directed by internal signals

(e.g. transmembrane domains). Alternatively, the ER association could be independent of signal-recognition particle (SRP) and thus occur post-translationally. Deletion of the second hydrophobic region, but not of the C-terminal dilysine ER-retention motif, of Nogo disrupts its ER association and is thus crucially involved in correct membrane association [19].

Some of the RTNs associate with cellular structures other than the ER. In myoblasts, RTN2 colocalizes with the intermediate filament desmin, whereas, in myotubes, it colocalizes with α -actinin and seems to be associated with muscular Z band [20]. Nogo-A localizes with Golgi markers in addition to the ER and is present in small amounts at the plasma membrane of oligodendrocytes and fibroblasts [6] (T. Oertle, unpublished).

The subcellular localization of RTNs might depend on their mRNA distribution. For example, rat RTN1-C mRNA is restricted to axonal poles of certain neurons and is enriched in synaptosomal fractions [21]. This compartmentalization is thought to be due to 'zipcodes' present in the 3'-untranslated region of RTN1 mRNA [22]. Consistent with an enrichment of mRNA in synaptosomal fractions, RTN1-C and Nogo-A are concentrated in growth cones of neuroblastoma cell lines (e.g. SK-N-SH) and olfactory neurons, respectively [23,24]. It is tempting to speculate that this enrichment represents the association of RTNs with synaptic vesicles.

Membrane topology

The membrane topology of RTNs is of specific interest, particularly because the two very large (~35 amino acid) putative transmembrane domains could both span the membrane either once or twice (Fig. 2). Immunofluorescence studies have shown that, in the prevalent ER-associated topology, the N- and C-termini of RTNs face the cytoplasm ([6,16]; M. van der Haar, unpublished) (Fig. 2a). The 66-amino-acid loop between the two hydrophobic domains of Nogo-A cannot be detected by antibodies without prior permeabilization of the ER, suggesting that it assumes a lumenal orientation

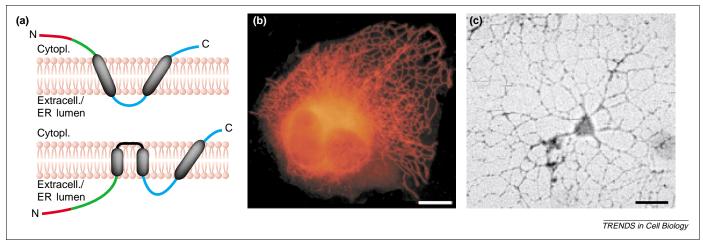


Fig. 2. Membrane topologies and subcellular localization of RTN1 and Nogo/RTN4. (a) Two proposed topologies for the C-terminal hydrophobic regions of RTNs. The lengths of the hydrophobic stretches (\sim 35 amino acids) could allow them to span the membrane once or twice. Because deletion of the second putative TM domain leads to a partial cytoplasmic localization of the protein, it is possible that the first hydrophobic region does not cross the membrane. There are also other possible topological models (not shown). (b) Immunocytochemical localization of RTN1-A in the endoplasmic reticulum (ER) of a transfected COS cell. Scale bar, 4 μ m. (c) Surface staining of endogenous Nogo-A on a cultured oligodendrocyte. Scale bar, 10 μ m.

Table 1. Summary of published and unpublished data on the expression pattern of the main reticulon transcripts

