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## Channelopathies linked to plasma membrane phosphoinositides

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### Abstract

The plasma membrane phosphoinositide phosphatidylinositol 4,5-bisphosphate (PIP<sub>2</sub>) controls the activity of most ion channels tested thus far through direct electrostatic interactions. Mutations in channel proteins that change their apparent affinity to PIP<sub>2</sub> can lead to channelopathies. Given the fundamental role that membrane phosphoinositides play in regulating channel activity, it is surprising that only a small number of channelopathies have been linked to phosphoinositides. This review proposes that for channels whose activity is PIP<sub>2</sub>-dependent and for which mutations can lead to channelopathies, the possibility that the mutations alter channel-PIP<sub>2</sub> interactions ought to be tested. Similarly, diseases that are linked to disorders of the phosphoinositide pathway result in altered PIP<sub>2</sub> levels. In such cases, it is proposed that the possibility for a concomitant dysregulation of channel activity also ought to be tested. The ever-growing list of ion channels whose activity depends on interactions with PIP<sub>2</sub> promises to provide a mechanism by which defects on either the channel protein or the phosphoinositide levels can lead to disease.

### Keywords

PIP<sub>2</sub>; Phosphoinositides; Channelopathies; Ion Channels; Channel-PIP<sub>2</sub> interactions; Channel activity; Modulation of channel activity

## Introduction

Phosphatidylinositol 4,5-bisphosphate (PtdIns(4,5)P<sub>2</sub> or PIP<sub>2</sub>) is the most abundant phosphoinositide localized at plasma membranes of eukaryotic cells. It is a well-recognized lipid precursor molecule that has for more than three decades garnered appreciation as a regulator of many physiological processes. Since the mid-1990s, when three reports of PIP<sub>2</sub> regulation of K<sub>ATP</sub> channel activity appeared [53, 60, 78], there has been an explosion of reports demonstrating a dependence of the activity of most ion channels on the presence of phosphoinositides. Numerous reviews have appeared discussing in detail the activity dependence of specific ion channel types. General reviews also appear annually highlighting general principles that may apply across different channel types (e.g., [63, 83, 195]). Yet, as our appreciation grows regarding the central role these signaling phospholipids play in regulating channel activity, one wonders why the number of ion channel diseases described to be linked to phosphoinositide defects are relatively sparse. Here, we first review diseases known to be caused by dysregulation of phosphoinositide levels and ask how expected concomitant effects on ion channel activity might contribute to the disease phenotype. Next, we update the ever-growing list of ion channels, whose activity is reported to depend on phosphoinositides, and summarize key features of their physiology and pathophysiology. We then review ion channel channelopathies that have been directly linked to altered interactions with PIP<sub>2</sub>. We finally conclude by asking whether, given the central role of phosphoinositide control of ion channel activity, we ought to be clarifying whether mechanisms of disease for phosphoinositide-dependent channels operate by affecting phosphoinositide regulation of their activity.

## PIP<sub>2</sub> and disease

Aberrant regulation of PIP<sub>2</sub> gives rise to a plethora of diverse diseases, as might be expected for a ubiquitous signaling phospholipid with central importance in such diverse functions as neuronal signaling, regulation of apoptosis, and actin remodeling. Many diseases currently attributed to aberrant PIP<sub>2</sub> regulation are linked to disorders of the phosphoinositide pathway, which is briefly reviewed below.

The precursor phosphatidylinositol (PtdIns) is subject to reversible phosphorylation at the 3, 4, and 5-hydroxyl positions of the inositol ring, potentially giving rise to seven different phosphoinositide molecules. Due to tight temporal and spatial restriction of the kinases and phosphatases governing phosphoinositide generation, different phosphoinositides are largely confined to different membranous compartments, with PIP<sub>2</sub> concentrated at the plasma membrane. Indeed, PIP<sub>2</sub> interaction with integral membrane proteins appears to play a major functional role, with PIP<sub>2</sub> substrates including enzymes with the pleckstrin homology domain, scaffolding proteins, and ion channels, the subject of this review. The seminal importance of PIP<sub>2</sub> in regulated secretion pathways has been demonstrated in neuroendocrine cells, including the ability of PIP<sub>2</sub> to direct and accelerate targeting of synaptotagmins involved in vesicle fusion. PIP<sub>2</sub>, generated by 5-phosphokinases from PtdIns4 at the plasma membrane, is essential for the early steps of endocytosis, including adaptor protein recruitment and actin molecular motor operation. The endocytic pathway

further requires 5-phosphatase activity and subsequent removal of PIP<sub>2</sub> from endocytic microdomains to complete vesicle fusion and release [208].

Due to PIP<sub>2</sub> involvement in several essential cellular tasks at the plasma membrane, it is not surprising that aberrant PIP<sub>2</sub> generation could give rise to diseases with variable clinical phenotypes. The oculocerebrorenal syndrome of Lowe, characterized by mental retardation, cataracts, and renal Fanconi syndrome, is linked to mutations in the OCRL1 gene, a known inositol 5-phosphatase with a preferred in vitro substrate of PIP<sub>2</sub>. How loss of OCRL1 function leads to the severe clinical pathology in Lowe syndrome is unclear but may underscore the importance of tight regulation of phosphoinositide generation. There has been much interest as well in lithium treatment of bipolar disorder and impact on phosphoinositides. Lithium is known to inhibit inositol monophosphatase, leading to reduced pools of myoinositol, a precursor to PtdIns. Whether inositol depletion by lithium accounts for the mood-stabilizing effects in bipolar disease patients remains a controversial issue, especially since new cell signaling targets for lithium have been found, including PKC and GSK3β [69].

There has been a flurry of interest recently in neurodegenerative diseases and PIP<sub>2</sub> metabolism, and importantly, the protein aggregates postulated to have a central role in neurodegeneration have direct or indirect impacts on membrane PIP<sub>2</sub>. Oligomeric Aβ<sub>42</sub> peptide, known to accumulate in the brains of Alzheimer's disease patients, was shown to decrease PIP<sub>2</sub> levels in both acute and chronic treatments of primary cortical neurons in culture without altering the levels of PIP<sub>2</sub> metabolic enzymes, and in a reversible manner. The selective PIP<sub>2</sub> decrease was shown to involve phospholipase C-mediated hydrolysis and calcium, while synaptojanin-1 (an inositol 5-phosphatase) haploinsufficient neurons were protected from the PIP<sub>2</sub> decreasing effect of oligomeric Aβ<sub>42</sub>, possibly due to their already increased PIP<sub>2</sub> levels [8].

If proper PIP<sub>2</sub> levels are indeed crucial to normal synaptic function, then it is perhaps not surprising that dysregulation can produce cognitive deficits. SYNJ1, coding for synaptojanin-1, is localized to chromosome 21q and is subsequently a potential player in the cognitive deficits of Trisomy 21 or Down's syndrome. A mouse model of Down's syndrome displayed elevated levels of synaptojanin-1, and transgenic overexpression of synaptojanin-1 in normal mice was linked to deficits in behavioral learning. Utilizing the Morris water maze task and limited training, transgenic SYNJ1 mice spent equal amount of time in each maze quadrant, while wild-type mice spent the majority of time in the quadrant containing the hidden platform. Only with extensive training could the transgenic mice reach equivalent scores on the maze with the wild-type mice, indicating a deficit in spatial learning ability linked to phosphoinositide metabolism [210].

Further evidence of the role of PIP<sub>2</sub> in central nervous system (CNS) function comes from its interaction with myelin basic protein (MBP), an essential component in the myelination pathway that may be disrupted in demyelinating diseases like multiple sclerosis. PIP<sub>2</sub> was shown to interact with MBP in both primary oligodendrocytes and an oligodendrocyte precursor cell line, oli-Neu. A mutant form of MBP that does not localize to the plasma membrane is unable to localize to PIP<sub>2</sub>-rich regions, and a reduction in PIP<sub>2</sub> levels by

synaptojanin-1 overexpression and wortmannin treatment resulted in less MBP targeted to the plasma membrane. Further disruptions in either PIP<sub>2</sub> charge or localization prevented MBP recruitment to the membrane, implicating PIP<sub>2</sub> as the anionic phospholipid required for proper MBP localization and function [141].

Given its ubiquitous nature, diseases associated with PIP<sub>2</sub> function can have far-reaching multi-organ pathological consequences, as shown in the ciliopathy Joubert syndrome. The central tenet of ciliopathies is that an impairment of cilia function in several cell types results in dysregulated proliferation in response to external cues and subsequent formation of cystic masses in multiple organs. Individuals with Joubert syndrome were found to have associated mutations in the INPP5E gene, an inositol 5-phosphatase, that impaired normal activity on the substrates PIP<sub>3</sub> and PIP<sub>2</sub>. Primary fibroblasts isolated from patients with mutant INPP5E had reduced cilia number and length after serum stimulation compared to control fibroblasts. Interestingly, this implicates aberrant regulation of phosphoinositides in impaired function of the cilia [17].

