

CHAPTER 1

Molecular Mechanisms of Axonal Growth

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Abstract

Outgrowth of axons during neuronal development, as well as their regeneration after injury, of the adult nervous system is controlled by specific extracellular cues which are diffusible, or bound to cell membranes or extracellular matrix. The exact molecular mechanisms through which these extracellular signals are integrated by the growing axon, are not yet well defined. However, it is widely accepted that most, if not all, signaling cascades triggered by guidance cues eventually converge onto the cytoskeleton. The action of extracellular guidance factors is thus modulated not only by specific membrane receptors, but also by cytoskeletal and cytoskeleton-associated molecules within the axon. In fact, the cytoskeleton represents a point of convergence and integration of both neuron-intrinsic and extrinsic factors. Moreover, in recent years, there has been increasing evidence for the involvement of a coordinated cross-talk between actin filaments and microtubules, the two main components of the growth cone cytoskeleton. Their reorganization is complex and involves numerous cytoskeleton-associated proteins whose function is regulated via activation or inhibition of particular signaling pathways.¹⁻⁴

Introduction

The growth cone, highly motile distal tip of the axon, shares many properties with other motile structures, such as the leading edge of migrating cells. This is reflected in a similar cytoskeletal organization of these subcellular compartments, and the use of common signaling pathways, such as the one involving Rho-GTPases (see below). Despite these similarities, the behavior of neurons appears more complex than that of other cell types, in that they extend very long processes, and exhibit quite “sophisticated” responses when confronted to extracellular cues. Expression of cytoskeleton-associated molecules specific for the neuronal growth cone may, at least in part, explain some unique features of this motile structure (for review refs. 5-8).

Here, we will describe in some detail the cytoskeletal network within the neuronal growth cone, and how its organization is regulated in response to extracellular factors by integration of signaling pathways.

The Neuronal Growth Cone and Its Cytoskeletal Organization

Neurites should be thought of as exceptionally differentiated cellular processes. The growth cone tipping an axon (or dendrite) is an extremely motile and dynamic structure that explores the environment. To guide an axon towards the appropriate target, the growth cone fulfills different functions: it acts as sensor of environmental cues, signal transducer, and motility device. Growth cone advance is mediated by the polymerization/depolymerization of cytoskeletal

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elements, and their specific interactions. The axonal cytoskeleton is composed of three main filamentous polymers: neurofilaments, microtubules and actin microfilaments. Within the growth cone, microtubules and actin filaments are actually the major cytoskeletal components, and have been the focus of most studies. Their spatial organization and relative position in the growth cone define different, functionally specific zones, described in Figure 1.

The Peripheral Domain

The peripheral domain (P-domain) is the most distal part of the growth cone, a highly dynamic, actin-rich structure. This domain bears lamellipodia, membranous flat veil-like protrusions, from which extend many filopodia. These very thin, finger-like structures contain mainly actin filament bundles, and undergo permanent elongation and retraction cycles as they organize their content in response to the environment.^{9,10} In the P-domain, equilibrium between actin polymerization and depolymerization (actin “treadmilling”) constantly generates protrusion forces, and retrograde flow of actin (see below).

The Transition Zone

The transition zone (T-zone) is situated at the interface between the actin-rich P-domain and the MT-rich central domain. The molecular motor myosin, concentrated in the T-zone, can serve to contract the actin network, thereby inducing the formation of an actin-filament arc.¹¹ Movements of this arc, in association with retrograde actin flow, limit the penetration of MTs into the P-domain.

The Central Domain

The central domain (C-domain) represents the main site of MT polymerization. Neurofilaments, which transport vesicles and organelles along with the MTs, are also present. The size of the C-domain varies in correlation to the growth mode of the axon: Relatively large when the growth cone is pausing, whereas the C-domain exhibits a thinner shape during fast advance mode.

Actin Filaments and Associated Proteins

Actin filaments (AFs) are helical polymers formed by addition of ATP-actin monomers. AFs are polarized structures characterized by a “pointed” and a “barbed” end. Dissociation of ADP-actin is favored at the pointed end, suggesting that polymerization occurs at the barbed end, and depolymerization at the pointed end.^{7,12}

Actin is present in both the P-domain and the T-zone, where it is organized in two different types of networks:^{10,13,14} filopodia are composed of thick actin bundles, while in lamellipodia, AFs are organized in a loose meshwork. Similarly, contraction of the actin meshwork in the T-zone by myosin action results in formation of a thick actin arc, oriented perpendicularly to the axon.¹¹

In the P-domain, AFs polymerize close to the distal membrane, and polymers are retrogradely transported to the T-zone by a myosin-dependent mechanism.¹⁵ Increased contractile forces in the T-zone then induce severing and depolymerization of AFs. This permanent actin treadmilling accounts for the high dynamics of the P-domain. Moreover, the retrograde actin flow generates a backward force suspected to limit MT invasion into the P-domain.