Tissue/cell	RTN1-A	RTN1-C	RTN2-A/-B	RTN2-C	RTN3	RTN4-A	RTN4-B	RTN4-C	RTN4-D-G
Central nervous system Cerebral cortex	+ [65] + [22,23,62,63]	+ [1,65,72] + [1,22,23,62,63]	+ [12,65] + [12]	+/- [12,65] +/- [12]	+ [16,66,A,B] + [60,A,B]	+ [4,6,7,33,58,67, 68,71,A,D] + [33,A]	+ [4,6,7,33, 58,A,D] + [33*,A]	+ [4,6,7,33, 58,70,A] + [A];	- [4,7,11, 58,69 [#] ,D]
Olfactory cortex	+ [64]					+ [24,67]		+/- [33]	
Entorhinal cortex	+ [62]				+ [60]	. [0.4]			
Piriform cortex Hippocampus	+ [62] + [22,62]	+ [22]	+ [12]	- [12]	+ [60,66,A,B]	+ [34] + [33,34,68,A]	+ [33*]	+ [A];	
Прросапраз	+ [22,02]	+ [22]	T [12]	[12]	+ [00,00,A,D]	+ [55,54,00,7]	+ [55]	+/- [33]	
Cerebellum	+ [22,23,62,63]	+ [22,23,62,63]	+ [12]	+/- [12]	+ [A,B]; - [60]	+ [33,67,68,A]	+ [33*]	+/- [33]	
Corpus callosum Putamen Amygdala Nucleus caudatus Thalamus	+ [62]	+ [1]	+ [12] + [12] + [12] + [12] + [12]	- [12] +/- [12] - [12] +/- [12] - [12]	+ [A] + [60,A]	+ [24,33,68] + [68] + [34,68,A] + [68] + [68]	+ [33*]	- [33]	
Substantia nigra Brain stem	+ [62] + [22]	. [22]	+ [12]	- [12]	+ [A,B]	+ [68]			
Spinal cord	+ [22]	+ [22]	+ [12]	+/- [12]	+ [A,B]	+ [4,33,34,67,68, 71,D]	+ [4,33,34* *]	+ [4,33,34* *]	
Retina Optic nerve	+ [61]	+ [61]			+ [66,A]	+ [33,A] + [4,6,24,33,D]	+ [33*] + [4,6,33,D]	+ [33,73] + [4,33]; - [6]	
Peripheral	+/- [23]	+ [23]			+ [A]	+/- [4,24,33,68];	+ [4,33*];	- [4,33]	- [4,58]
nervous system Adrenal gland	+/- [23]; - [22]	+/- [23]; - [22]				- [6,34] + [A]	- [6,34**] + [34**]		
Lung	- [22]; +/- [23,65]	- [22,65,72]; +/- [23]	+/- [12,65]	+ [12]	+/- [16,66,A]	- [6,7,33,58,68]; + [71,A]	- [6]; + [7,33,58,D]	- [6,7,33, 58,70]; + [A]	- [7,58,69 [#]]
Liver	- [22,23,65]	- [1,22,23,65,72]			+/- [16,66,A]	- [6,7,33,58,68,71]	- [6,7,58,D]; +/- [33]	+ [A] - [6,33,70]; + [7,58]	- [7,58,69#]
Kidney	- [22,23]	- [1,22,23,72]			+/- [16,66,A]	- [6,7,33,58,68]; + [71,A]	- [6]; + [7,33,58,D]	- [6,70]; +[7,33,58]	- [7,58,69#]
Spleen	- [22]; + [65]	- [22,65,72]	+/- [12,65]	+/- [12,65]	+/- [16,66,A]	- [7,33,58,71]	+ [7,33,58,D]	- [7,33,58,70]	- [7,58]
Stomach Small intestine	+/- [23] +/- [65]; - [23]	- [23,72] +/- [65]; - [23,72]	+ [12]	+ [12]	+/- [66] +/- [66]	- [7,58,71]	+ [7,58]	+/- [7,58]	- [7,58]
Colon	+/- [23,65]	+/- [65]; - [23]	- [12]; +/- [65]	+/- [12]	+ [A]	- [7,58]	+ [7,58]	+ [58]; +/- [7]	- [7,58]
Pancreas	+/- [23,65]	- [23,65]	- [12]	+/- [12]	+ [A]	- [7,58]; + [C]	+ [7,58,A]	- [58]; + [7,A]	- [7,58,69#]
Thymus Prostate	- [22,65] +/- [65]; - [23]	- [22,65,72] +/- [65], - [23]	- [65 <u>]</u>	+/- [65]	+ [A] +/- [66,A]	- [7,58] - [7,58]	+ [7,58,D] + [7,58]	- [7,58] + [7,58,A]	- [7,58] - [7,58]
Testis Ovary	+/- [22,65] - [23]; +/- [65]	- [22,72] - [23]	+/- [12] - [12,65]	- [12] +/- [12,65]	+/- [16,66,A] + [A]	+ [7,11,33,58,A] - [7,58]	+ [7,11,33,58,D] + [7,58]	- [7,33,58, 70] - [7,58]	+ [7,11,58,69 [#] ,D] - [7,58]
Placenta	+7 [00]		- [12]	+ [12,65]	+ [A]	- [7,58]	+ [7,58,A]	- [7,58]; + [A]	- [7,58,69 [#]]
Mammary gland Cervix Skin Adipose tissue	- [23] - [23] +/- [23]	+/- [23] - [23] - [23,72]	– [12]	+ [12]	+ [A] + [A] + [A]		+ [A] + [A]	+ [A] + [A] + [A] + [A] + [70]	
Heart	- [22,23,65]	- [1,22,23,72]	- [12,65]	+ [12,65]	+/- [16,A]	- [6,7,68];	– [6];	- [6,7,33,58];	- [7,58,69 [#]]
Skeletal muscle	- [23]	- [23,72]		+ [12,65]		+ [33,71,A,D] - [4,33,68]; +/- [7,24,58,67]	+ [7,33,58] - [4,33]; + [7,58]	+ [70] + [4,7,33,58,70]	- [7,58,69 [#]]
Smooth muscle Blood cells	- [23] + [23,65]	+ [23] - [23,65]	+/- [12,65]	+/- [12] +/- [65]	+ [A]	- [7,58]	+ [7,56] + [A] + [59**]; - [7,58]	- [7,58]	- [7,58]