Many of the diseases described thus far have a central theme: either too much or too little PIP<sub>2</sub>, resulting from impairment of normal phosphoinositide metabolism. We would predict that dysregulation of PIP<sub>2</sub> levels would result in dysregulation of channel activity in the cells and tissues where it occurs. This prediction points us in the direction of examining for possible electrophysiological phenotypes in such cases of PIP<sub>2</sub> dysregulation.

We will continue next by examining proteins that normally interact with PIP<sub>2</sub> but are not directly involved in its metabolic regulation, namely, PIP<sub>2</sub>-sensitive ion channels. Ion channels are involved in a diverse array of biological processes such as in the control of cellular excitability of neurons or neuroendocrine cells and neurotransmitter and insulin release, in cellular excitability of muscle cells of all types and muscle contraction, in sensory modalities, in salt transport across epithelia, and in T-cell activation.

## Ion channels and transporters regulated by phosphoinositides

Tables 1 and 2 list ion channels whose activity has been reported to depend on phosphoinositides and their tissue distribution. This list builds on previous efforts by other investigators in the field over the past 5 years (e.g., [63, 194, 195]). The danger of compiling lists of this sort in such a rapidly evolving field is that they are both unlikely to be all inclusive and certain to be outdated even before published. Nonetheless, Tables 1 and 2 do make the point that very different ion channel types, both in terms of structural and functional diversity, utilize PIP<sub>2</sub> to control their activity in the plasma membrane.

Several studies have concluded that channel-PIP<sub>2</sub> interactions control directly channel gating (e.g., for Kir channels [52, 119, 122, 218]). Yet, the details of how channel-PIP<sub>2</sub> interactions lead to channel gating and which gates are affected are awaiting further structural and functional analysis.

Analysis of 25 crystallographic structures of a diverse group of proteins that were solved in complex with phosphoinositides revealed a number of generalizable common features [175], among which were that (a) there was a strong electrostatic component in the protein–

phosphoinositide interaction, involving at least two positively charged residues, and (b) the ability of a specific phosphoinositide to bind a protein depended in its ability to fit into a binding site, and its affinity depended on the number of specific interactions in which it would engage. As three-dimensional structures of ion channel complexes with phosphoinositides become available along with molecular dynamic simulations, they promise to give us insights as to the missing details of the specific channel-PIP<sub>2</sub> interactions and how they lead to channel gating (e.g., [119, 175]).

Below, we give a brief description of the PIP<sub>2</sub>-sensitive channels described in the literature thus far and in the order they appear in Tables 1 and 2, with a special emphasis into their key physiological and potential pathophysiological roles, particularly as suggested by transgenic animal models. There exist many comprehensive reviews detailing our current knowledge of these channels. Here, we aim to give our readers an overview of the physiology and pathophysiology that PIP<sub>2</sub>-sensitive channels are involved in.

### Kir channels

Inwardly rectifying K<sup>+</sup> (Kir) channels pass K<sup>+</sup> ions better in the inward than outward direction, a phenomenon mediated by a physical block of outward current by Mg<sup>2+</sup> ions and polyamines that bind to the transmembrane and cytoplasmic regions of these channels. They possess two transmembrane domains that form the basic pore-conducting structure in K<sup>+</sup> channels. They are major contributors to the resting membrane potential of cells they are expressed in [76]. All Kir channels depend on the presence of PIP<sub>2</sub> to maintain their activity. Kir channel structures have allowed mapping onto the protein structure of amino acid residues, mutation of which alters channel-PIP<sub>2</sub> interactions [119]. Interestingly, diverse modulators of Kir channel activity, such as the βγ subunits of G proteins, intracellular Na<sup>+</sup>, and phosphorylation by different kinases (Kir3) and protons (Kir1.1), depend on phosphoinositides for their effects and act in close proximity to residues implicated in phosphoinositide binding [120]. This has led to the hypothesis that modulators exert their effects by altering channel-PIP<sub>2</sub> interactions.

Kir1 channels (first referred to as ROMK—rat outer medullary K<sup>+</sup>—channels) come in six alternatively spliced mRNA isoforms that give rise to three distinct proteins (Kir1.1–1.3) with differing lengths in their NH<sub>2</sub> terminus. They show weak rectification and are blocked by internal acidification. Kir1.1 is localized at the apical surface of kidney epithelial cells and physiological as well as transgenic work supports its function in renal NaCl absorption. Kir1.1 knockout in mice results in Bartter's syndrome, an autosomal recessive renal tubulopathy characterized by renal salt wasting and metabolic alkalosis, among other phenotypes [76].

Kir2 channels (first referred to as IRK—inwardly rectifying K<sup>+</sup>—channels) are constitutively active and exhibit strong inward rectification. There are five Kir2 subfamily members (Kir2.1–2.4 and a recently discovered Kir2.6) that can exist as homomers or heteromers [76, 178]. These channels keep the resting potential close to the K<sup>+</sup> equilibrium potential and contribute to the long-lasting action potential plateau in a number of different cells. Dysfunctions in Kir2.1 caused by mutations reducing its activity result in Andersen's syndrome, an autosomal-dominant disorder, characterized by delayed ventricular

repolarization (manifested as a prolonged QT interval on an electrocardiogram), syncope, and sudden death [209]. Kir2.1 knockout mice reproduce some phenotypes of Andersen's syndrome and show defects in vascular tone. Gain of function mutations in Kir2.1 can lead to short QT syndrome that can lead to sudden cardiac death, syncope, and/or atrial fibrillation [76].

Kir3 channels (first referred to as GIRK—G protein-sensitive inwardly rectifying K<sup>+</sup>—channels) are distinguished from other inward rectifiers in that their activity is regulated by G proteins. Kir3.1–Kir3.4 exist as homomers (except Kir3.1) or heteromers. Kir3.2 and Kir3.3 predominate in the nervous system, while Kir3.4 in the atria of the heart. Kir3 currents exhibit strong inwardly rectifying characteristics. ACh released by the vagus nerve activates K<sub>ACh</sub> (Kir3.1/Kir3.4), slowing the heart rate and shortening the atrial myocyte action potential and effective refractory period. Kir3.1 or Kir3.4 knockout mice lack the typical K<sub>ACh</sub> currents. Kir3.4 knockout mice exhibit unchanged ambulatory heart rate, reduced heart rate variability, and resistance to atrial fibrillation [76]. Neuronal Kir3 channels modulate synaptic transmission underlying memory storage, control of seizure activity, reinforcement of addictive substance use, and regulation of pain sensation. Consistent with their broad distribution and negative feedback on excitatory synaptic transmission, Kir3.1- and Kir3.2-knockout mice exhibit many behavioral phenotypes including hyperactivity, reduced anxiety behavior, diminished administration of addictive substances, lower seizure threshold, hyperalgesia, and diminished opioid induced analgesia [133, 134, 163].

Kir4 and Kir5 channels can form heteromers with each other. Kir5.1, like Kir3.1, is not functional as a homomer but confers distinct phenotypes to heteromers with Kir4 subunits (e.g., intracellular pH and Na<sup>+</sup> sensitivity). Kir4.1 and Kir4.2 exist also as functional homomers. Kir4 subunits show intermediate inward rectification as homomers but much stronger rectification as heteromers with Kir5.1. Physiological functions of Kir4.1 channels include Na<sup>+</sup> reabsorption in the basolateral membranes of the distal convoluted tubules of the nephron; aiding in proton secretion by regulating the activity of a proton pump in gastric parietal cells; significant contributions to the endocochlear potential that is essential for proper audition; and significant contributions to the resting potential of astroglial cells in brain, spinal cord, and retina. Kir4.1 knockout mice have shown a multitude of phenotypes including deafness, epilepsy and seizures, ataxia, and hypomyelination [76].

