

Chapter 3

Adenosine Receptors: Structure, Distribution, and Signal Transduction



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Abstract Adenosine receptors A_1 , A_{2A} , A_{2B} , and A_3 are effector proteins triggered by the endogenous nucleoside adenosine to exert its numerous vital physiological effects, behaving like a guardian angel. This chapter offers an overview of the updated knowledge concerning the structure, distribution, and signal transduction of adenosine receptors. They are a family of G protein-coupled receptors widely distributed through the body, from central nervous system to peripheral organs, important and ubiquitous regulators of numerous cellular signaling. Their presence on every cell renders them an attractive opportunity for the pharmacological research and development of new drugs but also a challenge in the difficulty to produce tissue-selective ligands avoided of side effects. To aid this process, several efforts have been invested to reveal the molecular structure and the consequent mechanism of ligand binding of these receptors, and until now more than 30 structures have been published for the human A_{2A} subtype. Finally, the principal adenosine receptor signaling pathways including adenylyl cyclase, phospholipase C, inositol triphosphate, diacylglycerol, phosphatidylinositol 3-kinase, and mitogen-activated protein kinases determining their effects on several transcription factors, such as hypoxia-inducible factor 1, cyclic AMP (cAMP)-responsive elements, nuclear factor- κ B, and exchange protein directly activated by cAMP as the most relevant, are presented.

Keywords Adenosine receptors · Signal transduction · cAMP · Distribution · Kinases

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3.1 Introduction

Adenosine is a purine nucleoside released by almost all cells mediating its effects through activation of four G protein-coupled adenosine receptors, classified as A₁, A_{2A}, A_{2B}, and A₃ (Borea et al. 2016). The first demonstration of their existence has been offered more than 40 years ago by the observation that methylxanthines such as caffeine and theophylline were able to antagonize the cardiac and cerebral effects of adenosine. These receptors are characterized by different affinity for adenosine, G protein coupling, as well as intracellular signal transduction inside cells. In general adenosine interacts with A₁, A_{2A}, or A₃ subtypes with an EC₅₀ in the range 10 nM–1 μM, while activation of the A_{2B} subtype needs concentrations higher than 10 μM, rarely obtained in physiological conditions but present in hypoxic/injured tissues (Eltzschig 2009). Anyway, the affinity of adenosine to its receptors may also depend on the effect investigated, e.g., cAMP level determination versus MAPK activation or the number of receptors expressed (Chen et al. 2013). Specifically, on the one hand, A₁ and A₃ adenosine receptors show high and low affinity for adenosine, respectively, and are able to reduce adenylyl cyclase activity. On the other hand, A_{2A} and A_{2B} subtypes display high and low affinity for the nucleoside, respectively, and activate adenylyl cyclase, thus stimulating cyclic AMP (cAMP) levels (Fredholm et al. 2011; Borea et al. 2017). Adenosine receptors are present in every organ, tissue, and cell of the body rendering them attractive targets for the research and development of new drugs in many pathological conditions related with raised adenosine levels (Gessi et al. 2011). Anyway this wide distribution implies the lack of specificity of a given receptor subtype that may be present in both tissues involved in disease but also in healthy organs with consequent side effects, rendering difficult the development of drugs for specific medical needs. In this chapter updated informations concerning the molecular structure, distribution, and signal transduction of adenosine receptors are provided.

3.2 Molecular Structures of Adenosine Receptors

Adenosine receptors have been cloned in the beginning of the 1990s and deeply pharmacologically characterized and consist of a similar structure represented by a core domain crossing the plasma membrane seven times, with an extracellular N-terminus, an intracellular C-terminus, and three intracellular and three extracellular loops (IL and EL, respectively) of different lengths and functions among the four adenosine receptor subtypes (Fredholm et al. 2000). These domains give specific characteristics important for receptor-ligand interactions. Specifically, the EL1, EL2, and EL3 of GPCRs contribute significantly to receptor function as evidenced by crystal structures, and cysteine amino acids forming disulfide bonds in the EL domains of GPCRs are important not only in ligand binding but also in receptor stability and function (Avlani et al. 2007; Schiedel et al. 2011). The N-terminus presents one or more glycosylation sites, while the C-terminus

possesses phosphorylation and palmitoylation loci, which are important for receptor desensitization and internalization. Specifically, mutation studies revealed that glycosylation is relevant for the recruitment of receptors to the plasma membrane, while palmitoylation sites, located at the end of helix 8 and absent in A_{2A} adenosine receptors, influence receptor degradation. Depalmitoylation of A_3 adenosine receptors, in contrast to what happens for A_1 subtype, induces a fast receptor desensitization through GPCR kinase phosphorylation induction (Pirainen et al. 2011). Adenosine receptors are characterized by a high homology sequence among them, ranging from 41% to 58% of sequence identity for the human species, with the most conserved region being in the extracellular region of the receptor reaching 71%.