No expression detected is marked with ' - ', very low expression levels with ' + /- ' and clearly detectable signals with ' + '. The data were obtained by analysing reticulon mRNA (by *in situ* histochemistry, northern blotting, reverse-transcription polymerase chain reaction and microarray and expressed-sequence-tag databanks) and protein (western blot, immunohistochemistry). Notice that the expression of *RTN1* transcripts in peripheral tissues has been shown to be due mainly to the presence of peripheral neuroendocrine cells and *RTN1*-positive macrophages.

Abbreviations: *, RTN4-A/-B; * * , RTN4-A/B/C; #, RTN4-E.

([6]; M. van der Haar, unpublished). However, antibodies against the 66-amino-acid loop region and antibodies against the N-terminus of Nogo-A can bind to the surface of differentiated oligodendrocytes in culture ([6]; M. van der Haar, unpublished), which suggests that, at least in these cells, Nogo-A can assume two membrane topologies (Fig. 2a,c).

Therefore, future studies are required to investigate: (a) whether the membrane translocation of RTNs is SRP dependent and, if so, which sequences function as insertion modules; (b) the three-dimensional structure of the transmembrane domains; (c) whether RTNs other than Nogo-A are localized to the Golgi and plasma membrane; and (d) which molecular mechanisms or

A Genbank dbEST

B Gillerion, O et al., unpublished.

C Pot, C. et al., unpublished.

D Merkler, D. et al., unpublished.

chaperones are responsible for the acquisition of the two proposed topologies.

RTNs as marker proteins and their roles in neuronal differentiation

RTN1-A and RTN1-C are both expressed in most neuroendocrine tumours, such as SCLCs, whereas they are absent in atypical carcinoids [25–27]. Only non-SCLCs showing a neuroendocrine immunophenotype also produce RTN1-A [28]. Thus, RTN1 is considered to be a highly sensitive and specific marker of neuroendocrine differentiation in lung cancer to be used in the diagnosis of this disease. Although it has been speculated that the presence of neuroendocrine markers could help to identify patients that are more likely to respond to chemotherapy, most clinical studies have shown that there are no biological markers that can reliably predict the response to chemotherapy in patients with non-SCLC [29].

