

# The secret life of ion channels: Kv1.3 potassium channels and proliferation

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## Abbreviations:

4-aminopyridine (**4-AP**); Antigen presenting cells (**APCs**); Calcium Release-Activated Ca<sup>2+</sup> channels (**CRAC**); Central memory T-cell (**T<sub>CM</sub>**); Effector memory T-cell (**T<sub>EM</sub>**); Extracellular matrix (**ECM**); Intermediate conductance calcium activated K<sup>+</sup> channels (**KCa3.1 channels**); Inwardly rectifier K<sup>+</sup> currents (**K<sub>IR</sub>**); Lipopolysaccharide (**LPS**); Membrane potential (**V<sub>M</sub>**); outwardly delayed rectifier K<sup>+</sup> currents (**K<sub>DR</sub>**); Oligodendrocyte progenitor cells (**OPCs**); phenotypic modulation (**PM**); Tyrosine kinases (**TK**); Vascular smooth muscle cells (**VSMCs**); Voltage-dependent potassium channels (**Kv channels**).

## Abstract

Kv1.3 channels are involved in the switch to proliferation of normally quiescent cells, being implicated in the control of cell cycle in many different cell types and in many different ways. They modulate membrane potential controlling  $K^+$  fluxes, sense changes in potential and interact with many signaling molecules through their intracellular domains. From a mechanistic point of view, we can describe the role of Kv1.3 channels in proliferation with at least three different models. In the "membrane potential model", membrane hyperpolarization resulting from Kv1.3 activation provides the driving force for  $Ca^{2+}$  influx required to activate  $Ca^{2+}$ -dependent transcription. This model explains most of the data obtained from several cells from the immune system. In the "voltage sensor model" Kv1.3 channels serve mainly as sensors that transduce electrical signals into biochemical cascades, independently of their effect on membrane potential. Kv1.3-dependent proliferation of vascular smooth muscle cells (VSMCs) could fit this model. Finally, in the "channelosome balance model", the master switch determining proliferation may be related to the control of the Kv1.3 to Kv1.5 ratio, as described in glial cells and also in VSMCs. Since the three mechanisms cannot function independently, these models are obviously not exclusive. Nevertheless, they could be exploited differentially in different cells and tissues. This large functional flexibility of Kv1.3 channels surely gives a new perspective on their functions beyond their elementary role as ion channels, although a conclusive picture of the mechanisms involved in Kv1.3 signaling to proliferation is yet to be reached.

## Introduction

The early studies linking K<sup>+</sup> channels to cell proliferation were carried on T lymphocytes in the early 80's (49). Since then, K<sup>+</sup> channels have been identified as important contributors to cell proliferation both in normal and cancerous cells (158, 170). K<sup>+</sup> channels are important for setting the resting membrane potential (V<sub>M</sub>) and the driving force for Ca<sup>2+</sup> influx, and both mechanisms contribute in many different ways to cell cycle progression (118). In addition, both are decisive for volume regulation of growing cells (92). Finally, it is increasingly recognized that K<sup>+</sup> channels can control cell proliferation through other signaling mechanisms independent of ion fluxes (71, 80). Their functional flexibility together with their location at the plasma membrane makes them suitable for coordinating multiple signaling pathways, integrating intra and extracellular signals.

A wide variety of K<sup>+</sup> channels has been shown to contribute to the regulation of different cell cycle checkpoints in different cancer cells (90, 93, 118, 126). These data rely on the observation that genetic or pharmacological blockade of K<sup>+</sup> channels inhibit cancer cells growth. Although cancer and normal cells can share some mechanisms, the aberrant expression, modulation and/or localization of K<sup>+</sup> channels in cancer cells have been shown to alter the downstream signals that converge on the cell cycle machinery. In this review, we will focus on what is known regarding the mechanisms by which a voltage dependent K<sup>+</sup> channel, the Kv1.3, modulate cell proliferation under physiological or pathological conditions in non-cancerous cells.

Interestingly, in three tissues in which a role for Kv1.3 channels in proliferation has been determined, different mechanisms have been proposed. ***In the immune system***, and particularly in T-cells, many studies argue in favor of a mechanism of Kv1.3 influence on proliferation involving K<sup>+</sup> efflux and membrane hyperpolarization. By favoring Ca<sup>2+</sup> influx, this hyperpolarization promotes the activation of Ca<sup>2+</sup>-dependent transcriptional factors leading to proliferation. This mechanism could be defined as the ***“membrane potential model”***. In contrast, in ***glial cells of the nervous system***, proliferation signals conveyed by Kv1.3 channels are related to changes in the balance of expression of several Kv channels, most notably Kv1.5 and Kv1.3. This model could be designated as the ***“channelosome balance model”***. Finally, the available data in ***vascular smooth muscle*** share some of the characteristics of this balance model, although data from heterologous expression systems point to the importance of Kv1.3 channels as voltage sensors, since the effect of Kv1.3 on proliferation could be reproduced by non-conducting mutants (40). This illustrates the so called ***“voltage sensor model”***. Clearly, these mechanisms are not exclusive, but from a didactical point of view it could be useful to dissect them independently.

## An overview of Kv1.3 channels

Kv1.3 (KCNA3) is a voltage-gated K<sup>+</sup> channel belonging to the shaker related (Kv1, KCNA) subfamily. The existence of voltage-dependent potassium (Kv) channels was first reported in excitable cells, although they are almost ubiquitously expressed. In 1984, a delayed-rectifier Kv

channel showing similarities with their counterparts in nerve and muscle was described in human T-cells (50) and classified as the n-type channel, for its prevalence in “normal” human T-cells (51, 99). After the finding of the *Drosophila* mutant *Shaker*, the cloning of a family of K<sup>+</sup> channels from the *Shaker* locus (81, 125, 134, 142) provided the tools to identify Kv channels. Using low stringency hybridization protocols Kv1.3 channel was isolated from mouse and rat brain (30, 64, 151, 152) in different laboratories and with different names. The adoption of a consensus nomenclature for Kv channels solved this confusion (28, 67).

### **Kv1.3 structure**

Kv channels are tetramers of pore-forming  $\alpha$  subunits, each one with six transmembrane helices (S1-S6) connected by intra- and extracellular loops (Figure 1A). The N- and C-terminal domains are intracellular regions of variable length. The basic structural elements have been confirmed from the crystal structure of their bacterial homologues KcsA and KaVP (52, 77, 102).

The transmembrane helices of each Kv $\alpha$  subunit contain two functionally and structurally independent domains: The K<sup>+</sup> selective pore (formed by S5 and S6 helices and their linker) and the voltage sensor domain (the S1-S4 transmembrane helices). The pore has a motif of five amino acids (TVGYG) forming the narrowest part of the channel (the selectivity filter) which is highly conserved among K<sup>+</sup> channels. The four pore domains arrange symmetrically around the conduction pathway, surrounded by the four voltage sensor domains. The S4 segment contains a positively charged amino acid every third position and accounts for most of voltage dependence of the channel gating. Membrane depolarization induces a structural rearrangement of S4 which translates into a displacement of the S4-S5 linker that opens or closes the conduction pathway (17, 77, 127).

The cytoplasmic domains participate in channel assembly and association with auxiliary subunits as well as in the regulation of inactivation and trafficking. Tetramerization of Kv $\alpha$  subunits is subfamily-specific and involves a highly conserved N-terminal domain (the T1 domain). Also, Kv $\alpha$  subunits can assemble with ancillary Kv $\beta$  subunits through this T1 domain, increasing functional heterogeneity (101, 143). More recently, a growing number of studies indicate that these cytoplasmic domains can have roles beyond regulation of K<sup>+</sup> fluxes, participating in cell signaling via protein-protein interactions (8, 95). The large divergence in the sequence of these regions within the same family suits with the subunit-specific nature of these interactions.

### **Kv1.3 biophysics**

Members of the Kv can be identified based on their specific biophysical and pharmacological properties. These properties are better characterized in isolation, by using heterologous expression systems. The correlation of these parameters with native currents may be poor due to the presence of a mixture of homo- and heterotetrameric channels, to their association with accessory subunits and to post-translational modifications (reviewed in 36). In the case of Kv1.3 channels the biophysical properties of the heterologously expressed channels are very similar

to the endogenous Kv1.3 currents observed in T-cells, as Kv1.3 is the only Kv subunit expressed.

Kv1.3 activation and inactivation is voltage-dependent. Activation threshold occurs at potentials between -60 and -50 mV. Open probability has a very steep voltage-dependence, with a midpoint around -40 mV (reviewed in 106). The voltage-dependence of inactivation is also very steep, with a midpoint around -45 mV for heterologous channels and between -60 and -70 mV for native T-cell currents, due to the modulatory effect of accessory Kv $\beta$ 2 subunits (1, 109). These biophysical properties determine a small range of voltages at which there is a finite probability that Kv1.3 channels are open and not inactivated (i.e. the window current region). In T-cells, this region overlaps with resting  $V_M$ , allowing its effective control by Kv1.3 currents (86, 120).

Kv1.3 activation time course is fast (a few milliseconds) whereas the inactivation time constant is much larger, ~200 ms at +50 mV (122). Kv1.3 channels inactivate with the slow C-type inactivation, caused by the rearrangement of the outer mouth of the permeation pathway (38, 76, 103, 138). C-type inactivation is sensitive to extracellular medium composition: it is slowed by elevated extracellular  $K^+$ , and, in the case of Kv1.3, is also slowed at acidic  $pH_e$  (98, 147). These changes are profound, and Kv1.3 channels require a considerable time to reopen again, exhibiting a remarkable cumulative inactivation (100, 123, 138). Many of these biophysical and kinetic properties are relevant for the modulation of firing patterns in excitable cells. However, their possible role shaping membrane potential in non excitable cells remains to be elucidated. In any case, it is clear that due to these distinct properties, replacement of Kv1.3 channels for other Kv1 channels will impact resting  $V_M$  also in non excitable cells (see below).