Kir6 channels associate into octamers with the sulfonylurea (SUR) receptors (four subunits each) to form the weak inwardly rectifying K<sub>ATP</sub> currents. K<sub>ATP</sub> channels are inhibited by ATP and stimulated by nucleotide diphosphates (NDPs), such as ADP. They serve as metabolic sensors responding to the ATP/ADP ratio. The Kir6 subunits are responsible for the ATP inhibition, and the SUR subunits for the NDP activation. Sulfonylureas inhibit while K<sup>+</sup> channel openers stimulate K<sub>ATP</sub> channel activity by binding to the SUR subunits. Kir6.2/SUR1 form the pancreatic K<sub>ATP</sub> channel, inhibition of which causes  $\beta$ -cell depolarization that leads to insulin release. Kir6.2/SUR2A form the ventricular cardiac K<sub>ATP</sub> channel that is activated (or less inhibited) under lower ATP/ADP ratios, such as during increased cardiac work load, hypoxia, or ischemia exerting a cardioprotective effect (shortening the action potential and limiting Ca<sup>2+</sup> influx through Ca<sup>2+</sup> channels). Kir6.1/



SUR2B form the vascular smooth muscle  $K_{ATP}$  channels that besides the ATP/ADP ratio, they respond to a number of vasodilators and vasoconstrictors. Glucose-sensitive hypothalamic neurons utilize either Kir6.1 or Kir6.2 complexed with SUR1 to regulate wakefulness, locomotor activity, appetite, sleep, energy conservation, feeding behavior, etc. Loss of function mutations cause excessive insulin secretion despite hypoglycemia (persistent hypoglycemia of infancy), while gain of function mutations cause reduced insulin secretion and hyperglycemia (neonatal diabetes mellitus) [76].

Kir7.1 is less homologous to the other Kir channels displaying a much lower single-channel conductance, ten times lower sensitivity to  $Ba^{2+}$  or  $Cs^{+}$  block, and inward rectification independent of  $[K^{+}]_o$ . The M125R mutation (Arg is conserved in all other Kir channels) normalized all three differences [49, 100]. Snowflake vitreoretinal degeneration patients show the heterozygous mutation R162W in Kir7.1. This mutation makes Kir7.1 behave like a non-selective cation channel, depolarizing the cells in which it is expressed [76].

### K2P channels

The K2P family of potassium channels is responsible for background “leak” potassium current, which is operative over all physiological membrane potential ranges, unlike Kv and Kir channels. K2P channel subunits contain four transmembrane domains with two pores arranged in tandem, with the functional unit a homoor heterodimer.

TREK1 responds to a wide variety of physiological stimuli, with activation by intracellular acidosis, membrane stretch, polyunsaturated fatty acids, lysophospholipids, and volatile anesthetics. Inhibition results from increased cAMP or Gq-coupled signaling. Exogenous  $PIP_2$  application was reported to reduce TREK1 response to various activating stimuli, including acidosis and membrane stretch.

TASK currents are responsive to low changes in extracellular pH and were recently implicated in stabilizing the adrenal zona glomerulosa membrane potential, which was depolarized in the TASK1/TASK3 knockout mouse. Brainstem TASK channels are also implicated in oxygen and  $CO_2$  sensing [51].

### Na<sup>+</sup> channels

Among Na channels, strong evidence for regulation by phosphoinositides currently exists only for a non-voltage-gated sodium channel: the epithelial sodium channel (ENaC or amiloride-sensitive sodium channel). These channels are composed of three subunits:  $\alpha$ -,  $\beta$ -, and  $\gamma$ -ENaC. Each subunit has two membrane-spanning domains, a large extracellular loop, and intracellular N- and C-termini. Analogy to the related acid sensing ion channels suggests that ENaC channels exist as a heterotrimer of the three subunits.

These channels are found on the apical membranes of various epithelia, and they especially play important roles in renal and pulmonary physiology. Passage through ENaC channels is the rate-limiting step for reabsorption of  $Na^{+}$ , and thus the channels are important for control of water homeostasis and blood pressure. In humans, loss of function mutations in ENaC are associated with pseudohypoaldosteronism type-I (PHA-I) characterized by volume depletion, hypotension, and hyperkalemia. In contrast, gain of function mutations are

associated with Liddle syndrome characterized by volume expansion, hypertension, hypokalemia, low aldosterone level, and metabolic alkalosis. In lung/airway epithelial cells, ENaC function is important for clearance of surface liquid. Loss of function mutations associated with PHA-I are additionally associated with neonatal respiratory distress syndrome due to pulmonary edema. Impaired ENaC activity is furthermore also linked to susceptibility to high-altitude pulmonary edema in patients [11].

Relevant phenotypes have also been observed for various mouse models. Knockout of the  $\alpha$ -ENaC subunit results in lethal respiratory distress syndrome. On the other hand, certain gain of function ENaC mutations can recapitulate cystic fibrosis-like symptoms in transgenic mice by causing increased clearance of liquid from lungs and increased inflammation [11, 85].

### Cl<sup>-</sup> channels

Among Cl<sup>-</sup> channels, evidence for regulation by phosphoinositides currently exists only for the cystic fibrosis transmembrane conductance regulator (CFTR) channel. This protein also functions as a member of the ATP-binding cassette (ABC) transporter superfamily of ATPases. It is the only known ABC transporter ATPase to also function as an ion channel. CFTR seems to be constructed from a single polypeptide containing several domains: two transmembrane domains containing six membrane-spanning helices each, two nucleotide binding domains, and a regulatory domain. Anion flow is vital for normal water movement across epithelia, and loss of function of the CFTR channel leads to cystic fibrosis characterized by thickening of mucous secretions, which impair function at various epithelial surfaces including airways, intestines, pancreatic ducts, testes, and sweat glands. Two thirds of all cystic fibrosis cases are due to the  $\Delta$ F508, but over 1,000 other disease-causing mutations are also recorded.  $\Delta$ F508 leads to failure of protein maturation and its eventual degradation. Many of the other mutations also lead to loss of function by truncation or by effects on open probability and conduction rate. However, most disease-causing mutations have not yet been characterized [61].

### P2X receptors

The entire family of P2X receptor cation channels that are gated by extracellular ATP has been shown to be PIP<sub>2</sub> sensitive [232]. There are seven different P2X receptor subunits (P2X1-7) that can assemble as homo- or heterotrimeric [31]. P2X receptor subunits consist of a large extracellular domain and two transmembrane helices. Both the N- and C-termini are intracellular [90]. P2X receptors have a widespread expression in the nervous system, with P2X2, 4 and 6 being the most abundant in neurons [94].

P2X1 receptors are abundantly expressed in smooth muscle cells and platelets [94]. P2X1 knockout male mice are infertile, due to a defect in purinergic neurotransmission in the vas deferens, which controls emission of sperm into the semen [94]. A severe bleeding disorder has also been linked to a single amino acid deletion in the P2X1 subunit [151]. Consistently, P2X1 knockout mice exhibit reduced thrombosis after injury of the walls of small arterioles [198].



P2X2 has a perisynaptic localization in excitatory synapses in the brain. There are presynaptic P2X2 receptors as well, which increase glutamate release onto inhibitory interneurons in the feed-forward circuit in the hippocampus [94]. In the periphery, P2X2 is important for myenteric neurotransmission, as knockout mice show impaired fEPSCs in myenteric neurons [94]. P2X2 has also a predominant role in the response to hypoxia in the carotid body, since excitation of primary afferent nerves by hypoxia is much reduced in mice lacking P2X2 [198]. Homomeric and/or heteromeric P2X2 and P2X3 receptors are essential players in taste transduction [198]. P2X2 or P2X3 knockout mice exhibit moderately diminished neural and behavioral responses to tastants, whereas double mutants show complete absence of nerve responses to tastants applied to the oral cavity.

P2X3 is implicated in neuropathic and inflammatory pain. P2X3 subunits are abundantly expressed in a subset of primary afferent neurons implicated in pain sensation, and P2X3 knockout mice exhibit greatly reduced mechanical allodynia, together with further defects in afferent sensation [94]. Moreover, P2X3 is expressed in bladder afferent nerves, and P2X3 knockout mice have also impaired ability to sense bladder filling [94].

The first described phenotype of P2X4 knockout mice was an increase in blood pressure [94]. P2X4 knockout mice also show lack of flow-induced calcium and NO production in lung microvessels and decreased vasodilation. The vascular phenotype of P2X4 knockout mice generally resembles the one in endothelial nitric oxide synthase knockout mice, supporting the idea that P2X4 subunits are involved in the modulation of NO production and release. P2X4 subunits have been implicated in pain sensation as well. Tactile allodynia is much reduced when downregulating P2X4 expression in the dorsal horn, using antisense oligonucleotides [94]. Moreover, P2X4 subunit expression is increased in microglia of the dorsal horn of the spinal cord following spinal nerve ligation, a common model for neuropathic pain. P2X4 and P2X6 subunits are also found in perisynaptic locations on hippocampal CA1 and cerebellar Purkinje cells. Long-term potentiation is impaired in the hippocampus of P2X4 knockout mice [198].