3.2.1 A_1 Adenosine Receptors

A_1 adenosine receptors are 326 amino acid long distributed among 7 transmembrane domains (TM) of which TM3 and TM7 result strictly conserved sequences for ligand interaction with the receptor, as reported from mutagenesis studies (Jespers et al. 2018). The A_1 AR orthosteric site is found inside the TM packet, but also EL2 has been implicated in the ligand affinity and signal transduction (Peeters et al. 2012; Nguyen et al. 2016a, b). In addition, in the A_1 adenosine receptor EL2, the presence of an allosteric site has been reported through molecular modeling characterization (Narlawar et al. 2010). Recently, the crystal structure of A_1 adenosine receptors bound to a selective covalent antagonist has been revealed (Glukhova et al. 2017). Interestingly, significant differences with respect to already presented A_{2A} adenosine receptor structure indicate a different conformation of EL2 and a bigger extracellular cavity presenting an alternative binding pocket accepting both orthosteric and allosteric molecules. It has been suggested that this configuration confers ligand selectivity instead of the simple amino acid sequence. From this knowledge more selective drugs could be projected with both agonist and allosteric properties, useful for the therapy of neuropathic pain, ischemia-reperfusion damage, and renal pathologies (Glukhova et al. 2017; Cheng et al. 2017).

As for allosteric sites located on the EL region, a crystal structure with an allosteric modulator has not been provided but through mutagenesis studies the amino acid sequence responsible for these ligands involved in the binding site of A_1 AR allosteric modulators (Jespers et al. 2018) has been reported.

3.2.2 A_{2A} Adenosine Receptors

A_{2A} adenosine receptors in human species are 412 amino acid long, but this number may slightly change from 409 to 412 in other species (de Lera Ruiz et al. 2014). At variance with other adenosine subtypes, it presents a long carboxy-terminal

domain, responsible for a major molecular weight (45 kDa) with respect to the other adenosine subtypes (Preti et al. 2015). A_{2A} adenosine receptors are formed by 7 TM of 20–27 amino acids with TM3 and EL2 containing cysteine residues giving a disulfide bond. In addition an extra short TM8 domain is present toward the membrane cytoplasmic surface (Jaakola and IJzerman 2010; de Lera Ruiz et al. 2014). Interestingly, two new cholesterol-binding sites have been described on it, one of which interacts with cholesterol only when bound to an inverse agonist, as demonstrated through numerous high-resolution crystal structure studies (Rouviere et al. 2017). Indeed, the last 10 years have seen a huge development of novel crystallization strategies that have introduced enormous changes in the knowledge of structural biology of GPCRs. Specifically, the A_{2A} adenosine receptor has been one of the best studied and characterized by a structural point of view, having more than 30 structures been described (Carpenter and Lebon 2017). In particular, crystal structures of A_{2A} adenosine receptors have been solved in complex with both agonists and antagonists, which provide informations concerning the binding sites and the conformational changes occurring following ligand-receptor interactions (Jaakola et al. 2008; Xu et al. 2011; Lebon et al. 2011, 2015; Doré et al. 2011; Hino et al. 2012; Congreve et al. 2012; Liu et al. 2012; Carpenter et al. 2016; Jazayeri et al. 2017; Carpenter and Lebon 2017). Specifically, the most observed phenomenon taking place after binding of the agonist is a contraction of the binding site due to TM3, 5, 6, and 7 rearrangements (Jespers et al. 2018). In addition an outward rotation of TM6 on the cytoplasmic side, consequent to receptor activation, allows G protein activation and signal transduction propagation. In addition it has been revealed that the ribose moiety is a key component of A_{2A} receptor agonists that helps to stabilize the intermediate-active state before the occurrence of the fully active receptor conformation, following G protein coupling (Carpenter and Lebon 2017). Numerous mutagenesis studies investigating the ligand binding of A_{2A} adenosine receptors have been performed. Interestingly, from them, the relevance of a glutamic acid and a histidine in TM1 and TM7, respectively, has been found taking part into the agonist binding process. In addition a relevant role for H bonds in ligand binding affinity has been revealed following the observation that loss of interactions between ligand and water is reflected in worsen affinity of both agonists and antagonists (Jespers et al. 2018). Overall from the data emerging by complementary techniques such as crystal structures as well as X-rays and mutagenesis studies, it is possible today to address a structure-based rationale design of new ligands interacting with A_{2A} adenosine receptors (Jespers et al. 2017).