### **Kv1.3 pharmacology**

Molecules inhibiting Kv1.3 channel fall into two structural categories: venom-derived peptides, and organic small molecules. They can affect Kv1.3 currents by blocking the ion-conducting pore from the external or internal side or by modulating channel gating through binding to the voltage-sensor domain or auxiliary subunits. The number of selective and specific Kv1.3 blockers is continually growing, due to their relevance in T-cell physiology.

Initially, Kv1.3 blockers were viewed as general immunosuppressants assuming that they inhibited calcium influx in all T-cell subsets. They were proposed as alternatives to cyclosporine and FK506 for prevention of transplant rejection. However, the discovery of a prominent role for Kv1.3 channels in a T-cell subset (called effector memory T-cell or  $T_{EM}$ ) involved in the pathogenesis of autoimmune diseases (171) changed the concept and the strategy. Now Kv1.3 blockers are regarded as immunomodulators that can selectively suppress human  $T_{EM}$  (173).

Many peptides obtained from scorpion venom such as charybdotoxin, margatoxin, kaliotoxin, agitoxin-2 and noxiustoxin can block Kv1.3 channels. They are peptides of 18-60 residues cross-linked by 2-4 disulfide bridges, forming molecules remarkably resistant to denaturation. Recently, another very potent Kv1.3 blocker, ShK, was isolated from the Sea anemone

*Stichodactyla helianthus* (27). Extensive work has focused on the development of more stable and specific Shk analogues for the treatment of autoimmune diseases (13, 29, 130, 156). These peptides bind tightly into the external vestibule of the channels with 1:1 toxin-channel stoichiometry, occluding the permeation pathway (review in 107, 151). Altogether, they constitute a large pharmacological armamentarium to target Kv channels with high potency and specificity (173).

The first small molecules that were used to pharmacologically identify K<sup>+</sup> channels were the classic Kv channel inhibitors 4-aminopyridine (4-AP) and TEA, and the Ca<sup>2+</sup> activated K<sup>+</sup> channel blocker quinine (173). They are organic cations that block open K<sup>+</sup> channels by binding to the inner pore from the cytoplasmic side. After Kv1.3 cloning, a high-throughput screening of library compounds was used to search for more potent and selective small molecule blockers with little success. Meanwhile, in the early 90's several reports suggested that extracts of *Ruta graveolens* alleviated multiple sclerosis symptoms, an effect related with their blocking effect on K<sup>+</sup> channels (21). 5-methoxypsoralen (5-MOP), a compound used for psoriasis treatment, was identified as the major K<sup>+</sup> channel channel-blocking principle of *R. graveolens*. Derivatives without photoreactivity, and with higher potency and selectivity for Kv1.3 channels such as the phenoxyalkoxypsoralen-1 (PAP-1) were developed afterwards (141, 161).

### **Kv1.3 modulation**

Ion channels associate with protein adaptors, kinases, second messenger producing enzymes, membrane receptors and cytoskeletal proteins, forming the so called channelosome. This macromolecular complex enables the spatio-temporal organization of cellular responses and regulates the channel localization, activity and function, converting ion channels in master regulators of functions such as adhesion, migration, and proliferation. Several types of proteins have been described within the Kv1.3 channelosome (Figure 1B).

#### **Auxiliary subunits**

Although heterologous expression of Kv $\alpha$  subunit recapitulates voltage-dependent K<sup>+</sup> fluxes, it is now clear that native Kv channels are heteromultimeric complexes coassembled with accessory subunits. These auxiliary subunits have, in addition to their influence on Kv channel kinetics, important roles in Kv channel sorting and trafficking to distinct cellular localizations (135). Kv1.3 associates with Kv $\beta$  and KCNEs auxiliary subunits.

Kv $\beta$  are cytosolic proteins that bind to T1 cytoplasmic domains of Kv $\alpha$  subunits with a four-fold symmetry so that Kv channels are tightly associated 4 $\alpha$ :4 $\beta$  octamers (135). In human T-cells, Kv $\beta$ 2 subunits accelerate the assembly of Kv1.3 channels, enhancing current levels (109). In addition to Kv $\beta$ , KCNE peptides, which have been widely studied in association with Kv7 and Kv11 cardiac channels, also contribute to Kv1.3 regulation. KCNE4 behaves as a dominant-negative partner of Kv1.3 (65), leading to decreased current density, slower activation and accelerated inactivation(146). Moreover, by masking a surface targeting motif at the C-terminus of Kv1.3, KCNE4 subunits retain Kv1.3 in the ER (145, 146).

### **Associated receptors and scaffold proteins**

**Integrins** are a family of cell surface receptors that mediate cell-cell and cell-matrix interactions. They are heterodimers formed by noncovalent association of  $\alpha$  and  $\beta$  subunits, each formed by a large extracellular domain (> 1500 aa), a single transmembrane helix and a short cytoplasmic tail. Each integrin has a large repertoire of specific extracellular ligands and cell surface receptors, including ion channels (3, 11). Integrin receptors coordinate bidirectional signaling, regulating cellular functions such as cell growth and differentiation, cell activation, adhesion and migration. By linking ECM molecules to actin cytoskeleton, they control cell responses as a function of the extracellular environment (the “outside-to-in” signaling). Also, their binding to extracellular ligands is modulated by interactions with intracellular signals and proteins (“inside-to-out” signaling) (3, 61, 62).

Physical and functional association of integrin with Kv1.3 channels was first reported in T-cells.  $\beta 1$  integrin mediates T-cell adhesion and migration following activation of Kv1.3 with different stimuli (97). Kv1.3 opening by membrane depolarization activates integrin signaling, an example of the “inside to out” mechanism. A physical link between Kv1.3 channels and  $\beta 1$  integrins has also been found in melanoma cells (4). The “outside to in” signaling (integrin activation modulates ion channel) has been recently described for hERG channels (9). In fact, when associated with integrins, ion channels function becomes bidirectional as well. These reciprocal regulatory interactions can rely on subtle structural rearrangements (as voltage-dependent conformational changes), driving a change that mechanically propagates across the bilayer.  $K^+$  channels response to changes in transmembrane potential includes changes in the location and the coupling of cytoplasmic loops and helices. As there is a tight coupling between the lipid environment and the conformation of the protein, these changes can affect the conformation of other proteins in the same lipid raft. In these cases neither a stable physical association nor ion fluxes will be required for the coupling between the channel protein and the integrin receptor (3, 63).

**Cortactin** is a F-actin binding protein that upon phosphorylation-mediated activation promotes polymerization and rearrangement of the actin cytoskeleton. Cortactin is a cytoplasmic protein with an amino-terminal acidic region followed by 6.5 tandem repeats responsible for F-actin binding (58) and a carboxy-terminal proline-rich region with several phosphorylation sites and a SH3 domain (85). The N-terminus is critical for regulating branched actin assembly while the C-terminus allows cortactin to function as a scaffold. Many proteins bind to the SH3 domain and in this way can be bridged to the actin cytoskeleton (48, 55). Cortactin represents a good candidate to mediate cytoskeleton modulation of ion channels function, as it can bind and regulate ion channels, and in particular Kv channels (33, 68, 72, 169). In T-cells cortactin and Kv1.3 interaction takes place upon activation of the immune synapse (the specialized junction between the T-cell and the antigen presenting cell, APC). However, binding of Kv1.3 C-terminus with the SH3 domain has also been shown in HEK cells (68). These results suggest that actin dynamics regulates the membrane mobility of Kv1.3 channels, contributing to Kv1.3 localization.

**PDZ proteins.** Proteins containing PDZ domains anchor membrane receptor proteins to cytoskeletal components, holding together and organizing signaling complexes at the membrane. Interaction of Kv1 channels with adaptor PDZ-containing proteins of the MAGUK family was first reported in neurons (84). The PDZ domains enable protein-protein interaction with multiple partners, regulating the activity, the transport and clustering of the channels at the membrane and supporting the assembly of macromolecular complexes.

Kv1.3 channels associate with two different PDZ proteins: PSD95 (or Dlg4) and SAP97 (or Dlg1), through a PDZ-binding motif located at the C-terminus (107, 155). The interaction of SAP97 with Kv1.3 was first described in T-cells (69). SAP97 binds both Kv1.3, and the tyrosine kinase Lck, allowing the physical proximity between them that is required for Kv1.3 **current** downregulation by protein kinase A (91). PSD95 association with Kv1.3 can affect both channel location (promoting clustering of the channels at specific membrane domains) and channel activity through the PSD95 SH3-gk domain. In Jurkat cells both PSD95 and SAP97 interact directly with Kv1.3, but only PSD95 participates in Kv1.3 targeting (155). Altogether, it seems that while association with SAP97 regulates Kv1.3 channel phosphorylation, association with PSD95 determines mainly Kv1.3 location (91)

**Caveolins.** Caveolae are a type of lipid raft, defined by the presence of the cholesterol binding proteins caveolins. Caveolins are integral membrane proteins with cytoplasmic amino- and carboxy-terminal domains, which emerge as signaling platforms creating a cluster of lipids and proteins where effector proteins and their substrates interact. (70). Kv1.3 channels present a caveolin-binding domain (FQRQVWLLF) at the cytoplasmic N-terminal domain. Targeting of Kv1.3 to caveolar rafts reduces the channel's lateral mobility, increases Kv1.3 currents and enhances C-type inactivation (131) whilst disrupting the rafts inhibits channel activity (20). Interestingly, the presence Kv1.5 could impair Kv1.3 targeting to caveolae. In macrophages Kv1.3/Kv1.5 ratio changes in response to stimulation. This change regulates the targeting of the channels to microdomains enriched in signaling molecules and consequently their functional response (164, 166).