P2X7 is expressed abundantly in cells of the immune system, including macrophages and microglia [31]. P2X7 seems to be critically involved in cytokine release, as P2X7 knockout mice do not release interleukin-1 $\beta$  in response to ATP [94]. P2X7 is also implicated in pain perception, as P2X7-deficient mice show reduced or absent behavioral responses to inflammation of the paw (chronic inflammatory pain) and tactile allodynia (neuropathic pain) [198]. Moreover, P2X7 is normally expressed in osteoclasts and osteoblasts. Bone metabolism is impaired in mice with a P2X7 deletion, giving rise to a unique skeletal phenotype with excessive resorption of the trabecular bone [94]. Interestingly, P2X7 knockout mice have also been shown to exhibit antidepressant-like behaviors and increased responsiveness to a low dose of the antidepressant drug imipramine [6].

## iGluRs

Thus far, ionotropic glutamate receptors (iGluRs) have been shown to be regulated by phosphoinositides in atypical ways. iGluRs are ligand-gated channels responsible for the vast majority of excitatory neurotransmission in the nervous system [46]. They are divided into subclasses (NMDA, AMPA, and kainate) according to their pharmacological behavior

(i.e., agonist specificity) [118]. NMDA receptors are obligate heterotetramers consisting of GluN1 (NR1) and GluN2A-D (NR2A-D) or GluN3A-B (NR3A-B) [140]. AMPA receptors subunits (GluA1-4 or GluRA-D) and kainate receptors subunits (GluK1-5 or GluR5-7) can form homotetramers, but the native receptors are most likely heterotetramers [35, 125]. The membrane topology and domain organization is common in all iGluR subunits [188]. The amino-terminal domain, implicated in subtype-specific receptor assembly and allosteric modulation, and the ligand-binding domain are extracellular. The transmembrane domain consists of three transmembrane helices (M1, M3, and M4) and a re-entrant loop (M2). The C-terminal domain is cytoplasmic.

iGluRs have well-established roles in synaptic plasticity and neuronal development [37]. Given the physiological significance of iGluRs in the nervous system, it is not surprising that they have been linked to an array of pathological conditions, including Fragile-X syndrome, schizophrenia, Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, ischemic stroke, and neuropathic pain [19, 46, 54]. iGluRs have also been implicated in depression [72] and epilepsy [156]. CNS disorders are generally considered multifactorial, and often, a specific etiology has not been established [19]. However, aberrant iGluR function has been implicated in several mouse models for CNS disorders.

NMDA receptors act as coincidence detectors at postsynaptic sites. Upon activation, they allow calcium to flow into the cell, an event that is critical for most forms of synaptic plasticity [129]. They are activated by PIP<sub>2</sub> through interactions that are mediated by the cytoskeletal associated protein  $\alpha$ -actinin [137]. The cytoskeleton might also play an important role in these interactions [132]. Several mouse models for Huntington's disease have demonstrated an increase in NMDA receptor-mediated currents in striatal neurons and altered synaptic plasticity [54].

AMPA receptors mediate fast excitatory neurotransmission and are also critically involved in synaptic plasticity. Depending on their subunit composition, they are either constantly trafficked to and from the synapse (GluA2/3) or they are recruited in an activity-dependent manner (GluA1/2) [185]. It has been shown that PIP<sub>3</sub> regulates AMPA receptor mobility at the synapse and is necessary for maintaining AMPA receptors in the synaptic compartment [4]. Knockout mice for GluA1 have been shown to exhibit behavioral and neurochemical alterations that have been linked to major depressive disorder [34]. Also, a mouse model for Fragile-X syndrome exhibits exaggerated AMPAR-associated LTD in the CA1 region of the hippocampus and in Purkinje cells of the cerebellum [19].

Kainate receptors can be found at both pre- and postsynaptic sites. At postsynaptic sites, kainate receptors not only produce synaptic currents but also regulate neuronal excitability. Presynaptic kainate receptors are known to regulate transmitter release and affect both excitatory and inhibitory neurotransmission [156]. GluK1 knockout mice show decreased responses to capsaicin or inflammatory pain, whereas GluK2 knockout mice exhibit reduced fear memory [97]. Finally, several kainate receptor subunits have been implicated in animal models of epileptic seizures [19]. No regulation of kainate receptors by phosphoinositides has been reported yet.

## Ca<sup>2+</sup>-release channels

Ca<sup>2+</sup> release channels include ryanodine receptors and inositol triphosphate (IP<sub>3</sub>) receptors. These channels predominantly localize to the sarcoplasmic and endoplasmic reticula, respectively. They are considered intracellular receptors, where they participate in the release of internal calcium stores.

IP<sub>3</sub> receptor subunits consist of a large cytoplasmic N-terminus, six membrane-spanning helices, and a short cytoplasmic C-terminus. Three different genes with various splice variants encode these subunits which then homo- or heterotetramerize to form functional channels. These channels participate in the release of intracellular Ca<sup>2+</sup> stores in response to IP<sub>3</sub> released from hydrolysis of membrane PIP<sub>2</sub>. While this fundamental signaling mechanism is vital to a myriad of physiological processes from learning/memory to apoptosis, no human diseases directly involving mutations of IP<sub>3</sub> receptors are known. It is hypothesized that perhaps this is due to functional redundancy among the various isoforms and splice variants. Knockout of type 1 IP<sub>3</sub> receptors causes neurological defects and early death. Knockout of both type 2 and type 3 is required to generate a pancreatic acinar cell secretion mouse phenotype [58].

Ryanodine receptor (RyR) subunits are likely to be composed of four transmembrane domains with cytoplasmic termini. Three genes encode RyR subunits: RyR1 and RyR2 are found in the terminal cisternae of muscle sarcoplasmic reticulum, where they are responsible for the release of internal Ca<sup>2+</sup> stores in excitation–contraction coupling; the exact role of RyR3 is unclear. RyR3 is found in all cells, RyR1 is considered the skeletal muscle isoform, and RyR2 is considered the cardiac muscle isoform, although both RyR1 and RyR2 have also been shown to be present in peripheral lymphocytes. Mutations in RyR1 and RyR2 are associated with autosomal-dominant diseases of skeletal and cardiac muscle, such as malignant hyper-thermia, central core disease, catecholaminergic polymorphic ventricular tachycardia, and arrhythmogenic right ventricular dysplasia type 2. No disease-associated mutations are known for RyR3, while RyR3<sup>(-/-)</sup> mice show defects in memory and learning. Knockout of RyR1 or RyR2 is lethal early in embryonic development [23].

## Other channels

Gap junctions are defined as clusters of few to hundreds of tightly packed intercellular channels that allow small molecules to be directly transferred between neighboring cells [104]. The connexin family consists of 21 members in humans. Cx43 is the most widely expressed connexin, found in 35 distinct tissues [104], and it is inhibited by depletion of PIP<sub>2</sub> [205]. Mutations in Cx43 have been linked to the pleiotropic developmental disorder ODDD. Patients suffering from this disorder exhibit syndactyly, craniofacial abnormalities, brittle nails, hair abnormalities, conductive hearing loss, lens defects, cornea defects, abnormalities of the teeth, and occasional neurological and heart symptoms [104]. Of the described loss-of-function mutations, two affect positively charged residues (K134E and R202H).

The volume-regulated anion channel (VRAC) is mainly permeable to Cl<sup>-</sup> under physiological conditions and is activated by classical “cell-swelling protocols” [144]. The

molecular identity of VRAC is presently unknown. VRAC is regulated by PIP<sub>3</sub> in mouse ventricular myocytes [219].

### Transporters and exchangers

The plasma membrane Ca<sup>2+</sup>-ATPase (PMCA) belongs to the P-type class of ion-motive ATPases. Its expression is ubiquitous and plays a critical role in Ca<sup>2+</sup>-homeostasis in the cell. There are four isoforms of PMCA pumps (PMCA1–4), with PMCA1 and 4 expressed ubiquitously in animal cells, whereas PMCA2 and 3 have more specific expression (nervous tissue, with PMCA2 also expressed in the inner ear) [26]. The physiological role of PMCA pumps is to drive Ca<sup>2+</sup> out of the cell by coupling it with hydrolysis of ATP. PMCA1 is activated in the presence of PIP<sub>2</sub> [33]. The phenotypes of knockout mice for PMCA1, 2, and 4 have been reported [162]. Deletion of PMCA1 is embryonic lethal, consistent with a housekeeping function of this form of the enzyme. PMCA2 knockout mice develop pronounced deafness, with defect in both vestibular and auditory systems. Several findings are consistent with an important role of PMCA2 in hearing. The major phenotype of PMCA4 is male infertility.

The Na<sup>+</sup>/Ca<sup>2+</sup> exchanger family consists of three genes (NCX1, NCX2, and NCX3). NCX1 is the dominant form found in most types of cells [18]. The Na<sup>+</sup>/Ca<sup>2+</sup> exchanger catalyzes the exchange of one intracellular Ca<sup>2+</sup> with three extracellular Na<sup>+</sup> [38]. NCX1 activity is potentiated in the presence of PIP<sub>2</sub> (i.e., [78]). Human NCX1 is upregulated in pressure overload, end-stage heart failure, and senescence, and it may play a role in excitation contraction coupling [38]. Deletion of NCX1 is embryonic lethal, as the embryos do not have beating hearts. A role of NCX1 in pacemaker function has been suggested [38].