Dozens of actin-associated proteins have been described in the neuronal growth cone, and were classified according to their function (for review see ref. 16). There are two main groups regulating actin polymerization/ depolymerization:

Actin Nucleation/Polymerization

Actin nucleation/polymerization factors increasing the number of free barbed ends incidentally increase actin polymerization. The Arp2/3 complex, thus, not only favors de novo actin polymerization, but also by binding sideways to preexisting filaments, creating a new branch and hence a new barbed end (for review see ref. 17). Members of the formin protein family

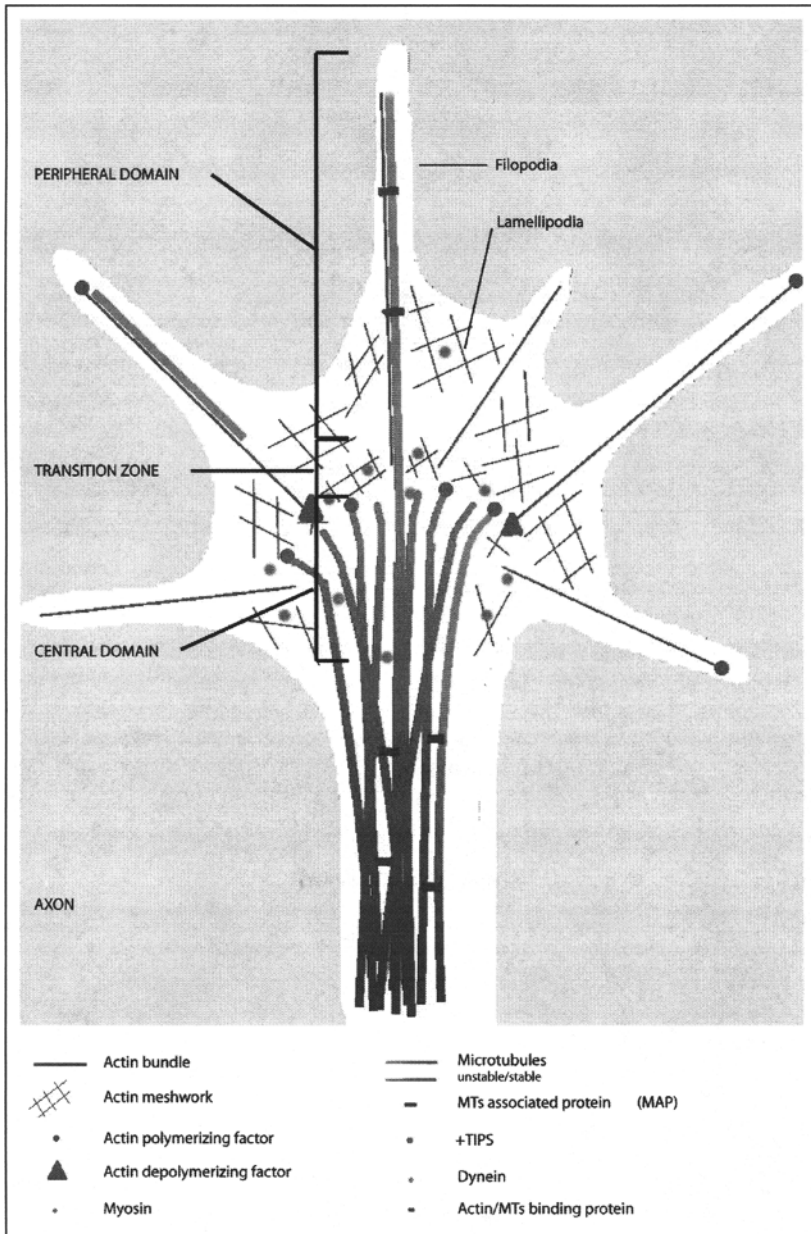


Figure 1. Cytoskeleton growth cone organization. The growth cone, tipping an axon, is divided in three different, functional zones. The C-domain is the polymerization site of MTs, which are thereafter stabilized in the axon shaft. The T-zone limits MTs penetration in the C-domain, and contains a high density actin meshwork associated with myosin. The P-domain is very dynamic and mainly contains actin, organized in bundles in filopodia, and meshwork in lamellipodia. Transient interactions between actin filaments and MTs are observed in the P-domain that are mediated by still unknown factors. MTs- and actin- associated proteins regulate their transport, polymerization and stabilization.

bind to the barbed end of elongating actin polymers, enhance filament elongation, and prevent binding of actin capping molecules (for review see ref. 18).

Actin Depolymerization/Severing

Actin depolymerizing factors (ADFs), as well as cofilins, are important regulators of actin dynamics in the growth cone. Although encoded by different genes, ADFs and cofilin have very similar effects, are regulated by reversible phosphorylation, and colocalize in the cells (for review see ref. 7). When phosphorylated, both bind to the rear end of actin filaments, generating actin fragments. Interestingly, actin severing leads to generation of new free barbed ends, thereby promoting actin polymerization, a mechanism perpetuating the retrograde actin flow (for review see refs. 7,19). Other proteins, such as gelsolin, stop actin polymerization by capping barbed ends, and thereby induce depolymerization (for review see ref. 20).

Thus, modulation of actin polymerization by extracellular guidance cues via actin-associated proteins provides a mechanism to regulate the progress of growth cones.