3.2.3 A_{2B} Adenosine Receptors

A_{2B} adenosine receptors in human species are 328 amino acid long, organized following the typical GPCR architecture consisting of 7 TM domains presenting the highest homology between A_{2B} and the other adenosine receptors. This core is formed by hydrophobic amino acids linked by three EL and three IL and terminates

with an extracellular N-terminus and an intracellular C-terminus. Combination of homology modeling of rhodopsin GPCR structure and mutational studies of the A_{2B} adenosine receptors leads to the knowledge of its binding site, where TM regions 3, 5, 6, and 7 are involved in agonist and antagonist recognition (Beukers et al. 2000, 2004; Aherne et al. 2011). Interestingly, the EL2 of A_{2B} receptor, the longest of all the other adenosine receptor subtypes, presents four cysteine amino acids (C154, C166, C167, C171) responsible for disulfide bonds connecting EL and TM domains. Interestingly, only disulfide bond occurring between C171 in EL2 and C78 present in TM3 is essential for A_{2B} adenosine receptor-ligand binding and function, and it may also play a role in the transport of the receptors toward the membrane. As for the other cysteine residues in the ECL2 of the A_{2B} receptor, they may have different functions in comparison to the role that they play in the A_{2A} receptor (Schiedel et al. 2011). In addition subsequent site-directed mutagenesis studies have reported that introducing ECL2 of A_{2A} adenosine receptors in the structure of A_{2B} adenosine receptors provides a mutant A_{2B} receptor that displays higher affinity for both agonist and antagonists, thus suggesting that ECL2 is crucial for ligand binding. Therefore the major length of ECL2 in the A_{2B} adenosine subtype is responsible for the lower affinity of ligands to it in comparison to A_{2A} receptors, because it may hamper the ligand interaction to the binding site (Schiedel et al. 2011; Seibt et al. 2013; da Rocha Lapa et al. 2014). Other mutational studies have discovered the amino acids involved in ligand binding of three different classes of molecules including xanthine, adenosine, and aminopyridine derivatives. In particular, the amino acids Asn282 and His280 by forming H bond stabilize the binding site as occurs in the A_{2A} adenosine receptor. Trp247, Val250, and especially Ser279 are crucial for adenosine binding. Leu81, Asn186, and Val250 are important for binding of the xanthine antagonists (Thimm et al. 2013).

3.2.4 A_3 Adenosine Receptors

A_3 adenosine receptors in human species are 318 amino acid long. As with the other adenosine receptors, the A_3 is constituted by seven TM domains with an intracellular C-terminal sequence containing six Ser and Thr amino acids undergoing phosphorylation by GPCR kinases during rapid receptor desensitization occurring in the order of minutes. Specifically, this process triggered following agonist binding to the A_3 adenosine receptors causes subsequent internalization through clathrin-coated pits in rat A_3 adenosine receptors (Palmer and Stiles 2000; Trincavelli et al. 2002a, b; Madi et al. 2003; Pugliese et al. 2007; Jacobson et al. 2018). However, the fast desensitization has not been observed in A_1 , A_{2A} , and A_{2B} receptor subtypes where this process takes place after hours. The reason for this discrepancy has been attributed to the lack of Ser and Thr residues in the C-terminus, for example, of the A_1 subtype. Another reason explaining the rapid desensitization of A_3 receptors resides in the presence of Cys amino acids in its C-terminus tail, crucial for GRK activation. As the sequence identity between rat and human A_3 receptors is only