The Na<sup>+</sup>/H<sup>+</sup> exchanger catalyzes the electroneutral exchange of one intracellular H<sup>+</sup> for an extracellular Na<sup>+</sup> and, as a result, regulates intracellular pH and cell volume [166]. NHE1 (SLC9A1) is ubiquitously expressed and is activated by PIP<sub>2</sub> [1]. NHE1 also acts as a plasma membrane anchor for cortical actin filaments [166].

The NBCe1 transporter is an electrogenic Na<sup>+</sup>-coupled HCO<sub>3</sub><sup>-</sup> that belongs to the SLC4 family of transporters [174]. The NBCe1-A variant is first characterized and is expressed primarily in kidney. Two other variants exist: NBCe1-B has widespread expression, and NBCe1-C is expressed almost exclusively in the brain. The NBCe1-A variant is activated by PIP<sub>2</sub> [215]. In the kidney, NBCe1-A is responsible for the reabsorption of HCO<sub>3</sub><sup>-</sup> from the lumen to blood [174]. Four naturally occurring mutations of NBCe1 have been reported that cause persistent recessive renal tubular acidosis and ocular abnormalities [174]. Interestingly, two of these mutations are missense mutations that target two highly conserved arginines among the SLC4 family members.

### Kv channels

Kv channels, composed of tetramers of single alpha subunits, consist of a voltage sensor coupled to a pore domain, with varying biophysical properties that allow for a large degree of heterogeneity. They contain six transmembrane domains where the first four comprise the voltage sensor, while the last two make-up the channel pore, just like in Kir channels. They are activated in response to membrane depolarization and are responsible for repolarizing

the cell following an action potential. The Kv family is composed of Kv1–Kv9, with Kv5.x, 6.x, 8.x, and 9.x composed of silent subunits, which do not localize to the membrane on their own, but must associate with a Kv1–4 family member. Kv1.1, Kv1.4, and Kv3.4 were shown to have relatively fast N-type inactivation abrogated by addition of intracellular PIP<sub>2</sub>, presumably by immobilizing the inactivation domain [149].

Kv1.1 has been implicated in episodic ataxia, a rare disorder resulting in transient episodes of ataxia with otherwise intact neurological function. Kv1.1 knockout mice show increased incidence of spontaneous seizures, with altered hippocampal excitability and nerve conduction. The V408A Kv1.1 transgene is embryonic lethal when homozygous, whereas heterozygous mice display a similar phenotype to patients with episodic ataxia, including relief with acetazolamide treatment [88].

Kv1.3 has recently become a candidate for multiple sclerosis treatment, owing to a correlation of myelin-reactive T cells with high Kv1.3 expression. Kv1.3 knockout mice have increased basal metabolic rates compared to wild type, which may explain their reduced body weight phenotype [216].

Kv1.5 polymorphisms (P532L and R578K) can result in reduced sensitivity to the antiarrhythmic quinidine. Kv1.5 mutants have also recently been implicated in familial atrial fibrillation according to genetic analysis [105].

Kv7.x (KCNQ) channels stand on their own as therapeutic targets, owing to an extensive body of work investigating their physiological and pathophysiological role. All members of the Kv7 subfamily have been shown to be PIP<sub>2</sub> sensitive [229].

The role of Kv7.1 in heart is well appreciated, since mutants can cause Long QT (LQT) syndrome. Defective Kv7.1 subunit assembly can result in the Jervell and Lange–Nielsen cardioauditory syndrome. A mouse model for this syndrome was produced by disrupting the Kv7.1 gene, resulting in inner ear defects and prolonged QT intervals.

The majority of Kv7.2 channels form heteromers with Kv7.3, resulting in the Kv7.2/3 M current, a slowly activating current that arises at sub-threshold potentials. Importantly, Kv7.2/3 can be inhibited by muscarinic AChR stimulation, resulting in Gq-coupled hydrolysis of PIP<sub>2</sub> and subsequent closure of the channel. Kv7.2/3 is implicated in benign familial neonatal convulsions, an autosomal-dominant disorder characterized by episodic partial and complex seizures starting early in life and disappearing soon afterward.

Disruption of Kv7.4, expressed mainly in the outer hair cells of the air and the auditory nuclei of the brainstem, results in congenital deafness.

Kv7.5 has unresolved function, but may contribute to the M current. There are no known diseases resulting from Kv7.5 mutations [24].

Kv11.1 (HERG, for human ether-a-go-go related gene) is also heavily researched for its role in LQT syndrome. HERG channels have the unique characteristic of faster inactivation than activation, with subsequent recovery of inactivation that is faster than deactivation. This results in a sustained outward current as the membrane repolarizes, causing the steep slope

of phase 3 repolarization in atrial and ventricular myocytes. The Kv11.1 B isoform knockout is predisposed to sinus bradycardia [14].

### CNG channels

Cyclic nucleotide-gated (CNG) are important in vision and olfaction. Retinitis pigmentosa can result from mutation of phototransduction-specific cGMP-gated channel CNGA1, while knockout mice of olfactory-specific CNGA2 display a broad phenotype of failure to mate or fight, likely due to disruption of normal olfactory physiology and response to environmental cues [15].

### HCN channels

Among CNG channels are the HCN channels that are responsible for the  $I_f$  “funny” current in the heart pacemaker nodes, so-called due to their unusual property of activation by hyperpolarization from resting membrane potentials. HCN channels in the nervous system regulate rhythmic firing of pacemaking neurons, as well as contributing to routine neuronal functions. HCN channels are regulated by the cyclic nucleotides cAMP and cGMP, which serve to depolarize the half-activation voltage, essentially resulting in increased excitability for hyperpolarization-activated channels. The HCN4 knockout is embryonic lethal, presumably due to the loss of autonomic regulation of the heartbeat. The HCN2 knockout suggests that this channel may have overlapping function with HCN4, as knockout mice have a sinus dysrhythmia but maintain normal response to autonomic signals [16].

### Ca<sup>2+</sup>-activated K<sup>+</sup> channels

Ca<sup>2+</sup>-activated K<sup>+</sup> (or K<sub>Ca</sub>, Big K<sup>+</sup>, Maxi K) channels belong to the SLO family of large conductance channels, also referred to as SLO1, and thus far they are the only member of this family shown to depend on phosphoinositides [204] (also see [169]). They can be activated either by depolarization or by intracellular Ca<sup>2+</sup> alone or synergistically by both. Their predicted membrane topology resembles the Kv channel six transmembrane helices with a voltage sensor (helices 1–4) and pore (helices 5–6) domains but, in addition, has an extra helix (helix 0) that places the N-terminus extracellularly and a long cytosolic domain with two ring structures (RCK domains) and a distal region involved in the Ca<sup>2+</sup>-sensing mechanism. SLO1 channels are ubiquitously expressed regulating endocrine secretions and vascular, urinary bladder, and respiratory tone [39]. In the CNS, they space bursts of Ca<sup>2+</sup> action potentials (e.g., dendrites of cerebellar Purkinje cells), they underlie the fast phase of the after-hyperpolarization potential (somata of CA1 hippocampal pyramidal neurons), and they regulate synaptic transmission (in presynaptic terminals sensing Ca<sup>2+</sup> influx through Ca<sub>v</sub> channels) [181]. Malfunctions of SLO1 channels can lead to generalized epilepsy and paroxysmal dyskinesia, noise-induced hearing loss, hypertension, urinary incontinence, overactive urine bladder, and asthma [39, 181].

### Ca<sub>v</sub> channels

Ca<sub>v</sub> channels are calcium-selective voltage-gated channels with four subunits (voltage sensor and pore domains) linked in tandem to form a functional channel. Calcium channels are critical for electrochemical signaling in eukaryotic cells and are broadly classified as L-



type, P/Q-type, N-type, R-type, and T-type channels regarding their biophysical and pharmacological characteristics.

Due to its crucial role in calcium-induced calcium release signaling, defects in L-type  $\text{Ca}_v1.2$  function produce multi-organ dysfunction, best represented by Timothy syndrome, causing developmental and mental abnormalities, heart disease, hypoglycemia, immune deficiency, and autism [190].

Mutations in the neuronally restricted P/Q-type  $\text{Ca}_v2.1$  can result in familial hemiplegic migraine, spinocerebellar ataxia, and episodic ataxia [64].

N-type  $\text{Ca}_v2.2$  is expressed in the spinal cord and dorsal raphe nucleus, and knockout mice exhibit reduced pain sensation and aggressive behavior, consistent with their proposed roles in target cell types of ascending pain and control of aggression, respectively [96].