### **Post-translational modifications**

Covalent post-translational modifications such as glycosylation, palmitoylation or phosphorylation regulate ion channel functions, either directly or indirectly by modulating their interaction with adaptor proteins. Protein phosphorylation is the most common post-translational modification.

Regulation of Kv1.3 currents by phosphorylation was first described in the early 90's in T-cells by serine-threonine kinases (reviewed in (122)). Kv1.3 channels are also regulated by phosphorylation on tyrosine residues, through both receptor and non-receptor tyrosine kinases (TK). Tyrosine phosphorylation of Kv1.3 channels, after activation of either receptor TK (such as EGFR) or non-receptor TK such as Src, decreases Kv1.3 currents (75). Several aspects emphasize the complexity of this modulation: first, multiple tyrosine residues can be involved in the modulation of Kv1.3 (56). Second, Kv1.3 channel activity can be differentially modulated by



several TK receptors (45). Third, the effects of TK can be modulated by adaptor proteins within the Kv1.3 channelosome (47). These associations can change the channel responses and can also lead to a reciprocal modulation of TK expression and activity by the channel itself (46).

Kv1.3 channels are part of multiprotein signaling complexes whose functions go beyond anchoring the channel to the membrane. These complexes present some clear advantages, including the increased efficiency of the enzymatic reactions (as both the substrate and the effector have a restricted diffusion), the compartmentalization that may be essential for determining specificity in the signaling pathways and the increasing speed that can be necessary for the transmission of the signals that regulate some channels.

## **Kv1.3 channels and proliferation**

### **The immune system**

**T lymphocytes.** Long before the molecular nature of ion channels was unraveled, Kv1.3 currents were described and functionally characterized in T-cells (25). Also in this preparation a role of Kv1.3 channels in mitogenesis was proposed for the first time (49). Thus, it is not surprising that most of our knowledge regarding the kinetic and pharmacological properties of Kv1.3 channels, their molecular associations, their contribution to cellular homeostasis and their role in the pathways leading to activation and proliferation has been characterized in T lymphocytes.

The generation of an efficient immune response against an antigen requires clonal expansion of lymphocytes. Antigens are presented to T-cells by professional antigen presenting cells (APCs) such as B-cells, dendritic cells or macrophages. Interaction of the antigens with the T-cell receptor/CD3 complex (TCR/CD3) activates signaling cascades involving TK pathways. Some of these pathways such as the Ras/MAPK pathway can initiate the expression of genes required for T-cell proliferation through PLC activation and the production of IP3 and DAG. DAG activates PKC which phosphorylates and activates several transcription factors such as NFκB. Meanwhile, IP3 production evokes a biphasic increase in  $[Ca^{2+}]_i$  by releasing it from intracellular stores and by activating a sustained  $Ca^{2+}$  entry through “Calcium Release-Activated  $Ca^{2+}$  channels” (CRAC). CRAC channels activate in response to  $Ca^{2+}$  store depletion. In T-cells ORAI1 and STIM1 are the genes encoding this calcium entry pathway (26, 59, 129). The  $Ca^{2+}$  signal also contributes to the activation of the transcription factor NFAT (nuclear factor of activated T-cells), which binds to the promoter of the interleukin-2 (IL-2) gene. Upon IL-2 gene activation T-cells are committed to proliferate even in the absence of the antigen.

Kv1.3 channels and the intermediate conductance  $Ca^{2+}$ -activated  $K^+$  channels (KCa3.1 channels) are the main  $K^+$  conductances in T-cells. Their activation, either by membrane depolarization (Kv1.3) or by increases in intracellular  $Ca^{2+}$  (KCa3.1) leads to membrane hyperpolarization, increasing the driving force for  $Ca^{2+}$ . These two channels determine T-cells

resting  $V_M$ , thus regulating the magnitude of the  $Ca^{2+}$  signal required for gene transcription and cell proliferation.

Upon stimulation by APCs, naïve T ( $T_N$ ) cells upregulate the expression of KCa3.1. Following antigen clearance, >95% of the effector cells die while a small pool ultimately develops into long-lived memory T-cells. A single  $T_N$  cell can generate many subsets of memory T-cells with different functional properties and gene expression profiles. At least two clonally expanded populations emanate from this primary response, ones expressing C-C chemokine receptor 7 ( $CCR7^+$ ), that lack immediate killing activity, and  $CCR7^-$  cells that are capable of immediate cytotoxicity.  $CCR7^+$  cells are named central memory T-cells ( $T_{CM}$ ) because of their location in secondary lymphoid tissues, while  $CCR7^-$  cells were named effector memory ( $T_{EM}$ ) because of their rapid effector function *ex-vivo* (106). An important difference between them is the  $K^+$  channel expression pattern. Upon activation,  $T_N$  and  $T_{CM}$  cells upregulate the expression of KCa3.1, while  $T_{EM}$  upregulate the expression of Kv1.3 channels. Hence  $T_{EM}$  cells are highly dependent on Kv1.3 channels for  $Ca^{2+}$  signaling and cytokines production. In the presence of selective Kv1.3 blockers, they fail to migrate, proliferate and secrete cytokines. As  $T_{EM}$  cells participate in the pathogenesis of autoimmune diseases (6, 14, 31), these differences in  $K^+$  channel expression represent a great therapeutic opportunity for the use of Kv1.3 blockers.

**B lymphocytes.** Although less extensively studied, B lymphocytes show also dramatic changes in  $K^+$  channel phenotype during differentiation and activation, paralleling T-cell changes. Quiescent  $T_N$  and early memory B-cells upregulate KCa3.1 upon activation, while late memory cell of the T ( $T_{EM}$ ) and B (class-switched) lineages increased Kv1.3 channels when activated (172).

**Natural Killer (NK) cells.** NK cells participate in both innate and adaptive immune responses and play a major role in the defense against tumors and virus. Human NK cells express both Kv1.3 and KCa3.1 channels, but their expression varies between the different subsets of NK cells. As for B and T lymphocytes, these differences are important in regulating  $V_M$ , degranulation and proliferation of the NK cells subpopulations, that can be differentially targeted with selective blockers (87).

**Macrophages, Dendritic Cells (DCs) and Monocytes.** The responses of these cells are initiated by recognition of pathogen-associated molecular patterns (PAMPs) through receptors such as toll-like receptors (TLRs). Activation of these receptors induces proinflammatory cytokines that can in turn activate macrophages and DCs. Kv1.3 and Kv1.5 have been described in macrophages, most likely as heterotetramers (165, 166). Kv1.3 channel expression has been reported to increase upon activation and differentiation in response to inflammatory injury in macrophages, and its blockade inhibits migration and proliferation (163).

### **The nervous system**

Kv1.3 channels are expressed in the mature nervous system in several subsets of neurons and in all types of glial cells: astrocytes, oligodendrocytes, and microglia. In contrast to neurons, glial

cells undergo proliferation in response to physiological or pathological cues, and a role for Kv1.3 channels has been proposed in this response.

**Astrocytes.** While initially they were considered only as *gap fillers* among neurons, astrocytes are now thought to play a number of active roles in the brain, including transmitter uptake and release, blood flow regulation, maintenance of an appropriate neuronal environment, modulation of synaptic transmission and nervous system repair (2). They respond to insults through a process named reactive astrogliosis, which is a pathological hallmark of CNS structural lesions. However, the contribution of astrocyte proliferation to reactive astrogliosis is controversial. In healthy CNS tissue, astrocyte turnover is very low. Few actively dividing reactive astrocytes can be found after brain injury, and their source is not well established (7).

Changes in K<sup>+</sup> channels expression have been implicated in the injury-induced proliferation of astrocytes, but their molecular correlates are not fully characterized. Within a few hours after the injury, downregulation of inward rectifier K<sup>+</sup> currents (K<sub>IR</sub>) with concurrent upregulation of outwardly delayed rectifier K<sup>+</sup> (K<sub>DR</sub>) currents has been described. K<sub>DR</sub> currents increase in proliferating astrocytes and decrease with cell cycle exit and differentiation. Blockade of K<sub>DR</sub> currents with TEA or 4-AP inhibited glial proliferation and retarded scar repair, supporting their contribution to proliferation (104, 105). Kv1.5 has been proposed to mediate this proliferation-dependent K<sub>DR</sub> current, by a mechanism involving Src-mediated Kv1.5 phosphorylation (104).

**Oligodendrocytes.** The adult nervous system has a very limited capacity of neural replacement. However, oligodendrocytes regenerate neuronal myelin membranes in response to a wide variety of insults in a rapid and efficient way. This remarkable repair capacity relies on the presence of oligodendrocyte precursor cells (OPCs) in the adult CNS, with phenotypic characteristics of immature oligodendrocytes (168). While activation of OPCs can be observed in response to inflammatory or immunological insults, the proliferative response is only observed in response to demyelination or generalized tissue destruction (15).