72%, this point has been recently addressed. Specifically, it has been shown that the C-terminus of the human subtype is not involved in β arr2 recruitment, receptor desensitization, and internalization, suggesting that other different regions of the human A_3 adenosine receptors, either cytosolic or exposed upon receptor activation, are involved in this process. It has been observed that C-terminal truncation, in combination with mutation of the “DRY” motif located at the boundary between TM3 and IL-2, significantly decreased β arr2 recruitment (Storme et al. 2018). Interestingly, mutational studies demonstrated that the active shape of the human A_3 receptor needs the highly conserved Trp (W6.48) in TM6, important to activate signal transduction pathways, to interact with β -arrestin2, and to undergo receptor internalization (Gao et al. 2002; Stoddart et al. 2014). Furthermore, use of a novel fluorescent A_3 agonist has allowed for the observation of co-localization with internalized receptor β arr3 complexes (Stoddart et al. 2015).

3.2.5 Adenosine Receptor Heteromers

Homomer, oligomer, and heteromer formation has been recently recognized as a common phenomenon affecting numerous GPCRs including adenosine receptors (Ferré et al. 2010a, b; Navarro et al. 2010a, b, 2016b; Brugarolas et al. 2014). The possibility of homo- or hetero-oligomer formation lies on, at least in part, high receptor levels (Fredholm et al. 2011). Specifically, GPCR heteromers are new entities for signal transduction with different functions if compared to homomers. In the field of adenosine receptors, A_1 - A_{2A} oligomers are present in neural tissue, comprising two different receptors coupled to two different G proteins (Brugarolas et al. 2014; Navarro et al. 2016b). In particular the A_1 component, through G_i and the A_{2A} part via G_s , confers to the heteromer the possibility to signal in an opposite way on cyclic adenosine monophosphate (cAMP) intracellular pathway. Therefore, this complex constitutes a cell surface sensor of adenosine concentration, distinguishing between low and high nucleoside concentration (Navarro et al. 2016b). Indeed the A_1 unit of this complex interacts with G_i/o protein, thus decreasing cAMP levels, PKA, and GABA uptake, when adenosine levels are low. The A_{2A} monomer of the heteromer takes place in cAMP signaling when adenosine levels increase, due to its inhibition of A_1 component and activation of G_s proteins, thus obtaining GABA uptake increase (Cristóvão-Ferreira et al. 2013). In addition various physiological process, such as glutamate release, may be regulated on the basis of adenosine concentration (Ciruela et al. 2006). Heteromerization has been described as a general process involving other receptors inside adenosine receptor family including A_3 ARs, forming homodimers and A_1 - A_3 heterodimers (Kim and Jacobson 2006; Hill et al. 2014). In addition, heteromerization involves also the interaction of adenosine receptors with other GPCRs. For example, A_1 may form oligomers with P2Y1 (Yoshioka et al. 2001), D1 dopamine (Ginés et al. 2000), and mGlu1 α R receptors (Ciruela et al. 2001). As for A_{2A} receptors, the most studied combination in this field is represented by the A_{2A} -D₂ dopamine complex, detected in the striatum, and a viable therapeutic target in PD (Fuxe et al. 2005, 2007; Ferré et al. 2010b; Navarro

et al. 2016a). In addition they may oligomerize with mGlu5 (Ferré et al. 2002), P2Y1 (Arellano et al. 2009), and cannabinoid CB1 receptors (Carriba et al. 2007).

3.3 Distribution of Adenosine Receptors

Adenosine receptors are widely distributed throughout the body spanning from the central nervous system, cardiovascular apparatus, respiratory tract, gastrointestinal tissue, and immune system to different organs or tissues including the kidney, bone, joints, eyes, and skin, suggesting a wide influence of adenosine in almost all physiological processes (Peleli et al. 2017). This distribution reflects a significant function of adenosine in the neurons, heart, and kidney.