RTN1-C mRNA is specifically upregulated upon spontaneous and induced neuronal differentiation [30,31]. It has also been proposed as a marker of neuronal differentiation that is reduced (together with Nogo-C) in temporal cortices of Down's-syndrome patients [32]. Nogo-A seems to be downregulated in some neurons and in skeletal muscle after differentiation [33,34]. De-differentiation of skeletal muscle cells (e.g. after denervation) leads to upregulation of Nogo-A and a concomitant downregulation of Nogo-C [35,36]. In line with this observation, the Nogo proteins have been recently proposed as molecular markers for the diagnosis of amyotrophic lateral sclerosis (ALS) and peripheral neuropathies in which changes in Nogo-A and Nogo-C expression levels have been observed [36].

Autoreactive antibodies against Nogo-A have been detected in sera of pilocytic astrocytoma patients [37] and of patients with multiple sclerosis and acute neurological disorders (M. Reindl *et al.*, pers. commun.). Therefore, the presence of anti-Nogo-A antibodies could potentially be used as marker for these diseases.

Possible functions of RTNs

ER function, plasma-membrane formation and cell division

Because RTNs are found in almost all eukaryotic cells and organisms, they would be expected to exert basic functions in the cellular machinery. Single RTN genes seem not to be of vital importance, however, because organisms with RTN gene disruptions (Saccharomyces cerevisiae, Schizosaccharomyces pombe, Caenorhabditis elegans and Drosophila melanogaster) are viable (e.g. [17,18,40]). On the basis of the (few) existing data, the following hypotheses for cellular functions of RTN proteins can be formulated.

(1) RTNs could function as pore or transporter complexes in the ER. RTN1-A and RTN1-B isoforms form supramolecular aggregates of $\sim\!500\,\mathrm{kDa}$ composed of homo- and heteropolymers [15], whereas RTN1-A and RTN1-C do not seem to co-polymerize [23] (Table 2). Because the domain involved in multimerization is likely to be the common C-terminus, especially the highly homologous RTNs (RTN1, RTN3 and RTN4) could also form homo- and heteromers if co-expressed together in the

same cells. Their unusually long hydrophobic regions might form pore-like structures. The evolutionary conservation of RTNs is clustered to these hydrophobic regions, underlining their relevance (T. Oertle, unpublished). The interaction of (S. cerevisiae) RTN2 with SHO1 (Table 2) could also point to a function of RTNs related to osmosensitivity.

(2) RTNs could function in the transport of constituents from the ER to other membrane compartments such as the Golgi, endosomes, synaptic vesicles and the plasma membrane. In the case of C. elegans RTNL-C, its N-terminal transcript-specific region interacts with RME-1 [18] (Table 2), a protein localized to the endocytic recycling compartment and involved in the exit of proteins from the endocytic recycling compartment to the plasma membrane or to the *trans*-Golgi network [38]. This N-terminus has no homology to vertebrate RTNs but a stretch of the protein is homologous to the endosomal protein endofin. S. cerevisiae RTN2 interacts with SEC27 (Table 2), a protein involved in ER-to-Golgi protein trafficking [39]. The enrichment of RTNs in neuronal growth cones (structures particularly active in endo- and exocytic processes) supports this possibility. In addition, overexpression of *S. pombe rtn* leads to a reduced cell wall lipid content (~20%) and to cell lysis in the absence of sorbitol [40]. The multiplication of *RTN* genes in plants (T. Oertle, unpublished) could be associated with the increased need for specialized proteins involved in the formation and maintenance of the plant cell wall.