Microtubules and Associated Proteins

Microtubule protofilaments are formed by spontaneous association of α/β tubulin heterodimers. 13 such protofilaments finally associate to form a hollow microtubule of a diameter of 25 nm (for review see ref. 21). Regulation of expression of different α and β tubulin isoforms during axonal development and regeneration regulates MT stability.

The orientation of tubulin monomers makes MTs intrinsically polarized structures with a “plus” and a “minus” end. In the axon, plus ends are oriented distally toward the growth cone. Depolymerization mainly occurs at the minus end, while a constant cycle of polymerization/depolymerization takes place at the plus end.^{22,23}

The frequency of polymerization/depolymerization or “rescue/catastrophe” events, as well as the duration of pauses in between, characterizes the “dynamic instability” of microtubules. The term dynamic instability describes an intrinsic property of MTs that allows them to switch abruptly between phases of elongation and rapid shortening.²² MTs are organized in parallel bundles throughout the axon shaft, and splay out when they enter the growth cone C-domain.^{13,24} During pauses, MTs extend loops into the C-domain, and breakage of these loops upon regrowth results in highly dynamic, small polymers capable to enter the P-domain and associate with actin bundles. Indeed, while MTs were previously thought to be restricted to the C-domain, recent progress in imaging techniques has provided evidence for MT-actin interactions within the P-domain. This interaction is fundamental for outgrowth, guidance and branching of the axon.^{11,25-28} Local stabilization of MTs is also tightly regulated during these events^{29,30} by specific post-translational modifications on MTs, and by their interaction with specific associated proteins:

Post-Translational Modifications

Post-translational modifications of MTs include detyrosination/tyrosination, acetylation, phosphorylation, polyglutamylation and polyglycylation (for review see ref. 21). Unmodified tyrosinated tubulin polymers are enriched in the distal part of the axon, while modified detyrosinated or acetylated isoforms are found in the proximal part of the axon, on “older” and stable MTs.³¹ Although these modifications do not have a direct effect on MT stabilization,³² tubulin modifications are frequently used as markers of MT stability. They may, however, facilitate localization and interaction of microtubule binding proteins, such as plus end-tracking proteins (+TIPS³³) and Microtubule Associated Proteins (MAPs^{34,35}).

Proteins Associated to MTs

Proteins associated to MTs include two groups of proteins that interact with MTs and regulate their dynamic instability.

Structural MAPs such as MAP1A, MAP1B, MAP2, and Tau, bind, bundle, and stabilize MTs. Their association with MTs is regulated by post-translational modifications of tubulin, as

well as their own post-translational modification, such as phosphorylation (for review see ref. 36). MAPs are particularly abundant in the nervous system, and their subcellular localization is strictly regulated. Some MAPs are preferentially associated with neuronal processes: MAP2 is concentrated in dendrites, while tau and MAP1B are mainly found in axons (for review see refs. 37,38). As a consequence, the spatial distribution of MAPs defines subcellular zones, in which MTs are more or less stabilized. MAPs are generally important both during development and in the adult nervous system. Maturation of the nervous system is accompanied by a transition from MAPs typically expressed during the phase of axon growth, to other MAPs characteristic of mature neurons.^{39,40} Certain MAPs, such as MAP1B and tau, are present in the growth cone, and were shown to play an important role in neurite outgrowth from embryonic neurons *in vivo* and *in vitro*.⁴¹⁻⁴⁴

Other MAPs, identified more recently,^{46,47} act as potent MT destabilizers. Among these are stathmin and SCG10, members of the same gene family, which are expressed in neurons and promote MT depolymerization by increasing the rate of catastrophes (for review see ref. 48). SCG10 and stathmin are considered as growth-associated proteins, and their expression correlates with neurite outgrowth.

Although the dynamic state of MTs has been shown to be important for neurite elongation and growth cone turning, it is still not clear how MT dynamics are regulated. In fact, MTs are known to be particularly labile within the growth cone,^{31,49} despite the rather high concentration of MT-stabilizing MAPs, such as MAP1B and tau. Therefore, it has been proposed that the potent MT destabilizer, such as SCG10, might counteract the activity of stabilizing MAPs, contributing to the regulation of MT dynamics.^{46,48}

Recently, a novel type of MT binding proteins called +TIPs has been identified as being specifically associated with the distal ends of growing MTs. These proteins have gained considerable interest with respect to the regulation of MT dynamics and the intracellular transport via MTs (for ref and review, see refs. 50,51), and also due to their anchorage to actin filaments and adhesion sites. A few of them have been detected in neurons, namely, cytoplasmic linker protein-170 (CLIP-170), CLIP-115, end-binding protein 1 (EB1) and EB3. Functions of these proteins in growth cone MTs remains to be determined.