### TRP channels

The transient receptor potential (TRP) superfamily in humans is comprised of six subfamilies: canonical (TRPC1-7), melastatin (TRPM1-8), vanilloid (TRPV1-6), ankyrin (TRPA1), polycystin (TRPP2-3 and TRPP5), and mucolipin (TRPML1-3). The subunits are composed of six transmembrane regions (S1–S6) with a pore-forming loop between S5 and S6. These subunits assemble into homo- or heterotetramers and form cation-selective channels [143]. While most TRP channels allow for the entry of  $\text{Ca}^{2+}$ , exceptions such as the TRPM4 and TRPM5 channels are permeable to monovalent cations, but not to  $\text{Ca}^{2+}$  or  $\text{Mg}^{2+}$ . On the other hand, TRPV5 and TRPV6 are highly  $\text{Ca}^{2+}$  permeable, while TRPM6 and TRPM7 are highly permeable to  $\text{Mg}^{2+}$ . Furthermore, TRPV1, TRPML1, and TRPP3 are additionally highly permeable to  $\text{H}^+$  ions. TRP channels tend to respond to a wide variety of stimuli including ligand binding, temperature, osmolarity, mechanical forces, or voltage [146]. Given the size of this family of channels and the diversity of stimuli they respond to, it is not surprising to find them implicated in a large variety of fundamental physiologic processes.

TRPC2 is a pseudogene in humans; in a knockout mouse model, however, the processing of pheromone signals was disrupted, and the mice displayed behavioral abnormalities including defects in gender recognition. TRPC4 knockout mice exhibit altered endothelial function as well as changes in neurotransmission. Endothelium-dependent vasorelaxation as well as mechanisms for endothelial control of paracellular permeability are affected. The serotonin-induced release of GABA from thalamic interneurons is reduced in TRPC4 knockout mice. Transmission of this GABAergic signal may play a role in sleep/wake cycles or in visual processing, although relation to human disease is not yet clear. Six mutations in TRPC6 have been linked to late-onset type focal segmental glomerular sclerosis (FSGS) in humans. Three of the mutations were gain of function, while the remainder showed no evidence of altered function; this gave rise to the hypothesis that increased  $\text{Ca}^{2+}$  entry leads to  $\text{Ca}^{2+}$  overload and death of glomerular podocytes and the ensuing pathology of FSGS. TRPC6 knockout mice show an increased contractile response in vascular and tracheal smooth muscle and exhibit moderately increased blood pressures. These effects are thought to result from a compensatory upregulation of TRPC3 channels in the TRPC6 knockout mice, and

thus the importance of these channels for human diseases such as hypertension remains to be clarified.

TRPM5 knockout mice have disruptions in sweet, bitter, and umami taste perception. They also lose the temperature dependence of sweet taste. The role of TRPM5 in analogous human phenomena and its involvement in taste disorders remains to be proven. Several mutations in TRPM6 are strongly linked to hypomagnesemia with secondary hypocalcemia in humans. TRPM6 is among the  $Mg^{2+}$ -permeable TRP channels, and defects in its activity are thought to lead to impaired active uptake of  $Mg^{2+}$  in the small intestine as well as impaired  $Mg^{2+}$  reabsorption in the distal convoluted tubule of the nephron. In a zebrafish model, mutations in TRPM7 caused severe growth retardation: endochondral ossification was accelerated, while intramembranous ossification was delayed. Additional abnormalities in the mutant zebrafish include the development of kidney stones and defects in embryonic melanophores and the touch response.

TRPV1 knockout mice have been studied extensively and exhibit several interesting phenotypes. These mice exhibit impaired inflammatory thermal hyperalgesia and do not exhibit pain behavior normally elicited by pungent vanilloids or painful heat. These mice not only exhibit reduced mechanosensation and nociception but inflammation-induced enhancement in these sensory signals is also abolished. Similarly, the knockout mice exhibit decreased swelling and hypersensitivity in a model for chronic osteoarthritis. In a model of allergic contact dermatitis, the TRPV1 knockout had a more pronounced pathologic phenotype compared to wild-type mice. Finally, the knockout mice also showed changes in bladder function. The mice display a higher frequency of spontaneous low volume urine spotting along with decreased bladder stretch detection. They also are resistant to bladder overactivity in the setting of acute bladder inflammation. TRPV3 knockout mice display diminished responses to innocuous and noxious heat and also have some hair abnormalities. Several rodents bearing TRPV3 mutations in the S4-S5 linker are spontaneously hairless, and some develop symptoms of atopic dermatitis similar to the human disease. The TRPV4 knockout mice have a mild phenotype showing moderate changes in blood osmolarity and water intake. They exhibit decreased secretion of antidiuretic hormone but normal response to the hormone. TRPV5 knockout mice have impaired osteoclast function but increased osteoclast number. These mice exhibit osteoporosis possibly due to compensatory upregulation of TRPV6 and an increase in 1,25-dihydroxyvitamin  $D_3$ . TRPV6 knockout mice exhibit reduced fertility, alopecia, dermatitis, impaired intestinal  $Ca^{2+}$  uptake, and impaired renal  $Ca^{2+}$  reabsorption.

TRPA1 knockout mice show impaired pain responses to endogenous inflammatory mediators and to topical application of a variety of noxious stimuli including mustard oil, acrolein, and allicin. Knockout mice also show resistance to bradykinin-induced hyperalgesia. Mutations in the homologous gene in *Drosophila* also lead to reduced avoidance to noxious thermal, chemical, and osmotic stimuli.

Mutations in TRPP1 or TRPP2 are the cause of autosomal-dominant polycystic kidney disease in humans. Other structural abnormalities are also linked to mutations of TRPP1: heart valve defects, aneurysms, colonic diverticula, and inguinal hernias. TRPP2 mutations

can also lead to heart defects such as problems in septum formation. TRPP2 mutations in transgenic mice recapitulate many of these phenotypes: cyst formation, septal defects, whole body edema, renal failure, and early death. TRPP2<sup>(-/-)</sup> mice show similar defects but almost always die in utero. TRPP2<sup>(+/-)</sup> mice have intermediate survival but do not develop cysts or renal failure. Another knockout allele of TRPP2 resulted in the malformations mentioned above but additionally demonstrated cardiac, pulmonary, and gastric situs inversus among other laterality defects.

TRPML1 mutations are linked to mucopolidosis type IV, an autosomal recessive lysosomal storage disorder characterized by psychomotor retardation, ocular abnormalities, agenesis of the corpus callosum, hypoferrremia, and achlorhydria. The mechanism by which TRPML1 mutations lead to defects in lipid storage and lysosome function remains unclear. Knockout of TRPML3 is lethal, but several mutations have been characterized in mice. These mice have defects in maturation of stereocilia and melanocyte function leading to an overall phenotype which includes deafness, vestibular defects, and a characteristic tri-color coat [146].

## Channelopathies and PIP<sub>2</sub>

Mutations in the genes encoding ion channel proteins may lead to altered channel function and thus underlie channelopathies. Increasing evidence suggests that some disease-causing mutations exert their effects on channel activity by altering channel-PIP<sub>2</sub> interactions. As mentioned above, the interaction between PIP<sub>2</sub> and channel residues is thought to involve a largely electrostatic component: positively charged side chains of channel residues near the inner membrane leaflet are attracted to the negatively charged phosphoinositol headgroups of PIP<sub>2</sub> [55, 89]. However, uncharged residues near these critical PIP<sub>2</sub>-interacting regions can also alter apparent PIP<sub>2</sub> affinity of the channel, possibly through allosteric mechanisms involving nearby positively charged residues (e.g., [122]). Thus, a variety of charged and uncharged residues in critical PIP<sub>2</sub> interacting regions of various channels has been found to both alter PIP<sub>2</sub> affinity and also lead to disease.

Mutations in the KCNJ2 gene leading to loss of function in Kir2.1 have been tied to the Andersen–Tawil syndrome (ATS) [47]. ATS occurs either sporadically or in an autosomal-dominant pattern and is characterized by periodic paralysis, cardiac arrhythmias, and dysmorphic features, although the presence and severity of these features can vary considerably [157]. Several of the KCNJ2 mutations underlying the syndrome have been shown in vitro to impair channel-PIP<sub>2</sub> interactions and thus decrease its open probability [122]. Kir2.1 residues, when mutated, have been found to both underlie ATS in patients and shown to alter channel-PIP<sub>2</sub> interaction in vitro include R67, R189, R218, G300, E303, and R312 [47, 122]. Another Kir2.1 residue potentially linked to ATS, L217, has not directly been tested in vitro for effects on PIP<sub>2</sub> affinity, but its location within the critical PIP<sub>2</sub>-interacting region of the channel and especially its proximity to the PIP<sub>2</sub>-interacting R218 residue led its discoverers to hypothesize that it too leads to a loss of function phenotype by disrupting channel-PIP<sub>2</sub> interactions [44].