The expression of K<sub>DR</sub> channels correlates with the proliferative potential of oligodendrocytes. OPCs exhibit large Kv currents, that are absent in postmitotic oligodendrocytes (5, 37). In proliferating OPCs there is an increase in the synthesis of both Kv1.3 and Kv1.5 mRNA during G<sub>1</sub> phase of the cell cycle that is accompanied by an up-regulation of outward Kv currents. Currents through Kv1.3-containing channels seem to play a crucial role in G<sub>1</sub>/S transition, as Kv1.3 blockade inhibits S-phase entry (37). In contrast, the functional contribution of Kv1.5 channels to proliferation is unclear, since Kv1.5 antisense oligonucleotides reduced OPCs Kv1.5 protein expression and Kv current density with no effect on proliferation (5).

Several results indicate a good correlation between the functional expression of Kv1.3 currents and OPCs proliferation: 1) selective Kv1.3 blockers inhibit OPCs proliferation; 2) in acute isolated cells, Kv1.3 expression decreases as OPCs progress through the lineage becoming less proliferative (37); 3) overexpression of Kv1.3 channels in OPCs mimics the effect of mitogens like PDGF, suggesting that Kv1.3-channels are essential mediators of PDGF-driven

proliferation (159). In this regard, it has been shown that PDGF-induced increase of  $K_{DR}$  in OPCs cells is sensitive to TK inhibition (36).

Other Kv channels apart from Kv1.3 have been described to regulate OPCs proliferation, either as activators (as Kv1.4) or inhibitors, as for Kv1.6 (159). The mechanisms for these synergic or antagonistic effects on proliferation are poorly understood.

**Microglial cells.** They are the primarily scavenger cells of the CNS, sharing many properties with macrophages. They represent the first line of defense in CNS, with functions that include phagocytosis of cellular debris, regulation of astrocytosis, neutralization of infectious agents and coordination of neuroimmune responses. Microglia activation involves a stereotypic pattern of responses: increased expression of immunomolecules, proliferation, recruitment to the site of injury and release of inflammatory mediators (60).  $K^+$  channels participate in several of these responses, but it is hard to unravel their specific role(s) in each aspect of microglial function, including proliferation, secretion, migration or chemokine release. Nevertheless,  $K^+$  channel upregulation is a hallmark of microglial activation (137). It has been suggested that unstimulated microglia cells express only  $K_{IR}$  channels, but upon activation there is an increased expression of Kv channels (117), mainly Kv1.5 and Kv1.3 channels. The seminal study of Kotecha and Schlichter (88) showed expression of both Kv1.3 and Kv1.5 proteins in cultured microglia cells. Both currents were involved in microglia proliferation but their relative roles changed with time in culture. Quiescent microglia cells expressed predominately Kv1.5 currents whilst Kv1.3 currents become predominant upon proliferation.

Similar results are reported in other models of microglial cells proliferation. Deletion of Kv1.5 channels increased microglia proliferation upon facial nerve axotomy, and cultured microglia treated with Kv1.5 antisense oligonucleotides showed an increase proliferation rate (121).

However, proliferation represents only an intermediate level of activation. The induction of the expression of both Kv1.3 and Kv1.5 channels is required for full microglial activation, albeit each channel plays a different role. Upregulation of Kv1.5 channels is required for increased nitric oxide production, but leads to cell cycle arrest, while Kv1.3 channels do appear to have a role in microglial proliferation and migration as well as in cytokine release (32, 149). Finally, simultaneous upregulation of both channels have been suggested in the case of stimulation of microglia with lipopolysaccharide (LPS), which increases a Kv current with biophysical properties compatible with heterotetrameric Kv1.5/Kv1.3 channels (121). LPS stimulation induces cytokine release, but decreases proliferation.

These observations have also therapeutic implications. If Kv1.5 is more important for resting cells and Kv1.3 is required for proliferating microglia, it may be possible to downregulate overactive microglia without compromising the functions of resting microglia.

### **Vascular smooth muscle cells**

Vascular smooth muscle cells (VSMCs) in the vessel wall retain a considerable degree of plasticity, being able to switch from a quiescent contractile state to a synthetic, migratory and

proliferative one, in response to chemical, mechanical or inflammatory stimuli (119, 167). This functional change of VSMCs is known as phenotypic modulation (PM). VSMC plasticity contributes to the development and homeostasis of blood vessels, but it has also ill-fated consequences as it is central to the process of intimal hyperplasia, a pathological lesion in vascular diseases displaying unwanted remodeling (112). PM of VSMCs during vascular diseases involves activation, proliferation, migration and dedifferentiation of VSMCs, and in all these events the contribution of different ion channels and transporters is also required.

A large number of ion channels, including several  $K^+$  channels have been involved in the PM of VSMCs (12, 35, 79, 89, 110, 114). In a large-scale analysis of the changes of ion channels expression upon PM both “*in vitro*” and “*in vivo*” models, only two ion channel genes were up-regulated in both models: Kv1.3 channel and its accessory subunit Kv $\beta$ 2.1 (42). Proliferating VSMCs exhibited increased Kv1.3, and Kv1.3 selective blockers inhibited cultured VSMCs migration and proliferation (35, 42). This effect has been also demonstrated in “*in vivo*” proliferative models (35, 43). As the increased contribution of Kv1.3 channels associates to a decreased expression of Kv1.5 channels, the Kv1.3/Kv1.5 ratio has been proposed as a marker of VSMC phenotype (40, 41). Interestingly, Kv1.3 and Kv1.5 channels have opposite effects on proliferation when overexpressed in heterologous expression systems: Kv1.3 channels increased HEK cells proliferation while Kv1.5 channels decreased it (40).

## **Kv1.3 channels and proliferation: Mechanisms**

Ion channels can regulate many signaling pathways involved in proliferation by modulating the electrical, mechanical and chemical properties of the cells. The complexity of this regulation explains why data on the signaling pathways activated by ion channels often remain described at a phenomenological level. We will try to dissect some of the potential mechanisms participating in the crosstalk between Kv1.3 channels and the biochemical pathways linked to proliferation, using data from the three “model” systems described previously (T-cells, glial cells and VSMCs). Initially, we can consider two non-exclusive mechanisms: either cells use Kv1.3 channels to regulate  $V_M$  and hence cell cycle, or Kv1.3 channels serve as sensors of changes in  $V_M$ , acting as signaling molecules connecting bioelectrical membrane signals with intracellular biochemical pathways. In other words, we can speculate that Kv1.3 is important in proliferation because it is a  $K^+$  channel that regulates  $V_M$  or because is a membrane protein that can undergo conformational changes in response to changes in  $V_M$ . In fact, it is very likely that both mechanisms contribute to proliferation, as their individual participation is difficult to dissect. Moreover, evidence points to the importance of Kv1.3 channelosome in the proliferative response, and again, signaling through these closely associated proteins can be dependent on  $K^+$  fluxes (permeation) or conformational changes (gating).

### **Kv1.3 as $K^+$ channels: the membrane potential model**

In non-excitable tissues, Kv channels regulate  $V_M$  and cell volume, and both processes have been linked to cell cycle progression. Two complementary observations have led to the

proposal that Kv channel activity is crucial for cell cycle progression: 1) Kv channel blockers inhibit proliferation whilst channel openers stimulate it, and 2) Kv channel expression and/or activity is upregulated by mitogens (170). Accepting this causal relationship between Kv channel activity and cell proliferation, two different hypotheses have been put forward to expound the underlying mechanism.

The first one proposes that Kv channels modulate cell cycle progression by controlling resting  $V_M$ .  $K^+$  conductance govern resting  $V_M$  in all cells, so that changes in  $K^+$  channel activity would determine cell cycle oscillations of  $V_M$ . Current models of these changes outline a rhythmic, slow oscillation of  $V_M$  with a hyperpolarizing spike occurring before S phase initiation and a prolonged depolarization being required for the G2/M transition (19). The resulting changes in  $V_M$  can regulate for instance  $Ca^{2+}$  fluxes. Also, regulation or recruitment of signaling molecules to the membrane can be dependent on  $V_M$  (96).

In the second hypothesis, the important signal contributing to proliferation will be  $K^+$  efflux upon Kv channel activation. Although the mechanism is not well described, cell proliferation is influenced by cell volume, which is in turn dependent of ion and water fluxes (reviewed in 72, 90). A bell-shaped relationship between cell proliferation and volume has been defined experimentally, indicating that proliferation is optimal within a cell volume window. This model could describe any change in rate of proliferation, suggesting a phenomenological correlation between cell volume and division. In this context, the cell volume increases upon  $K^+$  channels inhibition will be the mechanism responsible for decreased proliferation (53).

The contribution of Kv1.3 (and KCa3.1) channels to T-cell mediated activation and proliferation is related to its prominent role controlling  $V_M$  and indirectly,  $Ca^{2+}$  driving force (Figure 2). The contribution of these channels to resting  $V_M$  will vary depending on the T-cell subtype and on its activation state (see above). The voltage-dependence of activation and inactivation of Kv1.3 determines a membrane potential window at which the ion channels are active, while KCa3.1 channels are mostly silent at rest. This, together with the high input resistance of the membrane of unstimulated T-cells allows effective  $V_M$  control by a reduced number of channels with the resting conductance dominated by Kv1.3 channels (156, reviewed in (23, 122).