(3) RTNs might also play role in structural stabilization of the ER network, for example by linking the ER to the cytoskeleton via protein-protein interactions. Indeed, the proline-rich nature of the N-termini of RTN1, RTN2 and RTN4 with many potential SH3-domain-binding sites [11] suggests that RTNs could interact with a range of cytoskeletal and signalling molecules. In line with this prediction, Nogo-A has been shown to co-immunoprecipitate with α -tubulin and myelin basic protein (MBP) [41] (Table 2).

(4) Last but not least, RTNs could have a role in cell division. Overexpression of *S. pombe rtn* inhibits cell separation after division in the absence of thiamine [40]. During mitotic cell division, both *D. melanogaster* Rtnl1 [42] and mammalian Nogo-A [41] have been shown to be in a ring-like structure surrounding the spindle apparatus. RTNs might be responsible for the distribution of endomembranes to the two daughter cells during mitotic division.

Nogo and inhibition of neurite outgrowth and cell spreading

The main focus of present RTN research is on Nogo-A, a protein that has been purified and cloned as a potent inhibitor of neurite outgrowth, and is thought to be an important negative regulator of the regenerative and plastic capabilities of the adult central nervous system [4–6,43]. Its potential to inhibit nerve growth is shown by the fact that peripheral nerves regenerate well after a lesion, whereas ectopic expression of Nogo-A in Schwann cells leads to delayed recovery of the crushed sciatic nerve [44]. Two main regions of Nogo are likely to be responsible

Table 2. Intracellular proteins known to interact with members of the reticulon family

Reticulon	Interacting partner	Refs
(HUMAN) RTN1-A	(HUMAN) RTN1-A	[15]
(HUMAN) RTN1-A	(HUMAN) RTN1-B	[15]
(HUMAN) RTN1-C	Bcl-x _L	[58]
(HUMAN/RAT) RTN4-A	α-Tubulin	[41]
(RAT) RTN4-A	Myelin basic protein (MBP)	[41]
(HUMAN) RTN4-B	Bcl-2	[58]
(HUMAN) RTN4-B	Bcl-x _L	[58]
(HUMAN) RTN4	NIMP	[71]
(HUMAN) RTN4	UQCRC1, UQCRC2	[71]
(CAEEL) RTNL-C	RME-1	[18]
(YEAST) RTN1	YOR285w	[39]
(YEAST) RTN1	YDL089w	[39]
(YEAST) RTN1	HAT2 (YEL056w)	[73]
(YEAST) RTN2	INP54 [inositol (1,4,5)-trisphosphate 5-phosphatase]	[39]
(YEAST) RTN2	SHO1 (osmosensor)	[39]
(YEAST) RTN2	KAP104 (karyopherin)	[73]
(YEAST) RTN2	SEC27 (endoplasmic-reticulum-to- Golgi trafficking)	[73]
(YEAST) RTN2	YMR110c (aldehyde dehydrogenase III)	[39]

for its neurite-growth-inhibiting effect: the first region includes two stretches located in the N-terminal Nogo-A-specific region; the second region is the 66-amino acid loop-region between the two hydrophobic domains in the C-terminus (Nogo-66) [5,6,45] (T. Oertle, unpublished). Both regions induce the downstream activation of the small GTPase RhoA in responsive neurons [46] (Fig. 3).