Intermediate Filaments

Neurofilaments (NFs) are the major intermediate filaments in neurons. The NF network is composed of a NF-L (low molecular weight NF, 70 kD) core, associated to NF-M (medium molecular weight NF, 150 kD) and NF-H (high molecular weight NF, 200 kD) chains.⁵³ The function of NFs in transport of vesicles, membrane material and organelles has been extensively studied (for review see ref. 54). In contrast, even if NFs are found in the C-domain of the growth cone, they do not seem to interact with axonal growth and pathfinding. Thus, transgenic mice lacking axonal NFs are perfectly viable, and do not present any major defect in their neural connections.⁵⁵

Molecular Motors

These molecules present a molecular motor domain capable of generating forces on cytoskeletal polymers by means of ATP hydrolysis. They serve in transporting vesicles back and forth along the axon shaft, and in addition, can generate forces on the cytoskeleton by moving polymers relatively to each other.⁵⁶ Kinesin and dynein proteins are microtubule-dependent motors and the polarized structure of MTs induces specificity in the direction of motor molecules. Most kinesins move towards the plus end of MTs, whereas dynein complex moves towards the minus end (for review see ref. 57). Myosin proteins are actin-dependant motors and rather move to the plus end of actin filaments.⁵⁸

The diverse cytoskeletal proteins expressed in the growth cone act in concert to mediate axonal growth and pathfinding. They are regulated by extracellular cues, but also by the axon-intrinsic program. Thus, throughout development and regeneration, the expression of particular components, and their transport and final localization in the axon are tightly regulated.

The subsequent assembly of components and their interactions in the growth cone eventually modulates axonal outgrowth and pathfinding.

Mechanisms of Axonal Elongation

Synthesis of Cytoskeletal Proteins

The bulk of new cytoskeletal proteins is produced in the cell body. Recently, however, there is increasing evidence for a local synthesis in growing and regenerating axons, at least in small amounts (estimated at 5%⁵⁹), which can play a crucial functional role. Thus, it has been demonstrated that ribosomal proteins, translational initiation factors, and ribosome-bound mRNA are present in axons. Moreover, protein synthesis occurs even when processes are separated from their cell bodies.^{60,61} The rapidly growing list of identified intra-axonally synthesized proteins includes cytoskeletal proteins (intermediate filaments as well as actin and tubulin), heat shock proteins, endoplasmic reticulum proteins, metabolic proteins, anti-oxidant proteins, and proteins associated with neurodegenerative diseases (see ref. 62). When communication between processes and the cell body is interrupted by axotomy or colchicine treatment, blocking local protein synthesis in regenerating axons results in rapid retraction of growth cones, indicating a physiological importance for local synthesis during axonal regeneration⁶⁰ as well as during development⁶³ to respond to guidance factors.

Cytoskeletal Protein Transport

After their synthesis, cytoskeletal proteins have then to be transported to the site of axonal growth. The first studies on axonal transport were performed in the adult during axonal regeneration, and used radio labeled-methionine for tracing of newly synthesized proteins. They showed a correlation between the rate of axonal regeneration, and the rate of the slow axonal component (SC⁶⁴). Tubulin and actin are transported in two peaks, differing in their velocity and content. In mammals, the slower peak, SCb, is mostly composed of tubulin, while actin moves faster in association with the SCa peak (reviewed in ref. 65).

The polymerization status of actin and tubulin during their transport, as well as the exact mechanism of their transport are still unclear and have been much debated in recent years. Novel methods using fluorescent proteins and time lapse imaging may now yield new insight into this problem.⁶⁶ Two models have been proposed: The classical "cargo" model assumes that tubulin and neurofilament polymer transport uses the classical motor molecules. The "sliding filament" model^{67,68} suggests that short tubulin polymers can be moved anterogradely on longer MTs by dynein. NF transport was suspected to be linked to this MT transport with the NF "piggy backed" on MTs, but recent evidences suggest that it may rather rely on the classical cargo model.^{67,68}

Less is known about anterograde transport of actin. Myosin seems to be the motor for at least a subpopulation of para-axially aligned actin filaments.⁶⁸

Axonal Elongation

During axonal elongation, 3 phases can be distinguished (reviewed in refs. 16,69): In the initial protrusion phase, lamellipodia and filopodia extend from the tip of the axon, forming the growth cone. This phase is mainly governed by actin dynamics, which in turn, are regulated by Rho family GTPases, but is also modulated by MTs dynamics.⁷⁰ The engorgement phase that follows protrusion, consists in the invasion of MTs and organelles into the growth cone. It depends on the dynamic instability of MTs, since inhibition of these dynamics leads to a reduction in axonal growth.^{27,71,72} During the final consolidation phase, the formation of actin protrusion stops, and MTs become bundled. This phase probably relies on the activity and interaction of microtubule- and actin-associated proteins, although it is still not well elucidated.

Axonal elongation is modulated by extracellular factors that the growth cone senses in the environment. Extracellular guidance cues elicit diverse intracellular signaling cascades. Here

we will particularly focus on the signaling mediated by Rho-GTPases, as the consequences of their activation on reorganization of the cytoskeleton has been well characterized.