Control of  $V_M$  does not require a particular spatial distribution of channels in the membrane of T cells. However, Kv1.3, KCa3.1 and CRAC channels are recruited to the immunological synapse during antigen presentation (115, 116, 124, 136) which most likely provides additional signaling functions. Concentration of CRAC channels will produce a high localized  $[Ca^{2+}]_i$  within nanodomains close to the APC, which can trigger localized  $Ca^{2+}$  binding or activation of enzymes or other signaling proteins. As mitochondria also accumulate in the subsynaptic region, they remove  $Ca^{2+}$  and contribute to maintain CRAC current. The accumulation of Kv1.3 and KCa3.1 channels at the synapse facilitates the clustering and modulation of associated proteins. It will also result in a localized increase in  $[K^+]_e$  upon channels activation. The subsequent membrane depolarization will favor Kv1.3 activation, but there are also direct effects of increase  $[K^+]_e$  on Kv1.3 channels, including augmented single channel current and

decreased inactivation (24), that together with membrane depolarization will tend to increase Kv1.3 channel activity. This augmented activity of Kv1.3 dependent on  $[K^+]_e$  is tightly regulated. Larger increases in  $[K^+]_e$ , (as in necrotic areas within solid tumors), lead to an inhibition of T-cell activation, that is independent on the effect of  $[K^+]_e$  on  $V_M$  but depends upon changes in  $[K^+]_i$  (54).

### **Kv1.3 as voltage-dependent proteins: The voltage sensor model.**

In addition to allowing ion permeation, ion channels can also have non-conducting functions that enable them to interact with cell signaling pathways and directly regulate biochemical events (80). Certain types of ion channels such as the transient receptor potential channels (TRPs) are truly bifunctional proteins, with protein kinase domains in their cytosolic domains (139). Although no enzymatic activity has been described for the  $K_v\alpha$  subunits, such activity could be present on the associated molecules within the channelosome. In fact, the macromolecular complex includes accessory subunits such as  $K_v\beta$ , that show enzymatic activity (66). Therefore, the proteins within these complexes may contribute to this double life of Kv channels by transducing voltage-dependent conformational changes into cytoplasmic or nuclear signals affecting proliferation. The studies dissecting the contribution to the cell cycle of either conducting or non-conducting properties of Kv channels are scarce. As mentioned, it is now widely recognized that even though ion fluxes through the channel can also participate in this response, the final outcome is the triggering of a signaling pathway that other types of channels with similar electrical properties cannot recapitulate (80, 95).

The effect of Kv1.3 on proliferation in native cells was reproduced upon heterologous expression in HEK293 (40). Moreover, while Kv1.3 increases HEK proliferation, Kv1.5 has the opposite effect. These antagonistic effects give support to the idea that concurrent changes in the expression of these two channels in the native systems (discussed below) are in fact a requirement for the functional changes associated with dedifferentiation and proliferation. These observations also widened the possibilities for exploring the mechanism through which Kv1.3 increases proliferation. Several extreme Kv1.3 mutant channels have been used to determine the role of permeation, voltage sensor and channel location on proliferation. Non-conducting mutants induced proliferation to the same extent than WT channels. However, the effect was lost in voltage-insensitive channels or channels not expressed at the plasma membrane (40), indicating that Kv1.3 channels only need their voltage sensing capability to impact proliferation, while  $V_M$  modulation by Kv1.3 channels is nonessential. Electrical signals ( $V_M$  changes during cell cycle) are converted into a biochemically supported transduction pathway in the Kv1.3 molecule, whose conformational changes activate proliferation signaling (Figure 3). In fact, absolute values of  $V_M$  in HEK cells are irrelevant for proliferation since wild type and non-conducting Kv1.3 channels show a similar effect on proliferation with a very different effect on  $V_M$ , while Kv1.3 and Kv1.5 have similar effects on  $V_M$  and opposite effects on proliferation (40).

Effects on proliferation of non-conducting channel mutants have been also described for another  $K^+$  channels, such as Eag1 and  $Ca^{2+}$ -activated  $K^+$  channels (71, 111). However, in all

cases these data were obtained in heterologous systems, due to the clear difficulties to break up gating and permeation of native channels. Nevertheless, there are some clues suggesting that the pro-proliferative effect of Kv1.3 in VSMCs may not be simply related to its role as a K<sup>+</sup> channel. In femoral VSMCs the contribution of Kv1.3 channels to resting V<sub>M</sub> does not recapitulate the effects of Kv1.3 on VSMC proliferation. Kv1.3 blockade leads V<sub>M</sub> depolarization and inhibits proliferation. However, when depolarization was induced by blockers of other K<sup>+</sup> channels or by high [K<sup>+</sup>]<sub>e</sub>, cell proliferation was unaffected (42). Moreover, proliferation inhibition by Kv1.3 blockade was still present in VSMCs incubated in high (20 mM) [K<sup>+</sup>]<sub>e</sub>, which suggest a role for Kv1.3 channels in VSMCs proliferation beyond membrane depolarization.

These findings open interesting questions for future research. First, they indicate that the original hypothesis of depolarization inducing growth (18) is too simple and then, probably inaccurate. Although the general idea that cell cycle progression is marked by changes in V<sub>M</sub> still holds true (110) the relationships between cell cycle stages and V<sub>M</sub> are complex, because **1)** V<sub>M</sub> variations are cell-type specific, **2)** the control of V<sub>M</sub> is highly non-linear as many of the proteins that determine V<sub>M</sub> are themselves voltage-regulated and **3)** the expression and function of ion channels may fluctuate along the cell cycle (10, 110, 158). Second, if Kv1.3 behaves only as a sensor, and the changes in V<sub>M</sub> needed to proceed along cell cycle are not due to its activation, we need to identify the channel(s) and the signals responsible for cell cycle oscillations of V<sub>M</sub>. An attractive hypothesis linking changes in V<sub>M</sub> to G1 restriction point associates changes in V<sub>M</sub> with the polyamine synthesis occurring before entry in the S phase, since several K<sup>+</sup> channels are known to be inhibited by these molecules (128). The change in V<sub>M</sub> would be an indirect check of the correct increase in polyamine needed for DNA packing, and Kv1.3 sensing of V<sub>M</sub> changes could facilitate cycle progression. Third, if K<sup>+</sup> flux is not a requirement, then the voltage-dependent conformational change of Kv1.3 needs to be transduced via associated proteins within the Kv1.3 channelosome. The molecular identification of the putative docking sites in the Kv1.3 molecule, the nature of the interacting molecules, and the mechanisms involved need to be identified.

The opposite effect of Kv1.3 and Kv1.5 on HEK proliferation provided a useful tool to scrutinize the molecular determinants of Kv1.3-induced proliferation. Kv1.3-Kv1.5 chimeras indicate that these molecular determinants located exclusively on Kv1.3 C-terminus (78). Alanine mutation of consensus phosphorylation residues showed that Kv1.3-induced proliferation was fully abolished by three point mutations, two of them located in a short region near the S6 helix (the YS-segment). Remarkably, YS segment recapitulates Kv1.3-induced proliferation in a Kv1.5 backbone, but only at one specific location. Altogether, it seems that voltage-induced conformational changes of Kv1.3 channels regulated the accessibility of these phosphorylation sites, which function as specific docking sites to activate proliferation signaling cascades. Channel phosphorylation increases with the closed to open transitions and decreased in voltage-insensitive channels, which reside in the inactivated state (78).

### **Kv1.3 as multiprotein complexes: the channelosome model**



In Kv1.3 KO mice, the levels of various signalling molecules (TK, adaptors, PDZ-containing proteins...) are significantly elevated in olfactory bulbs (57). In addition, the synaptic glomeruli of these animals show profound effects on development that are not seen in the absence of other ion channels that are also expressed in olfactory neurons such as Kv3.1 (73). Kv1.3 channel seems to be a central signalling molecule as it appears unlikely that these effects of Kv1.3 absence can be attributed simply to changes in membrane excitability. Nevertheless, it is conceivable that the complete absence of a channel protein will lead to a drastic reorganization of the associated proteins, including modulatory subunits, scaffolds, receptors or cytoskeletal elements. They all can participate in Kv1.3 signaling, and for many of them such roles have been described. Additionally, changes in the distribution, the location or the association between Kv1.3 and some of these interacting proteins may contribute to the proliferative responses. To explore these aspects it is useful to study systems where cells switch from quiescent to proliferative phenotypes. Activation of proliferation in normally post-mitotic cells can be particularly useful to explore the underlying mechanisms, because as shown for microglia activation, they do not necessarily recapitulate the normal "*in vivo*" switch during early postnatal development (88).

With the notable exception of T-cells, in all the systems described so far cells express other Kv1 channels, whose expression is also remodeled upon activation and/or proliferation (42, 83, 149, 159). Notably, associated changes in Kv1.5 channels (often decreased expression) accompany Kv1.3 upregulation in proliferative cells. This is the case in OPCs (5), in microglial cells (88) and VSMCs (40, 41). The relative amount of homo or heterotetrameric Kv1 channels could be relevant. In fact, a very attractive hypothesis is that the master switch determining Kv1 effect on proliferation is not the upregulation of Kv1.3 channels but the control of the Kv1.3 to Kv1.5 ratio. In most VSMCs preparations, PM does not change the expression of Kv1.3 mRNA (41, 43). However, all other Kv1.x mRNA decreased upon proliferation. This decrease is particularly drastic for Kv1.5, which changes from being the most abundant Kv1 transcript in quiescent cells to almost disappear in proliferating cells (40, 42).

The implications for cell proliferation will be different depending on whether the response depends upon Kv1.3 conformational changes or whether Kv1-mediated fluxes are also necessary. Biophysical implications of a switch from Kv1.5 to Kv1.3 current include their different voltage dependencies. The resulting window currents will determine the ability of the cells to oppose both brief and long depolarization influences resulting from activation of other receptor or channels (39, 82, 113, 140). Lack of C-type and cumulative inactivation in Kv1.5 will result in an increased channel availability after repetitive stimulations. Also, if Kv1.3 and Kv1.5 have also roles in proliferation beyond their K<sup>+</sup> permeability, both channels might be subject to different regulations depending on their location and their associated proteins.