Nogo-66, but not the corresponding loop region of the other three RTNs, induces neuronal growth-cone collapse [6] via binding to a glycosylphosphatidylinositol-linked receptor in the plasma membrane called NgR [45]. NgR is also a receptor for two other myelin-associated inhibitory proteins known as MAG [47,48] and OMgp [49]. A coreceptor of NgR, the so-called low-affinity neurotrophin receptor p75, might be involved in signal transduction [50,51]. Indeed, soluble p75, soluble NgR and a peptide antagonist of NgR neutralize the inhibitory activity of myelin in vitro [50,52,53] and induce axonal regeneration after spinal-cord injury in vivo 52]. This suggests that the NgR-p75 receptor complex has a pivotal role in mediating myelin-associated inhibition. Many neuronal signalling molecules (e.g. neurotrophic factors or the axonal guidance molecules netrin and semaphorins) have complex multisubunit receptors that include more than one binding site (for example, the neurotrophin receptors p75 and trk, and the semaphorin receptors plexins and neuropilins). Nogo-A might follow the same rules (Fig. 3a). For the potent neurite-outgrowth and cell-spreading inhibitory site in the Nogo-A-specific part, binding to rat brain membranes and responsive cell lines (3T3 fibroblasts) can be shown biochemically (T. Oertle, unpublished). The Rho GTPase activation induced by Nogo-A fragments [46] argues for similar, convergent intracellular pathways as for Nogo-66/p75, or for common signal-transduction-receptor subunits for the different active sites of Nogo-A (Fig. 3a).

The predominant expression of Nogo-A in the myelinforming cells of the CNS supports the inhibitory effects of CNS myelin on neurite outgrowth *in vitro* and the poor capacity of the adult, myelinated CNS for regenerative and plastic neurite growth following lesions in vivo [54,55]. Indeed, in vivo application of antibodies against the Nogo-A-specific region induced sprouting of Purkinje cells in the adult cerebellum [56] and improved functional recovery following cortical stroke lesions [57]. The possible functions (perhaps as a repulsive axonal guidance molecule) of Nogo-A in developing neurons remain to be studied. The same is true for Nogo-B and Nogo-C: Nogo-B has an almost ubiquitous tissue expression pattern and both proteins possess the Nogo-66 inhibitory region. Short Nogo isoforms as well as NgR also occur in the lower vertebrate CNS, where regeneration does occur (T. Oertle, unpublished; M. Klinger et al., pers. commun.). In addition to a function as cell-surface signalling molecules, Nogo proteins-like the other RTNs-might also have intracellular roles in neuronal or non-neuronal cells.

Cancer and apoptosis

A recent study has suggested that Nogo-B might function as a pro-apoptotic protein. RTN1-C and Nogo-B interact with antiapoptotic members of the Bcl-2 family (Bcl-2, Bcl-x_L) [58]. When overproduced, Nogo-B and RTN1-C could sequester Bcl-2 and Bcl-x_L from mitochondria to the ER, thus reducing their antiapoptotic effect [58]. Strikingly, Nogo-B was also claimed to be a potent pro-apoptotic protein, specifically in certain cancer cells, when ectopically overproduced [7]. Transient transfection of Nogo-B into carcinoma cell lines (CGL4, SaOS-2) induced apoptosis, and this activity depended on the second hydrophobic region of the common RTN C-terminus [7]. However, these data contrast with other results, which show that neither spontaneous survival nor the extent of apoptosis induced by the chemotherapeutic drugs staurosporine or tunicamycin were enhanced in Nogo-B-transfected carcinoma cells (SaOS-2) or CHO cells. This thus questions the interpretation of Nogo-B as a cancer-specific pro-apoptotic protein [19].

Concluding remarks

Research in the field of RTNs has increasingly moved beyond descriptive studies of their expression patterns and genomic structures towards functional enquiries. The role of Nogo in neurite-outgrowth inhibition is currently being studied extensively. By contrast, the roles of RTN1, RTN2 and RTN3 in vertebrates, the possible intracellular role of Nogo/RTN4, and the function of the RTN genes in invertebrates, plants and yeast are poorly understood, and represent an exciting subject for future studies. The main questions that remain to be addressed include the exact membrane topology of RTN proteins, the identification of the putative receptor(s) on neuronal and non-neuronal cells transducing the inhibitory activity of the Nogo-Aspecific region, the intracellular interaction partners of RTNs, and the physiological roles of RTN genes in vertebrate and non-vertebrate species. We are only starting to comprehend the cell biology of RTNs, but their broad taxonomic and tissue distributions are a promising sign for a mesmerizing journey.