Regulation of the Cytoskeleton by Extracellular Cues, Role of Rho-GTPases

Regulation of Rho-GTPases

Rho-GTPases act as “molecular switches” by oscillating between an active, GTP-bound and an inactive, GDP-bound state. The three best-characterized members of this family are Rho, Rac and Cdc42. Their regulatory function on the actin cytoskeleton during axon outgrowth and guidance has been extensively demonstrated (for review see refs. 73-75). Rho, Rac and Cdc42 are generally considered to regulate formation of stress fibers (actin- and myosin-rich structures), lamellipodia, and filopodia, respectively.

The activity of Rho-GTPases is itself modulated by three families of factors. GAPs (GTPases activating proteins) facilitate hydrolysis of GTP by GTPases, and hence favor the inactive, GDP-binding state of Rho-GTPases.⁷⁶ GEFs (guanine nucleotide exchange factors) activate GTPases by facilitating GDP/GTP exchange.⁷⁷ Finally, GDIs (guanine nucleotide dissociation inhibitors) inhibit GDP dissociation and maintain GTPases in an inactive state. GEFs/GDIs/GAPs can be either specific for a given GTPase, or act simultaneously on several molecules.

In addition, Rho-GTPase activity can also be modulated by second messenger cyclic nucleotides. Indeed, cAMP-dependent protein kinase A (PKA) reduces Rho-GEF activity,⁷⁸ while activating Rho-GDIs.⁷⁹ RhoA is also directly inhibited upon phosphorylation by PKA.^{80,81} In addition to its action on Rho-GTPases, PKA can directly act on their downstream targets, including cytoskeletal components (see chapter by Piper et al.).

Binding of permissive or inhibitory factors to their neuronal receptors induces different signaling cascades, which in turn leads to activation/inactivation of Rho-GTPases. Since Rho, Rac and Cdc42 may also interact and thereby modulate themselves, it seems that the balance between the activities of different GTPases, rather than activation of a single group, will control the axonal response.

After binding to their membrane receptors, repulsive guidance cues activate Rho, while inhibiting Cdc42 and Rac activity by acting on GTPase modulators (see Fig. 2). For example ephrines, via Src kinase and RasGAP, inhibit p190RhoGAP.^{82,83} In parallel, the RhoGEF ephexin is activated,⁸⁴ which leads to RhoA activation.

Semaphorins activate Rho and inhibit Rac via a slightly different mechanism. The semaphorin receptors Plexins are able to directly bind Rac and Rho. This binding then activates Rho, while it sequesters Rac and inhibits its interaction with its downstream effector Pak.⁸⁵

In contrast, outgrowth- and regeneration-permissive factors activate Cdc42 and Rac, while inhibiting Rho. Neurotrophins for example, besides their trophic effect mediating gene transcription in the cell body, activate GEFs via a PI3-K signaling pathway,^{86,87} and thereby Cdc42. Binding of the neurotrophin receptor p75 to RhoA inactivates this Rho-GTPase, and further contributes to the attractive effect of neurotrophins.⁸⁸ Moreover, it has recently been demonstrated that RhoA-kinase and myosin-II are required for the maintenance of growth cone polarity and guidance mediated by nerve growth factor,⁸⁹ suggesting that localized activation of different RhoGTPases is necessary for axonal pathfinding.

Effect of Rho-GTPases on the Cytoskeleton

Activation of Rho-GTPases leads to an important cytoskeletal remodeling. Their effects converge on three main systems: actin polymerization/depolymerization, actin/myosin contractility, and microtubule reorganization, as represented in Figure 2.