A more complex scenario arises if we consider that Kv1.3 and Kv1.5 are likely to form heteromultimeric channels, like other Kv1 channels (133, 144, 151, 160), so that a range of possible Kv currents may be observed. However, regarding modulation by associated proteins,

these complexes could behave as dominant negative, so that the interaction(s) of either subunit with other scaffolds, enzymes or receptors will be hindered in the multimeric channel (Figure 4). In microglial cells, based on confocal images, Kv1.3/Kv1.5 heteromultimers seemed unlikely in quiescent cells (showing very little Kv1.3 immunoreactivity and largely intracellular), although their proportion could increase as the cells started to proliferate (88). At latter times in culture, the cells express Kv1.3 like currents, while Kv1.5 immunoreactivity decreased and remains mainly intracellular. The presence of heterotetramers Kv1.3/Kv1.5 has also been observed in microglial cells stimulated with LPS (121).

Heterotetrameric Kv1 channels are present in quiescent VSMCs (34, 133), but not in proliferating VSMCs, where only Kv1.3 currents are detected. Kv1.3 behaves as a housekeeping gene in VSMCs, as its expression cannot be stimulated by mitogens (41). It is conceivable that Kv1.5 downregulation could be the relevant change for VSMC proliferation, thus if Kv1.5 decrease is prevented PM will not take place. In this case, the role of Kv1.5 could be the activation of anti-proliferative signaling or the occlusion of the pro-proliferative Kv1.3 signals by Kv1.3/Kv1.5 heterotetramerization. In support of the first option, heterologous expression of Kv1.5 alone reduces proliferation (40). However, it is not clear whether this will be the case in native systems. In microglial cells, an antiproliferative role of Kv1.5 has been described since Kv1.5 antisense oligonucleotides increases proliferation. Using an “*in vivo*” model of microglia activation, LPS treatment decreased proliferation rate in WT animals but not in Kv1.5<sup>-/-</sup> animals (121). Notwithstanding, as Kv1.3 channels are also expressed in these cells, the antiproliferative role of Kv1.5 could also be explained by the occlusion of Kv1.3-induced proliferation. Kv1.5 overexpression in cultured VSMCs shows a decrease of proliferation rate similar to that observed with Kv1.3 blockers, and the two effects are non-additive (unpublished data). The interference of Kv1.5 with the pro-proliferative signaling pathways activated by Kv1.3 is the simplest explanation for these observations.

## Concluding remarks/Future directions

The work of many laboratories over the past decades points to a relevant role of Kv1.3 channels in the proliferative response of different cell types under physiological conditions. This finding is relevant as it provides novel therapeutical targets to prevent unwanted proliferation. It also adds tools to investigate the molecular processes regulating cell proliferation that are dependent on Kv1.3 channel function. In this regard, while the contribution of Kv1.3 to cell proliferation seems to be a shared feature of many cell types, the underlying processes linking Kv1.3 expression and/or activity to cell cycle progression are diverse and far from being fully understood (Figure 5). The diversity of mechanisms reflects the complexity of the functions carried out by Kv1.3 channels. Ion channels are pore-forming macromolecular complexes that allow the passive ion flow across membranes. However, they are not simple ionophores, but also integral membrane proteins that can mediate key steps in signal transduction in an exquisitely channel- and tissue-specific manner. In the case of voltage-gated channels, they can also act as transducers of bioelectrical signals into biochemical cascades. Because Kv1.3 channels are regulated by  $V_M$

and in turn they regulate  $V_M$ , bioelectrical signals can be highly non-linear, leading to complex recursion of the effects.

Still, the interactions of Kv1.3 channels with  $V_M$  are just one of the best known and more easily controlled cellular bioelectrical parameters. Subcellular organelles also have their own transmembrane potential, due to specific expression of ion channels. Kv1.3 channel expression is well documented in mitochondria, where they modulate cancer cells growth and apoptosis by regulating mitochondrial transmembrane potential (94, 153, 157). Mitochondrial Kv1.5 channels decrease associates with increased proliferation, while restoration of Kv1.5 channel led to apoptosis (22). It is tempting to speculate that the Kv1.3/Kv1.5 ratio at intracellular organelles could be also an important modulator of proliferation. The contribution of these subcellular altered bioelectrical signaling to cell cycle control warrants further research.

Many different  $K^+$  channels have been shown to regulate cell proliferation, highlighting the fact that  $K^+$  channel function, by modulating processes like membrane potential, cell volume and  $Ca^{2+}$  influx, is an important element in cell cycle regulation. This could be the case for Kv1.3 channels in T-cell activation and proliferation. Still, we tend to define  $K^+$  currents as the only effectors, ignoring other possible actions of the channel molecule itself. The specific requirement of Kv1.3 for proliferation in several cell types argues against this belief, suggesting that other permeation-independent mechanisms are also involved. Non-canonical functions can influence cell proliferation in the absence of (or in addition to)  $K^+$  efflux. This scenario could help to explain the proliferation-associated changes in Kv channels expression observed in several preparations (oligodendrocytes, microglia, VSMCs). In these cases the need of a dominant expression of Kv1.3 channels supports the involvement of molecule-specific interactions via mechanisms that are just starting to be identified. While heterologous expression studies suggest that Kv1.3-induced proliferation does not require  $K^+$  fluxes, more research is needed to extrapolate these observations to native tissues, where the contributions of canonical and non-canonical channel functions are more difficult to dissect. In addition, the differential effects on proliferation of Kv1.3-containing heteromultimeric channels described in some preparations adds complexity but also opens fascinating possibilities for the fine-tune control of cell proliferation.

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## Figure legends

**Figure 1.A.** Schematic picture of human Kv1.3  $\alpha$ -subunit highlighting some important domains. The S4 segment sequence with the charged residues in red (16), a N-glycosylation site (174) and the pore region sequence with a tryptophan residue critical for ion permeation and the K<sup>+</sup> selectivity filter highlighted (52, 132) are shown on top. The lower part shows the N- and C-terminal sequences with several well-characterized regions, including the SH3 domain, (107), the tetramerization T1 domain (150), the Kv $\beta$  association signature (135), and Caveolin binding domain (131) on the N-terminus, and the HRETE (148) or YMVIEE (108) forward trafficking motifs, the YS-segment (78) another SH3 binding domain and the PDZ binding domain (68, 107) on the C-terminus. The sequence of the S4-S5 linker (77) is also shown. The intracellular phosphorylatable residues are depicted as black dots. **B.** Schematic illustration of some of the described associations of Kv1.3 channels, including the cholesterol binding protein caveolin, and a heterodimeric integrin receptor at the cell membrane. Intracellular associated proteins include Kv $\beta$  subunits, PDZ proteins associating Kv1.3 with kinases, and cortactin binding F-actin. The focal adhesion complex links the cytoskeleton to integrin receptor. **C.** Functional domains of Kv1.3 channels. Kv1.3 channels are voltage sensors (sensor domain) that respond to changes in membrane potential with a conformational change. This conformational change activates K<sup>+</sup> permeability (pore domain) leading to changes in  $V_M$ . The cytoplasmic N- and C-terminal regions (signaling domain) can serve as docking sites for protein-protein interactions with other intracellular proteins that can activate different signaling pathways.

**Figure 2.** The membrane potential model of Kv1.3-induced proliferation. Activation of the immune synapse of a T-cell by an APC leads to PLC activation. PLC catalyzes the production of DAG (not shown) and IP3, which binds to its receptor on the ER, resulting in an initial small increased in cytoplasmic Ca<sup>2+</sup>. To sustain T-cell activation, an additional Ca<sup>2+</sup> influx is required. This influx is mediated by the voltage-independent Ca<sup>2+</sup> channel Orai, which is activated by STIM1 upon depletion of Ca<sup>2+</sup> from intracellular stores. This Ca<sup>2+</sup> influx activates KCa3.1, and by depolarizing the cell also activates Kv1.3. These K<sup>+</sup> channels led to membrane hyperpolarization that sustains Ca<sup>2+</sup> entry. The subsequent increase in [Ca<sup>2+</sup>]<sub>i</sub> mediates NFAT, translocation to the nucleus through the activation of calcineurin phosphatase. The normal values of resting  $V_M$  and of intra- and extracellular concentrations of K<sup>+</sup> and Ca<sup>2+</sup>, and their reversal potentials are also shown.

**Figure 3.** The voltage sensor model of Kv1.3-induced proliferation. Some of the elements of Kv1.3 channelosome that can participate in this process include integrin receptor, growth factor

(TK) receptors, caveolins, some scaffolding proteins and protein kinases such as MEK/ERK. Depolarization of  $V_M$  due to external and/or internal (the cell cycle) stimuli is sensed by Kv1.3 voltage sensor, and transduced into a conformational change of the channel intracellular domains that can promote phosphorylation and receptor or scaffolding protein associations, leading to the activation of pro-proliferative signaling pathways.

**Figure 4.** The channelosome model of Kv1.3-induced proliferation. The pro-proliferative role of Kv1.3 and the anti-proliferative role of Kv1.5 described in many preparations (see text) may be determining the assembly of Kv1.3 and Kv1.5 into homo- or heterotetrameric complexes, so that the relative proportion of both channels will control proliferation rate. Signaling of homotetrameric Kv1.3 channels will activate proliferation, while activation of Kv1.5 homotetramers will lead to an inhibition of proliferation. The pro-proliferative signals dependent on Kv1.3 activation will be occluded by the presence of Kv1.5 subunits in the heteromultimers, as Kv1.5 subunits will have a dominant-negative effect on Kv1.3-induced proliferation. Also, the biophysical differences between homo and heterotetrameric channels can play a role in cell proliferation.