3.3.1 A_1 Adenosine Receptors

In the brain A_1 adenosine receptors are highly distributed in different regions, including the cortex, hippocampus, cerebellum and spinal cord, autonomic nerve terminals, and glial cells (Chen et al. 2013; Ballesteros-Yáñez et al. 2018). In the heart, A_1 adenosine receptor expression has been detected with higher levels in atria and less in the ventricular myocardium (Varani et al. 2017). At vascular level A_1 adenosine receptors are present on coronary smooth muscle arteries and endothelial cells (Headrick et al. 2013). Furthermore, A_1 adenosine receptors are found in the lung endothelial cells, in smooth muscle cells of airway, in alveolar epithelial cells, and in macrophages (Sun et al. 2005). In the kidney, A_1 adenosine receptors are located in the collecting ducts of the papilla, inner medulla, and cells of the juxtaglomerular apparatus (Varani et al. 2017; Soni et al. 2017). A_1 adenosine receptors are expressed in pancreas tissues and adipocytes (Meriño et al. 2017). As for immune system, A_1 adenosine receptors are present on different immune cells, such as neutrophils, eosinophils, macrophages, and monocytes (Sachdeva and Gupta 2013; Boros et al. 2016). A_1 adenosine receptors have also been localized in the retina, intestine, skeletal muscle, and vascular cells of skeletal muscle (Varani et al. 2017).

3.3.2 A_{2A} Adenosine Receptors

A_{2A} adenosine receptors are mostly expressed in selected areas of the central nervous system as well as in peripheral immune cells. Specifically, concerning brain regions A_{2A} adenosine receptors are expressed at high level in striatal neurons, while lower presence has been detected in extra-striatal and in glial cells (Fredholm et al. 2011; Boison et al. 2012; Borea et al. 2017). In particular, they are numerous in the caudate and putamen, in the nucleus accumbens, as well as in the olfactory tubercle.

The presence of A_{2A} adenosine receptors has been demonstrated in the heart, in both atria and ventricle and in coronary vessels, but also in the lung and liver. Finally, high expression of A_{2A} adenosine receptors has been reported in platelets, lymphocytes, neutrophils, monocytes, macrophages, dendritic cells, vascular smooth muscle, and endothelial cells (Gessi et al. 2000).

3.3.3 A_{2B} Adenosine Receptors

At the central level, the A_{2B} adenosine receptors are expressed in astrocytes, neurons, and microglia (Koupenova et al. 2012; Merighi et al. 2015; Pedata et al. 2016). As for the periphery, they are found in the bowel, bladder, lung, vas deferens, and different cell types including fibroblasts; smooth muscle, endothelial, alveolar epithelial, chromaffin, and taste cells; platelets; myocardial cells; and retinal, intestinal and pulmonary epithelial, and endothelial cells. A_{2B} adenosine receptors are expressed in several immune cells including mast cells, macrophages, lymphocytes, neutrophils, and dendritic cells (Aherne et al. 2011).

3.3.4 A_3 Adenosine Receptors

A_3 adenosine receptors are present in several cells and tissues with a different degree of expression at central and peripheral level. In the brain tissue, they are present in low amount in the thalamus, hypothalamus, and hippocampus. At cellular level they are expressed in motor nerve terminals, microglia, astrocytes, cortex, and retinal ganglion cells while at cerebral vascular level in the pial and intercerebral arteries (Janes et al. 2014; Borea et al. 2016). A_3 adenosine receptors are present in the coronary and carotid artery and in the heart but only at low level. At the periphery A_3 adenosine receptors have been demonstrated in lung parenchyma and bronchi, enteric neurons and colonic mucosa, and epithelial cells. Finally, A_3 adenosine receptors have a wide distribution in immune and inflammatory cells including lymphocytes, neutrophils, eosinophils, monocytes, macrophages, dendritic cells, foam cells, mast cells, splenocytes, bone marrow cells, lymph nodes, synoviocytes, chondrocytes, and osteoblasts. Interestingly, A_3 adenosine receptors are overexpressed in different cancer tissues such as the colon, liver, lung, melanoma, and glioblastoma (Borea et al. 2015).

3.4 Signal Transduction of Adenosine Receptors

All adenosine receptors are coupled to G proteins and trigger several transduction pathways that may differ depending on the specific cell activated (Fredholm et al. 2001).