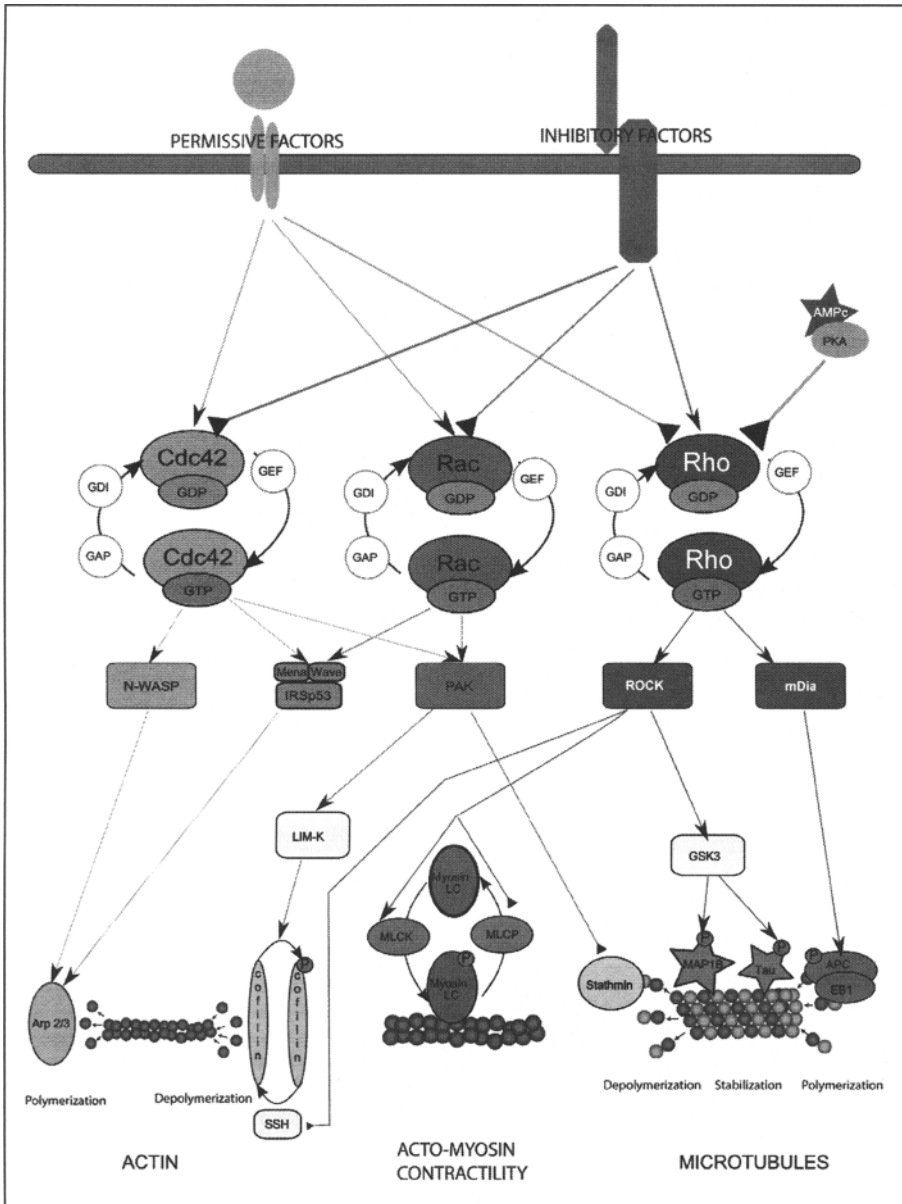


Figure 2. Rho GTPases signalling to the cytoskeleton. Rho-GTPases are controlled via their associated partners by extracellular cues. Specific effectors mediate actions of Rho-GTPases on the cytoskeleton. They focus on three main effects: actin polymerization/depolymerization, regulation of actomyosin contractility, and microtubules polymerization/depolymerization/stabilization.

Regulation of Actin Polymerization

Upon Cdc42 activation, N-WASP (N-Wiskott-Aldrich related protein), activates the Arp2/3 factor.⁹⁰ Arp2/3 stimulates de novo actin polymerization (for review see ref. 91). This factor is also activated by Rac effectors IRSp53 and WASP related protein SCAR/WAVE.⁹²

Conversely, actin depolymerization is induced by cofilin/ADF (Actin Depolymerizing Factor). Cofilin is activated by phosphatase SSH (slingshot), and inhibited by LIM kinase.⁹³ Rac and Cdc42 activate LIM-K,⁹⁴ while Rho and its downstream effector ROCK (Rho-associated kinase) activate SSH, and as a consequence, promote actin depolymerization.⁹⁵

Regulation of Acto-Myosin Contractility

Rho activation of ROCK increases myosin contractility by two converging pathways. ROCK activation induces phosphorylation of myosin light chain 2 (MLC2) by activating myosin light chain kinase, while at the same time inhibiting myosin light chain phosphatase.^{96,97} An increase in MLC phosphorylation and myosin activity then leads to contraction of the actin network.

Regulation of Microtubules

Rho-GTPases have been extensively described as actin modulators, but a growing number of studies also suggest a function in regulation of MT dynamics. In particular, it has been described that after Rho activation, the formin mDia not only favors actin nucleation,⁹⁸ but also stabilizes MTs via TIPS proteins EB1 and APC.⁹⁹ Rac1 activity has a MT stabilizing effect, since the Rac effector PAK inhibits the MT-severing protein Stathmin/Op18.^{100,101} These pathways have mainly been characterized in nonneuronal cells, but we assume that the same or similar mechanisms should also regulate neuronal cell motility. In neuronal cell lines, the Rho/ROCK pathway has been shown to induce hyperphosphorylation of two major MAPs, tau and MAP1B, by GSK3 β ,¹⁰² thereby destabilizing MTs. Interestingly, Rho-GTPase activity is inversely regulated by MT polymerization/depolymerization in nonneuronal cells: MT depolymerization leads to release of a RhoA activating GEF,¹⁰³ whereas their polymerization activates Rac1 by a still unknown mechanism.¹⁰⁴

This "retrograde signaling" from MTs to Rho-GTPases could be one way of coregulating MTs and actin dynamics during motile events. Indeed, a strict coordination of actin and MT systems is required for proper growth cone advance, turning and branching.^{13,25,29,105,106} Besides those based on regulatory interactions involving Rho-GTPases, several hypotheses have been put forward for a model of coupling between actin and MTs (for review see refs. 2,8,107). Structural interactions mediated by MT- and actin-binding proteins or protein complexes might physically couple actin and MT movements (for review and see refs. 8,45). For example, in addition to their interaction with MTs, some MAPs directly or indirectly interact with actin filaments. Another hypothesis proposes that actin and MT movements are controlled by the equilibrium between forces generated by molecular motors on the 2 types of filaments. According to this hypothesis, a balance between backward forces generated by myosin and forward forces generated by dynein or kinesins should control advance or retraction of the axon.⁵⁶

In summary, during axonal outgrowth, extracellular signals converge on the reorganization of cytoskeletal proteins, particularly actin filaments and microtubules, and thereby control the advance of the growth cone. On the other hand, specific expression and intrinsic modification of cytoskeletal proteins also modulates the neuronal response to extrinsic factors, allowing for diversity in the response to a specific guidance cue, and underlying the role of the cytoskeleton as a convergence point during axonal outgrowth.