Mutations in the *KCNJ1* gene leading to a loss of function in Kir1.1 have been tied to hyperprostaglandin E syndrome (HPS), the antenatal form of Bartter syndrome [86, 182, 184]. HPS is an autosomal recessive disease characterized by polyhydramnios, premature delivery, hypokalemic alkalosis, and hypercalciuria [182]. Several of the *KCNJ1* mutations underlying HPS have been shown in vitro to also impair channel-PIP<sub>2</sub> interactions and thus decrease Kir1.1 open probability [122]. Residues potentially tied to HPS that have also been shown to affect Kir1.1-PIP<sub>2</sub> interactions include R311 (equivalent to Kir2.1 R312 discussed above), C49, I51, A214, and L220 [122] (but also see [167]).

Some mutations in *KCNJ11* causing a loss of function in Kir6.2 have been tied to congenital hyperinsulinism (CHI) [66, 113, 168]. Loss of Kir6.2 currents leads to increased excitability of pancreatic  $\beta$  cells and thus an increased secretion of insulin. A few of the mutations linked to CHI can be mapped to the putative PIP<sub>2</sub> binding site on the Kir6.2 channel [68]. Residues that have been found to be mutated in patients with CHI that also have been shown to be important for channel-PIP<sub>2</sub> interactions include F55, R301, and K67 [68, 112, 113, 168].

Many mutations in *KCNQ1* causing a loss of function in Kv7.1 have been linked to LQT syndrome. The pathogenic mechanism behind at least a few of these mutations appears to be disruption of channel-PIP<sub>2</sub> interactions. Residues important for PIP<sub>2</sub> binding that have also been found to be mutated in LQT syndrome patients include R243H, R539W, and R555C [152].

Ryan et al. recently reported the discovery of *KCNJ18* and its product Kir2.6, which were previously unknown. Kir2.6 is primarily expressed in skeletal muscle and shares 96–99% amino acid identity with Kir2.2. Several mutations in this gene were identified in patients with thyrotoxic hypokalemic periodic paralysis (TPP). TPP is a sporadic disorder, which occurs in a subset of thyrotoxic individuals. It is characterized by episodic muscle weakness (clinically similar to the periodic paralysis found in ATS) and hypokalemia [157, 178]. A few of the Kir2.6 mutations found in TPP patients were also shown to alter channel-PIP<sub>2</sub> interactions. The R205H and K366R mutations turned out to be gain of function mutations and appeared to increase PIP<sub>2</sub> affinity. Increased Kir2.6 currents would tend to hyperpolarize the cell and decrease excitability, possibly leading to weakness/paralysis.

These examples establish a pattern whereby the alteration of channel-PIP<sub>2</sub> interactions can be the underlying pathogenic mechanism for either gain or loss of function mutations associated with channelopathies. Disease-associated mutations that can be mapped to channel residues adjacent to the intracellular leaflet of the membrane may potentially exert their effects through modulation of channel-PIP<sub>2</sub> interactions. It should be noted that although mutation of a residue may alter the channel-PIP<sub>2</sub> interaction, it may play additional roles such as participation in intersubunit hydrogen bonds which could also affect gating.

## Concluding remarks

In the last decade, we have witnessed an impressive number of ion channels that employ quite diverse mechanisms of gating, ion selectivity, and permeation to display similar dependence of their activity on the plasma membrane phosphoinositide PIP<sub>2</sub>. Channel (basic

residues)–PIP<sub>2</sub> (negative phosphate) interactions exhibit a strong electrostatic component, but non-charged residues can also affect channel–PIP<sub>2</sub> interactions either directly or allosterically. The fundamental and widespread role of PIP<sub>2</sub> in controlling channel activity begs the question of whether already identified channelopathies of ion channels, whose activity depends on this phosphoinositide, operate in part or in whole by altering channel–PIP<sub>2</sub> interactions. Moreover, dysregulation of the phosphoinositide pathway can result in either too much or too little PIP<sub>2</sub>. It is likely that in such cases along with the many other important functions that phosphoinositides control, ion channel activity could become dysregulated, giving rise to channelopathies. It feels that we have only scratched the tip of the iceberg, and the realization of the fundamental importance of PIP<sub>2</sub> in ion channel function in the past decade will guide us in the coming decade to an appreciation of the ways in which disruption of channel–PIP<sub>2</sub> interactions due to either channel or phosphoinositide malfunctions can lead to disease.

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**Table 1**

Phosphoinositide (PIP)-sensitive channels

Channel	Tissue distribution	References on PIP-sensitive channels
Kir channels		
Kir1.1 (ROMK1)	Kidney>skeletal muscle>pancreas>spleen>heart=brain>liver [70]	[48, 53, 84, 110, 114, 122, 131, 172, 183, 225, 226]
Kir2.1 (IRK1)	Forebrain, skeletal muscle, heart, macrophage cells, aortic endothelial cells [70]	[50, 53, 84, 122, 153, 171, 172, 189, 230]
Kir 2.2 (IRK2)	Heart, forebrain, cerebellum, skeletal muscle, kidney [70]	[172]
Kir2.3 (IRK3)	Heart, hippocampus, amygdala, caudate nucleus, thalamus, kidney [70]	[50,172]
Kir2.4 (IRK4)	Retina, heart, striatum [70]	[172]
Kir2.6 (IRK6)	Skeletal muscle	[178] [178]
Kir3.2 (GIRK2)	Brain, pancreas, testis [70]	[84]
Kir3.1/3.2 (GIRK1/2)	Brain [70]	[82]
Kir3.1/3.4 (GIRK1/4)	Heart atria [70]	[32, 84, 99, 108, 136, 171, 172, 197]
Kir3.4-S143T (GIRK4*)	Experimental construct	[99, 172, 230]
Kir4.1	Forebrain, cerebellum, striatum, kidney, retina [70]	[172]
Kir4.2	Kidney, pancreas>lung>prostate, testes, leukocytes [70]	[172]
Kir4.1/Kir5.1	Brainstem nuclei, kidney [70, 220]	[220]
Kir6.1	Heart, ovary, adrenal gland>skeletal muscle, lung, brain, stomach, colon, testis, thyroid, pancreatic islet cells>kidney, liver, small intestine, pituitary gland [70]	[131]
Kir6.2- 36	Experimental construct	[7, 131, 172]
Kir6.2/SUR1	Brain, pancreas [25, 70]	[7, 40, 53, 124, 172, 186, 187]
Kir6.2/SUR2A	Heart [25, 70]	[53, 71, 78, 101, 172, 183, 217]
Kir6.2/SUR2B	Vascular smooth muscle cells [25, 70]	[53]
Kir7.1	(Human) small intestine>stomach, kidney, brain, thyroid, choroid plexus, retinal pigment epithelium (rat) lung, testis [70]	[172]
KirBac1.1	Bacteria	[30]
K2P channels		
K <sub>2p</sub> 2.1 (TREK1)	Brain, heart [67]	[28, 29, 121]
K <sub>2p</sub> 3.1 (TASK1)	Brain, heart, lung, kidney, pancreas, others [67]	[27, 28, 41, 121]
K <sub>2p</sub> 4.1 (TRAAK)	Brain, kidney, small intestine, placenta, prostate [67]	[121]
K <sub>2p</sub> 9.1 (TASK3)	Brain [67]	[27, 121]
Na <sup>+</sup> channels		
ENaC ( $\alpha/\beta/\gamma$ )	Kidney, lung, gastrointestinal tract and skin [92]	[102, 130, 158–160, 191, 201, 202, 223, 228]
Cl <sup>-</sup> channels		
CFTR	Heart, exocrine glands (pancreas, airways, gastrointestinal tract and sweat glands) [79]	[79]
P2X receptors (ATP-gated)		
P2X1	Smooth muscle, brain, cerebellum, dorsal horn spinal neurons and platelets [93]	[10, 233]