3.4.1 *A₁ Adenosine Receptors*

The Gi-coupled A₁ adenosine receptor inhibits adenylyl cyclase (AC) activity thus decreasing cAMP levels. This leads to the inhibition of cAMP-dependent protein kinase A (PKA) activation and cAMP-responsive element-binding protein 1 (CREB-1) phosphorylation, resulting in the reduction of CREB transcriptional activation. In addition it also induces phospholipase C (PLC)-β stimulation, by link to Gq proteins, thus rising diacylglycerol (DAG) and inositol 1,4,5-triphosphate (IP₃) that, through interaction with its cytoplasmic receptor, rises intracellular Ca²⁺ concentrations, which activate calcium-dependent protein kinases (PKC) and/or other calcium-binding proteins. PKC may be phosphorylated also by DAG. In addition, βγ subunits of Gi/o protein are involved by A₁ adenosine receptor to induce PLC activation (Biber et al. 1997). In addition A₁ adenosine receptor enrolls pertussis-toxin-sensitive potassium (K) and K_{ATP} channels, expressed in neurons and myocardium, while reduces Ca²⁺ channels of Q, P, and N type. Recently, it has been reported that it increases PC12 cell damage following intermittent hypoxia through PKC and K_{ATP} mediators (Mei et al. 2018). Furthermore, the first report describing the link between A₁ adenosine receptor and the family of mitogen-activated protein kinase (MAPK) indicated the stimulation by it of extracellular signal-regulated kinase (ERK) (Schulte and Fredholm 2000) (Fig. 3.1). Since then many studies have found different effects on MAPK modulation depending on the cell investigated. For example, it has been reported that A₁ adenosine receptor in brain neurons increases p38 to reduce apoptosis in a rat model of brain injury (Zhai et al. 2016). Accordingly, it activates p38 and also c-Jun N-terminal kinase (JNK) in hippocampal neurons, thus inducing clathrin-mediated internalization of GluA2 and GluA1 subunits responsible for synaptic depression that caused hippocampal neurodegeneration after hypoxia/cerebral ischemia (Brust et al. 2006; Liang et al. 2008; Chen et al. 2014). Previous data in the hippocampus demonstrated that the increase in p38 phosphorylation induced by A₁ receptor was involved in brain-derived neurotrophic factor (BDNF) generation (Katoh-Semba et al. 2009). In astrocytes, A₁ adenosine receptor reduces ERK and AKT, thus provoking the inhibition of LPS-induced hypoxia-inducible factor (HIF)-1α activation with reduction of genes involved in inflammation and hypoxic injury (Gessi et al. 2013). In ear cochlea, it inhibits p38, ERK, and JNK activation and decreases cisplatin-induced signal transducer and activator of transcription (STAT-1) phosphorylation, thus reducing apoptosis and inflammation. This mechanism may be relevant to provide otoprotection against ototoxicity induced by this chemotherapeutic drug (Kaur et al. 2016). In cardiomyocytes, A₁ adenosine receptor phosphorylates p38, present downstream the mitochondrial K(ATP) channel, protecting cells from hypoxia injury (Leshem-Lev et al. 2010). Accordingly, in these cells it activates p38, ERK, and JNK phosphorylation, producing an increase of tissue transglutaminase (TG2) and cytoprotection (Vyas et al. 2016). An increase of p38 was also discovered in the reduction by A₁ adenosine receptor of beta-adrenergic-induced contractile function as a mechanism of adenoprotection (Fenton et al. 2010). In mouse coronary artery smooth muscle cells, it activates the PKC-alpha transduction pathway, causing ERK phosphorylation (Ansari et al. 2009). In foam cells, A₁ adenosine