During the past two decades, a huge amount of data has been acquired detailing the molecular mechanisms of axon outgrowth and guidance. Today, it seems possible to exploit these data also in view of a better understanding of phenomena related to axonal plasticity in adult nervous system. Thus, especially our growing knowledge of how exactly extracellular cues and intracellular pathways ultimately converge on the axonal cytoskeleton, is of particular interest for studies of axonal regeneration in the adult following a traumatic lesion.

Growth Cone of Regenerating Axons

In the adult nervous system, particularly of mammals, understanding why certain types of neurons regenerate their axons while others do not, may provide clues to establish a therapy for each type of lesion, be it traumatic, degenerative, or linked to developmental (genetic) anomalies.

In order to regenerate, adult neurons should have the intrinsic capacity to survive a traumatic or degenerative lesion, and to activate a cell-autonomous program that will end in plastic changes in their network. At the same time, this program is influenced by interactions between neurons and neighboring cells (glia in particular), mediated by cell- and substratum- adhesion molecules and their receptors, and by a variety of secreted factors into the extra-cellular space. A number of key players in these regenerative processes have already been identified. However, the relationship between individual molecular events, especially the triggering of gene expression and the corresponding cascade of signaling pathways, are still poorly understood. Here we summarize some relevant findings from studies that were undertaken to understand how the axonal cytoskeleton is reorganized in response to a lesion, particularly in response to axotomy.

Initiation of Axonal Regeneration after Axotomy

The regeneration of an amputated axon involves the transformation of a stable axonal segment, i.e., a stable structure specialized in propagating action potentials, into a highly motile and complex tip, a new growth cone, that will sense the surrounding environment and guide regenerating neurites to their targets. This is a critical step in the process of recovery from neural injury. Most of the studies on the initiation of the regeneration of damaged axon were done on *Aplysia* neurons^{108,109} where it has been shown that cytoskeleton reorganization promotes a growth cone formation, allowing elongation of a new axon.

Gene Expression Recapitulates Developmental Program during Axonal Regeneration

In response to injury, such as axotomy, adult neurons shutdown their specific differentiated functions and activate growth program through local intracellular signaling cascade. Coordinated sequence of gene expression is induced for synthesis and transport of proteins that maintain axonal plasticity, growth cones are formed and ultimately functional synaptic contacts are restored. In vertebrates, these events occur only in the peripheral nervous system (PNS). In contrast, most lesions in the central nervous system (CNS) result in abortive regeneration associated with decrease in protein synthesis and may ultimately induce atrophy or death. The coordination of gene expression pattern after axonal injury is complex and is determined by both intrinsic factors to neurons as well as environment factors.

Cytoskeleton Synthesis in Injury-Induced Axonal Plasticity

The contribution of cytoskeleton proteins to the axonal regeneration process is crucial. Although several studies on neuronal cytoskeleton were undertaken during the development, its regulation during axonal regeneration remains poorly understood. Nevertheless, cytoskeleton proteins in regenerating axon undergo quantitative and qualitative changes in synthesis, organization and protein transport, similar to that of growing axon during development.¹¹⁰

In vertebrates, the recapitulation of the developmental cytoskeleton-protein expression has been mainly demonstrated in the peripheral sensory neurons of the dorsal root ganglia (DRG) and motor neurons (MN, in the CNS). These neurons are able to regenerate after peripheral injury.

MN or DRG axotomy is followed by an increase in levels of specific tubulin isoforms, as well as beta actin and peripherin, while levels of neurofilaments (NF), known to regulate the axon caliber¹¹¹ decrease. The down regulation of NF gene expression was suggested to facilitate supplying structural elements toward the distal end of the regenerating axon, resulting in a selective acceleration in the transport rate of tubulin and actin (for review see ref. 112).

It is important to note that although the capacity of axonal regeneration is attributed to PNS neurons, it is now well accepted that, in response to CNS injury, there are some neuronal populations able to initiate an axonal growth program to regenerate. This has been observed during the first days after axotomy of rubrospinal neurons, where the amounts of GAP43 and cytoskeleton proteins such as actin and tubulin increase. Sustained only in few neurons, a decrease in these proteins occurs thereafter, associated with neuronal atrophy.¹¹³ This study demonstrated that for some CNS neurons, the failure to regenerate after axotomy is not due to the failure to initiate gene-expression changes, but mainly to due to the environment. Depending on extracellular cues, the signals converge in growth cone on cytoskeleton protein reorganization to promote axonal regeneration (PNS) or to impede regeneration (CNS).