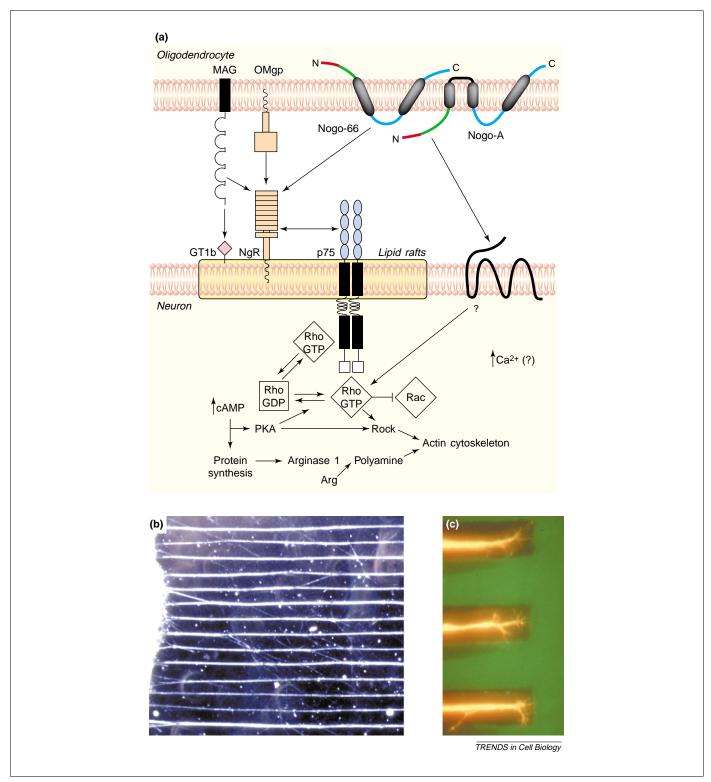


Fig. 3. Molecular basis of Nogo-A mediated neurite outgrowth inhibition. (a) Molecules that are currently known to be involved in the inhibition of neurite outgrowth by myelin-associated proteins. NgR is a common receptor subunit for Nogo-A via Nogo-66, MAG and OMgp, and is complexed with p75 as a probable signal-transduction unit. A concomitant activation of the small GTPase RhoA and inhibition of Rac, as well as an elevation of intracellular Ca²⁺, are thought to be the main downstream signals of Nogo and other inhibitory proteins. RhoA might be activated by the guanine-exchange factor (GEF) activity of the mastoparan-like domain present in p75. Experimental elevation of intracellular cAMP, which leads to protein-kinase A (PKA) activation, arginase-I upregulation and the synthesis of neurite-growth-promoting polyamines, as well as blockade of RhoA GTPase (with C3 exoenzyme) or of the Rho kinase Rock (e.g. with Y-27632), can together abolish Nogo-mediated neurite outgrowth inhibition. (b) Nogo-A mediated inhibition of chicken retinal ganglion cell axon growth on alternating stripes of laminin and laminin-Nogo-A. Notice the stripe-specific, strongly fasciculated outgrowth of ganglion cell neurites. Only a small proportion of neurites cross the Nogo-A-containing stripes. (c) Detail of an immunofluorescently labelled sample as shown in (b). Nogo-A substrate is shown in green, whereas axons are labelled in red with an anti-neurofilament antibody. The growth cones stop in the 'dead-end street' formed by the Nogo-A containing territory.

Acknowledgements

We thank O. Gilliéron and D. Merkler for providing unpublished data to complete Table 1, M. van der Haar for providing Fig. 2c, and A. Buss, D. Merkler, M. Kerschensteiner and S. DeMarco for critically reading the manuscript. We also thank E. Hochreutener and R. Schöb for excellent graphical work. Our own studies were supported by the Swiss National Science Foundation (grant 31-63633) and by the NCCR on Neural Plasticity and Repair.

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