**Figure 5.** Integrative flow of events between Kv1.3 channels and proliferation. Signals are initiated at the cell membrane by activation of Kv1.3 channels. Physically, the signal can be the  $K^+$  flux, changes in  $V_M$  or volume changes. A number of processes act as receptors for these signals (including changes in intracellular ions, conformational changes activated by voltage or other physical protein interactions), allowing their transduction into biochemical changes, that are amplified through interaction and cross-talk with several proteins and signaling pathways leading to proliferation.

Figure 1A, Pérez-García MT et al

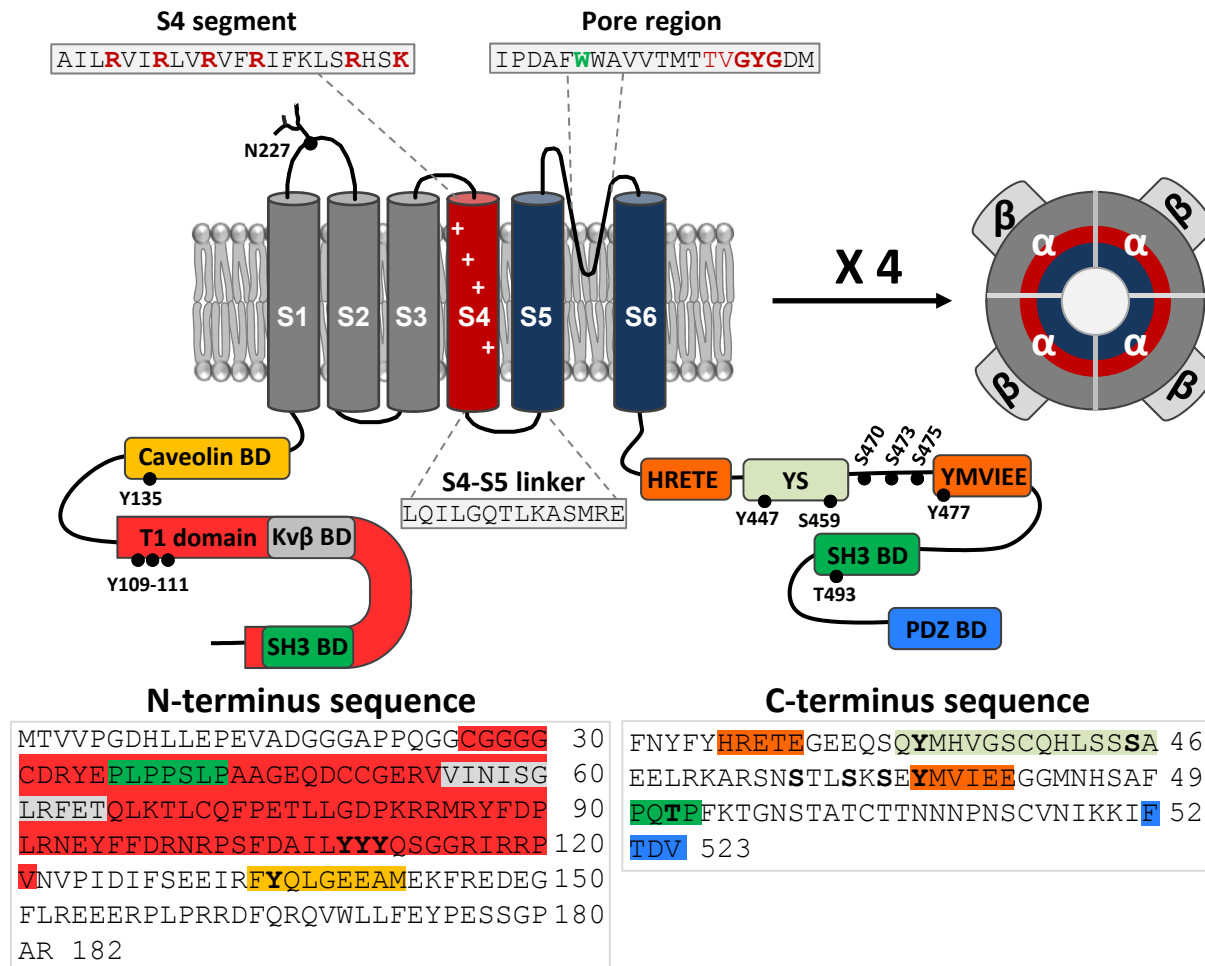
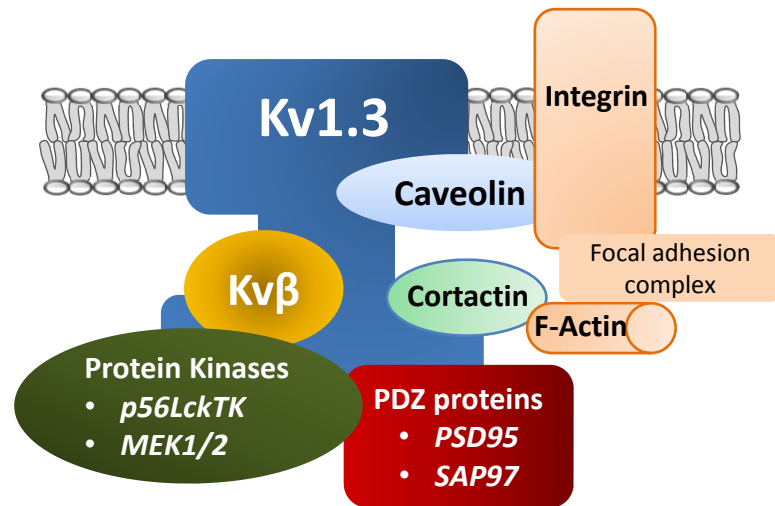