Channel	Tissue distribution	References on PIP-sensitive channels
P2X2	Nervous system (widespread) [93]	[59, 139, 233]
P2X3	Sensory neurons [93]	[139, 233]
P2X2/3	Sensory neurons [93]	[139]
P2X4	CNS synapses [93]	[9, 233]
P2X5	Brain, heart, spinal cord, adrenal medulla, thymus and lymphocytes [93]	[233]
P2X7	Macrophages, lymphocytes, microglia, osteoclasts, osteoblasts [31, 94]	[233]
Ionotropic glutamate receptors (iGluRs)		
Native NMDA receptors	Rat cortical pyramidal neurons [132]	[132]
NR1/NR2A	Mainly CNS [46]	[137]
NR1/NR2B	Mainly CNS [46]	[137]
NR1/NR2C	Mainly CNS [46]	[137]
Native AMPA receptors	Rat CA1 pyramidal neurons [4]	[4]
Ca <sup>2+</sup> -release channels		
Ins(1,4,5)P <sub>3</sub> receptor	Ubiquitous [58]	[65, 91, 127]
Ryanodine receptor (RyR1)	Skeletal muscle [165]	[98, 148]
Other channels		
Connexin Cx43	Widespread, dermal fibroblasts, glial cells, heart [104, 205]	[205]
Hair cell mechanotransduction channels	Frog saccular hair cells [81]	[81]
Volume-regulated anion channel (VRAC)	Widespread, epithelial cells [144]	[219]
Transporters and exchangers		
Plasma membrane Ca <sup>2+</sup> -ATPase (PMCA1)	Ubiquitous [26]	[33, 56, 142]
Na <sup>+</sup> /Ca <sup>2+</sup> exchanger (NCX1)	Cardiac myocytes, neurons, skeletal muscle, smooth muscle, kidney [18]	[5, 73, 77, 78, 161, 207, 222]
Na <sup>+</sup> /H <sup>+</sup> exchanger (NHE1)	Ubiquitous [147]	[1]
Na <sup>+</sup> /HCO <sub>3</sub> cotransporter (NBCe1-A)	Renal proximal tubule, eye [174]	[215]

This table summarizes ion channels that have been shown to be sensitive to phosphoinositide modulation and can be categorized in the following groups: inwardly rectifying potassium (Kir) channels, two-pore potassium (K2P) channels, sodium (Na<sup>+</sup>) channels, chloride (Cl<sup>-</sup>) channels, P2X receptors, ionotropic glutamate receptors (iGluRs), calcium (Ca<sup>2+</sup>)-release channels, and other channels. Transporters and exchangers that have been shown to be sensitive to phosphoinositides also appear in the corresponding group. The tissue distribution of each protein is provided on the second column, largely drawing from the IUPHAR database [70] but also from specific references that complement the database, as indicated. Specific references for the regulation of each channel/transporter by phosphoinositides are cited on the third column

**Table 2**

Phosphoinositide (PIP)-sensitive channels

Channel	Tissue distribution	References on PIP-sensitive channels
Kv channels		
Kv1.1/Kvβ1.1	Brain, heart, retina, skeletal muscle [70]	[149]
Kv1.3	(Human) T- and B-lymphocytes, alveolar macrophages, monocyte-derived macrophages, prostate epithelium, platelets, cerebral cortical grey matter, (rat) testis [70]	[135]
Kv1.4	(Human) brain, heart, pancreatic islet, (rat) skeletal muscle, arterial smooth muscle, retina [70]	[149]
Kv1.5/Kvβ1.3	(Rat) pulmonary arterial smooth muscle, spinal cord, brain, heart, (mouse) skeletal muscle, (human) pancreatic islet, atrial myocytes, atrium, ventricle [70]	[45]
Kv3.4	(Rat) parathyroid, prostate, brain, skeletal muscle, (mouse) pancreatic acinar cells [70]	[149]
Kv7.1 (KCNQ1)	(Human) heart=pancreas>kidney>lung=placenta, (mouse) intestine, stomach, liver, thymus [70]	[229]
Kv7.1 (KCNQ1)/KCNE1	Heart, inner ear [70, 123]	[123, 229]
Kv7.2 (KCNQ2)	(Human) brain (cortex and hippocampus), (rat) sympathetic ganglia, high expression levels in the cerebellum, cortex, and hippocampus [70]	[74, 75, 196, 229]
Kv7.3 (KCNQ3)	(Human) brain (cortex and hippocampus), (rat) sympathetic ganglia, lower expression levels in the cerebellum than in cortex and hippocampus [70]	[74, 75, 111]
Kv7.2/7.3 (KCNQ2/3)	Brain [70]	[57, 74, 111, 152, 170, 193, 196, 212, 224, 229]
Kv7.4 (KCNQ4)	Cochlea (outer hair cells), brainstem auditory nuclei [70]	[74, 75, 111, 229]
Kv7.5 (KCNQ5)	Brain, skeletal muscle [70]	[229]
Kv11.1 (HERG)	Heart, brain, gut, pancreatic beta cells, kidney, others [70]	[12, 13, 80]
CNG (cGMP-gated) channels		
Native rod CNG channel	Bovine rod outer segment [213]	[213]
Native olfactory CNG channel	Rat olfactory receptor neurons [227]	[227]
CNGA1	Retina, pineal gland, some neurons [70]	[213]
CNGA1/B1	Retina [70]	[213]
CNGA2	Olfactory neurons, hippocampus [70]	[20, 227]
CNGA2/CNGA4	Olfactory neurons [70]	[227]
CNGA3/CNGB3	Retina	[22]
Hyperpolarization-activated channels (HCN)		
HCN1	Brain, retina, sinoatrial node cells [70]	[154, 235]
HCN2	Brain, retina, heart [70]	[154, 155]
HCN4	Brain, retina, heart, testis [70]	[235]
K <sub>Ca</sub> channels		
K <sub>Ca</sub> 1.1 (SLO1)	Ubiquitous, brain, skeletal muscle, smooth muscle, adrenal cortex, cochlear hair cells, pancreas, colon, kidney [211]	[204]
Ca <sub>v</sub> channels		
Ca <sub>v</sub> 1.2 (L-type)	Heart, brain, prostate, bladder, uterus, stomach, colon, small intestine, placenta, adrenal gland, spinal cord [70]	[138, 234]

Channel	Tissue distribution	References on PIP-sensitive channels
Ca <sub>v</sub> 2.1 (P/Q-type)	Brain, heart, pancreas, pituitary [70]	[176, 214, 234]
Ca <sub>v</sub> 2.2 (N-type)	Brain, spinal cord [70]	[62, 106, 170, 214]
TRP channels		
TRPV1	Dorsal root ganglia, brain, kidney, pancreas, testes, uterus, spleen, stomach, small intestine, lung, liver [70]	[21, 36, 117, 126, 164, 192, 221]
TRPV1t (taste receptor variant)	Rat chorda tympani taste nerve [128]	[128]
TRPV5	Kidney, prostate, testes, placenta, pancreas, brain [70]	[107]
TRPV6	Intestines, stomach, placenta, salivary glands, liver, prostate, pancreas, kidney, testes, mammary glands [70]	[199, 200]
TRPM4	Small intestine, prostate, colon, kidney, testes, heart, lymphocytes, spleen, lung, brain, pituitary, skeletal muscle, stomach, adipose tissue, bone [70]	[145, 231]
TRPM5	Taste tissue, stomach, intestines, uterus, testis [70]	[115]
TRPM7	Ubiquitous, heart, pituitary, bone, adipose tissue [70]	[177]
TRPM8	(Rat) dorsal root ganglia, trigeminal ganglia, (human) prostate, testis, bladder>breast, thymus [70]	[21, 43, 116, 173, 206]
TRPA1	Brain, heart, small intestine, lung, skeletal muscle, and pancreas (mouse) dorsal root ganglia, trigeminal ganglia, nodose ganglia, nociceptive neurons, inner ear (organ of corti) [70]	[2, 42, 95]
TRPC1	Heart, brain, lung, liver>spleen, kidney, testis [70]	[179]
TRPC3	Pituitary gland>brain, heart, lung, dorsal root ganglia [70]	[109]
TRPC4	Heart, brain, pancreas, placenta, kidney [70]	[150]
TRPC5	(Mouse) brain, testis, kidney, uterus [70]	[203]
TRPC6	Heart, lung, kidney, muscle, intestine, stomach, pancreas, prostate, bone, brain [70]	[3, 87, 103, 109]
TRPC7	Kidney, intestine, pituitary gland, brain [70]	[109]
TRPC1/C5/C6	Rabbit coronary artery myocytes [180]	[180]

This table summarizes ion channels that have been shown to be sensitive to phosphoinositide modulation and can be categorized in the following groups: voltage-gated potassium (K<sub>v</sub>) channels, cyclic nucleotide-gated (CNG) channels, hyperpolarization-activated (HCN) channels, calcium-activated potassium (K<sub>Ca</sub>) channels, voltage-gated calcium (Ca<sub>v</sub>) channels, and transient receptor potential (TRP) channels. The tissue distribution of each channel is provided on the second column, drawing from the IUPHAR database [70] and from specific references complementing the database, as indicated. The tissue distribution shown for Kv1.1/Kvβ1.1 and Kv1.5/Kvβ1.3 heteromers pertains to Kv1.1 and Kv1.5, respectively. Specific references for the regulation of each channel by phosphoinositides are cited on the third column