Following a traumatic lesion, several inhibitory guidance cues are expressed in the CNS and are partly responsible for the poor regenerative response of axotomized neurons. Besides the inhibitory effect of these molecules, loss of regenerative capacities in the adult nervous system is thought to coincide with myelination. Indeed, several inhibitors of regeneration have been described on the myelinating cells surface, and, in the adult, contribute to the failure of regeneration in the CNS (for review see ref. 114). Furthermore, the effect of these molecules, as well as other extracellular factors, on axonal regeneration is modulated by the intrinsic neuronal state.

How Intrinsic Neuronal Properties Control the Success of Regeneration?

cAMP

The best characterized example of intrinsic neuronal state controlling axonal regeneration comes from demonstration that elevating intracellular cAMP concentration of adult neurons to reach that of young neurons allow them to regenerate on a central myelin substrate.¹¹⁵⁻¹¹⁷

Binding of myelin inhibitors to their receptors induces, repulsive guidance cues during development, an elevation of Rho activity via a RhoGDI.^{118,119} The exact mechanisms by which myelin inhibitors inhibit axonal regeneration are still unclear, but probably involve, as during the development, an actin depolymerization/contraction and a MTs destabilization. The precise effect of cAMP in overcoming myelin inhibition is not known. However, for a short phase, PKA action on Rho-GTPases may explain a part of the mechanism (see above). A second, transcription-dependant phase is induced by CREB activation. The multiple targets of this transcription factor are unknown, but one can reasonably consider that it may include cytoskeleton proteins. Moreover, it has been demonstrated that CREB activation leads to polyamines synthesis, which are known to modulate the cytoskeleton.^{121,122}

Cytoskeleton Associated Protein, GAP43/CAP32

One of the first and best studied example of a cytoskeletal regeneration-associated protein is GAP43, a phosphoprotein associated with growth cones, whose expression is also induced in adult regenerating axons (for review see ref. 123). GAP43 is one of the final targets of calcium signals. GAP43 is an actin capping protein that blocks microfilament elongation and appears to be an important regulator of growth cone motility during development. Phosphorylation of GAP43 by the protein kinase C (PKC) affects its interaction with actin filament and might therefore trigger actin polymerization and hence regulating axonal outgrowth (for review see ref. 135). Furthermore, it plays a significant role in regeneration, together with CAP23, a functionally related protein that is also upregulated by injury (ref. 124 and references therein).

Cytoskeleton Associated Protein, MAP1B

Several studies strongly suggest an axon growth-related function of MAP1B that is regulated by phosphorylation (for review see ref. 38). Although generally down-regulated in the adult, MAP1B is constitutively highly expressed in adult DRG and MN. After sciatic nerve lesion, the phosphorylated forms of MAP1B (MAP1B-P) is enriched in the more distal portion of the axon and is associated with peripheral regeneration of these neurons.^{125,126} In adult CNS, axonal MAP1B-P remains detectable in areas that retain axonal plasticity,^{127,128} and can also be reinduced

in injury-induced axonal reorganization.^{129,130} Adult DRG from MAP1B null allele mutant mice¹³¹ are able to regenerate their axons but exhibit two main abnormalities: (1) the number of terminal and collateral branching is significantly increased and (2) the turning capacity of growth cones, i.e., "choice" of a proper orientation, is impaired.⁴⁵ In developing neurons, both growth cone turning¹⁰⁶ and axonal branch formation²⁵ are known to involve local cross-talk between actin and MTs. MAP1B capacity to bind both actin filaments and microtubules¹³²⁻¹³⁴ suggests that MAP1B is involved in the locally coordinated assembly of cytoskeleton components required for branching and straight directional axon growth.⁴⁵ The developmental role of cytoskeleton-associated proteins in the organization of the cross-talk between MTs and actin-filaments⁸ appears thus to be maintained during axonal regeneration in the adult.

In conclusion, it seems evident that most, if not all signaling cascades triggered by extracellular stimuli converge onto the cytoskeleton. The subsequent reorganization of actin-filaments and microtubules is a complex phenomenon, and involves numerous cytoskeleton-associated proteins, whose function is fine-tuned via activation or inhibition of particular signaling pathways. Specific expression of some of these cytoskeleton-associated proteins in the neuronal growth cone may, at least in part, explain some unique features of this motile structure. Further studies, such as the one examining the coordinated cross-talk between actin filaments and microtubules during axonal branching and growth cone guidance to the appropriate target, will help determine the precise molecular mechanisms of axonal growth.

In contrast to neural development, the pathways involved in triggering cytoskeletal reorganization during regeneration are less well known, and this field of research is attracting great interest. Indeed, the ability of regenerating axons to respond to extracellular signals present in their environment depends on both the intrinsic neuronal state, and the presence (or absence) of specific cytoskeleton-associated proteins. It may be particularly interesting to determine a potential central convergence point of inhibitory extrinsic signaling. Modulating the intrinsic state of the neuron, and the response of the cytoskeleton to environmental factors, may provide clues for search of therapeutic targets to promote axonal regeneration after injury.

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