Figure 1B-C, Pérez-García MT et al

**B**



**C**

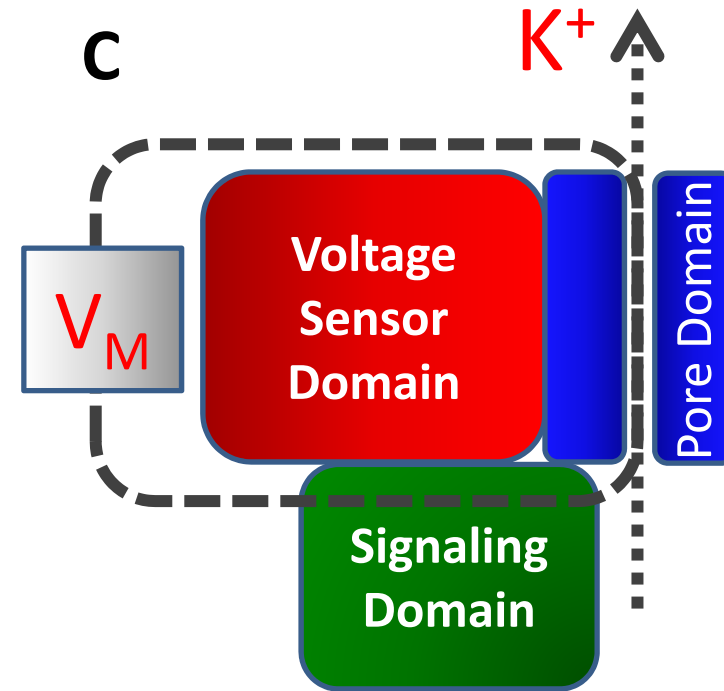


Figure 2, Pérez-García MT et al

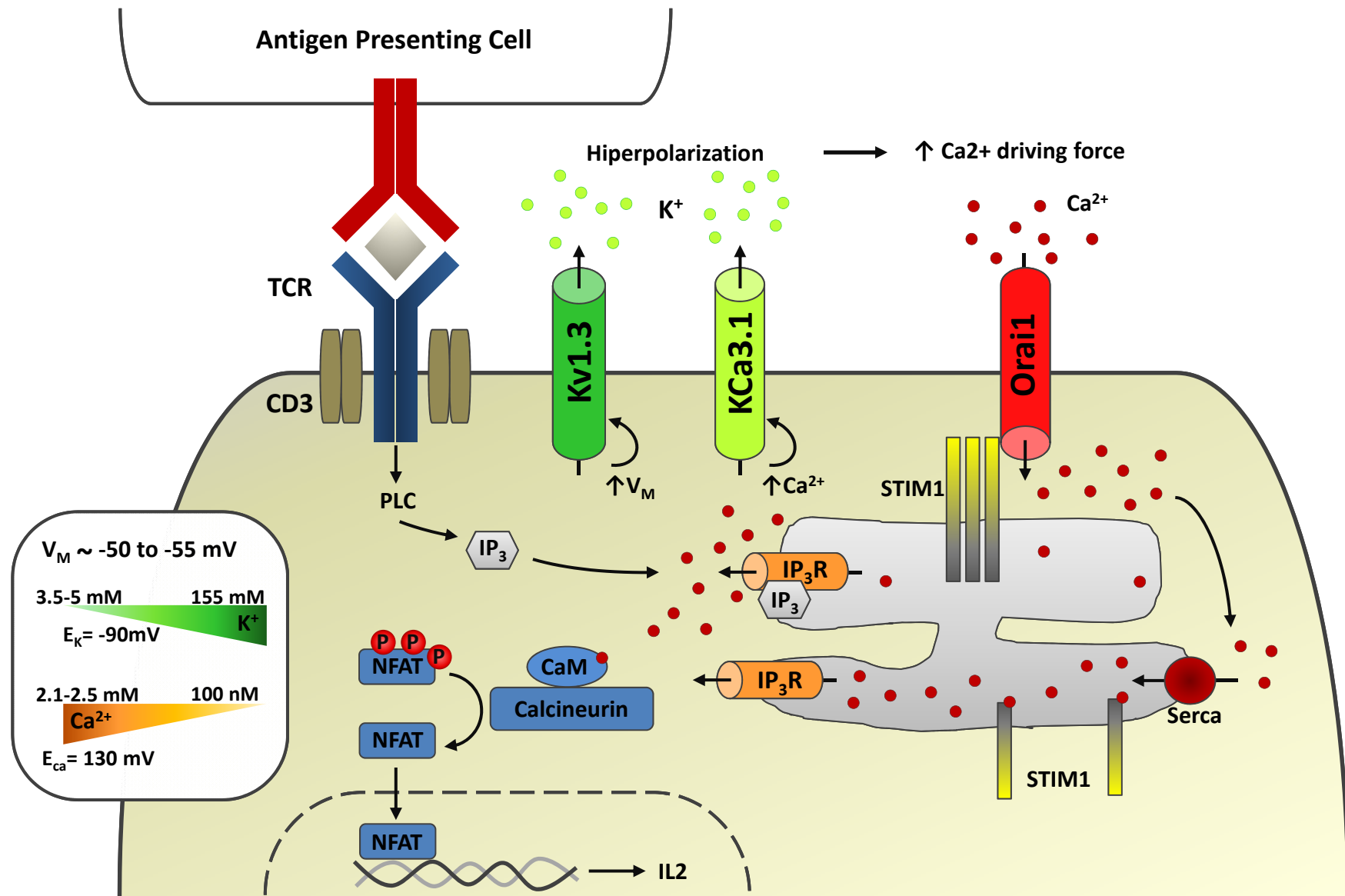


Figure 3, Pérez-García MT et al

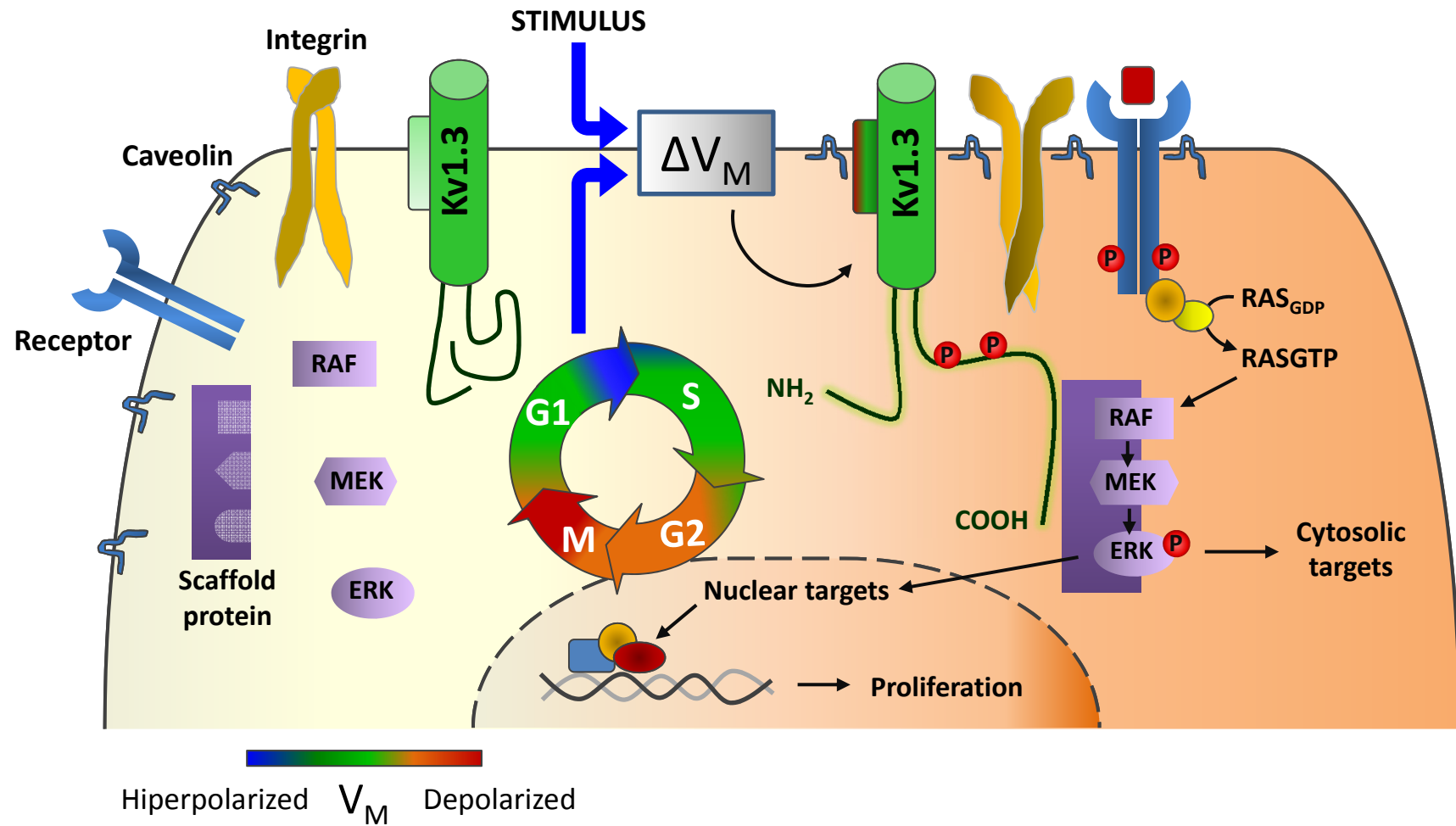


Figure 4, Pérez-García MT et al

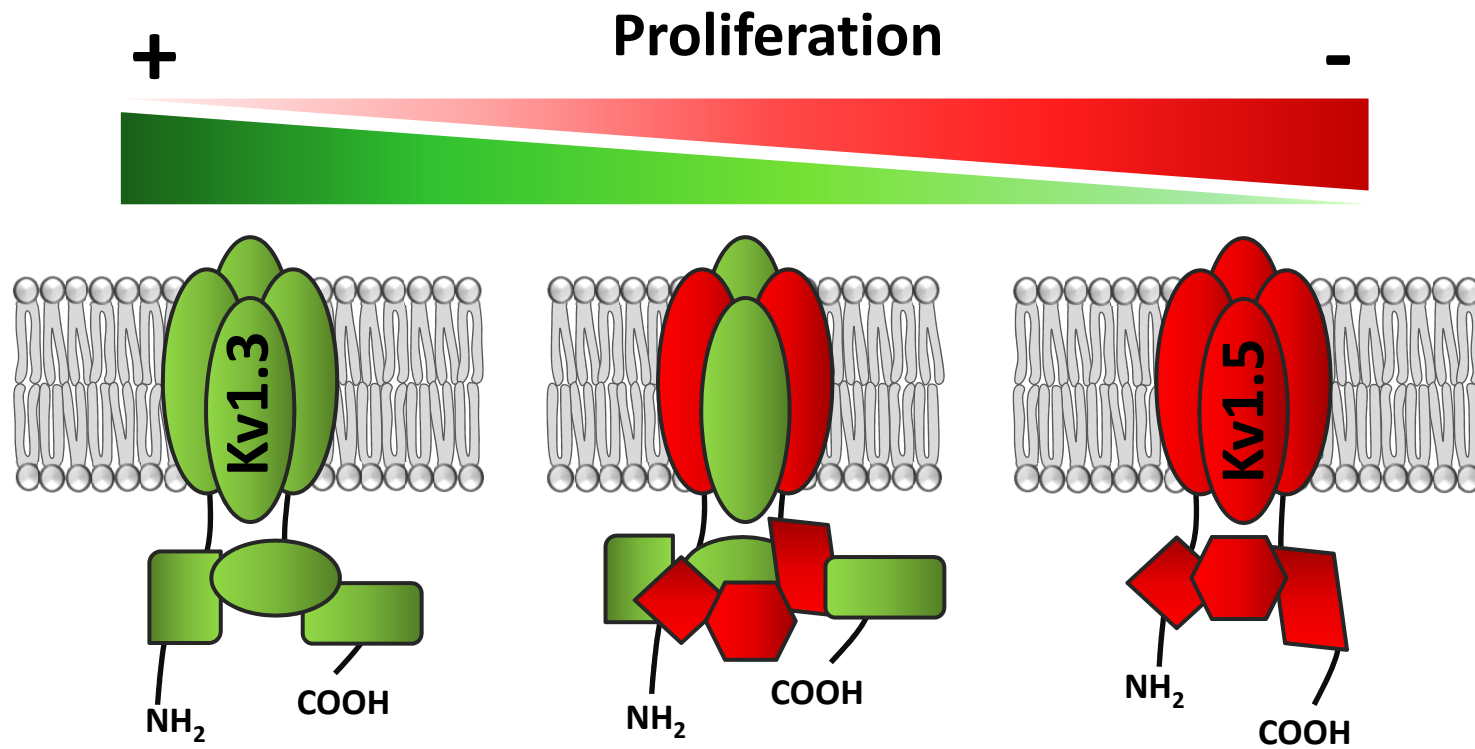




Figure 5, Pérez-García MT et al