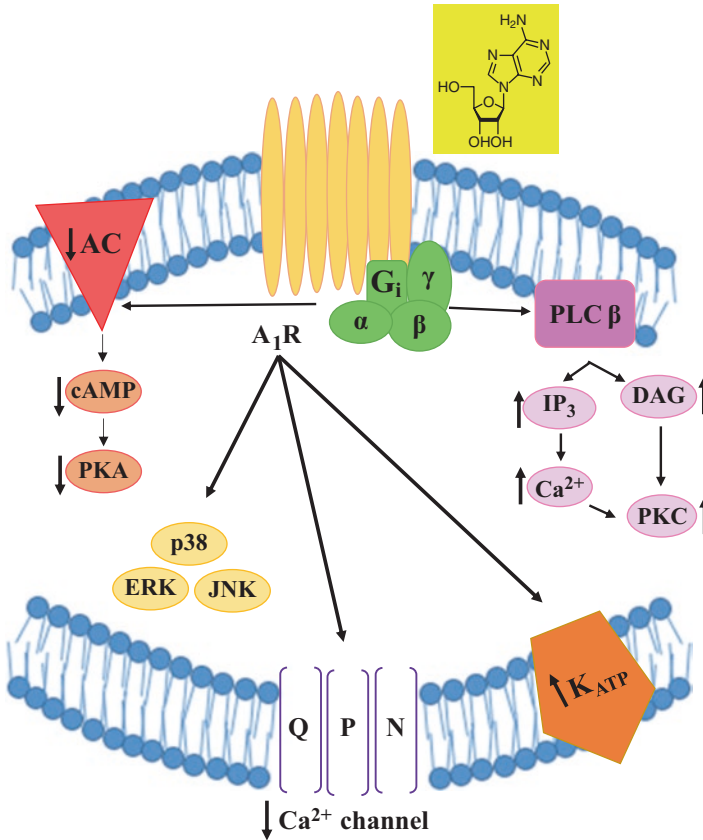


Fig. 3.1 Schematic picture of A₁ adenosine receptor signaling cascade. Adenosine activates A₁R to reduce AC activity and cAMP levels thus blocking PKA and CREB while stimulates PLC-β and Ca²⁺. In addition adenosine triggers K⁺ channels and inhibits Q, P, N, and Ca²⁺ channels. p38, ERK1/2, and JNK1/2 phosphorylation is determined by A₁R stimulation

receptor contributed to atherosclerosis by inducing HIF-1 accumulation through an increase of p38 and AKT phosphorylation (Gessi et al. 2010a). In contrast in neutrophils, it reduces p38 thus decreasing chemotaxis (Xu et al. 2017). Together, these data indicate that modulation of MAPK signaling, especially the one related to p38 phosphorylation, by A₁ adenosine receptor occurs in different organs and tissues thus affecting numerous pathological processes.

3.4.2 A_{2A} Adenosine Receptors

The Gs-coupled A_{2A} adenosine receptor stimulates AC activity, thereby increasing cAMP levels, with consequent PKA phosphorylation that causes activation of numerous proteins, including receptors, phosphodiesterases, cAMP-responsive

element-binding protein (CREB), and dopamine- and cAMP-regulated phosphoprotein (DARPP-32) (Preti et al. 2015). Interestingly, in hepatocyte membranes two different cAMP-responsive macrocomplexes activated by adenosine have been demonstrated that contain their own sequestered cAMP pools to generate their selective effects. One of these complexes responds to A_{2A} adenosine receptor that activates AC6, linked to A-kinase-anchoring proteins (AKAP)79/150, to produce cAMP available for AKAP79/150-tethered proteins, named protein kinase A (PKA) and phosphodiesterase 3A (PDE3A). The other complex responds to A_{2B} adenosine receptor, and the novel generated cAMP does not diffuse between these “signalosomes,” thus suggesting that a spatiotemporal regulation of cAMP exists in the cell to obtain receptor-specific responses (Guinzburg et al. 2017). In addition, in the brain, A_{2A} adenosine receptor regulates a specific neuron type of Gs protein named Golf, which is also related to AC (Kull et al. 2000). In the rat tail artery, it promotes noradrenaline release through both PKC and PKA recruitment (Fresco et al. 2004). A_{2A} adenosine receptor may also bind, through its long C-terminus, to various accessory proteins including D_2 dopamine receptors, α -actinin, ADP ribosylation factor nucleotide site opener (ARNO), ubiquitin-specific protease (USP4), and translin-associated protein X (TRAX) (Baraldi et al. 2008). Importantly, A_{2A} adenosine receptor plays a role in the regulation of MAPK affecting the transduction pathway of several cells from different organs and tissues (Baraldi et al. 2008; Chen et al. 2013) (Fig. 3.2). In neutrophils, A_{2A} adenosine receptor by increasing cAMP decreases phosphorylation of p38, ERK, PI3K/AKT, Hck, and Syk, thus inducing inhibition of their functions (Giambelluca and Pouliot 2017). Accordingly, in the same cells, the agonist ATL313 was able to suppress selectin-mediated activation of Src kinases (SFKs) and p38, thus reducing cell adhesion (Yago et al. 2015). In contrast, an increase in ERK, nuclear factor (NF)- κ B, and pSTAT was involved in the reduction of inflammatory cytokines produced by methotrexate through A_{2A} receptor activation in T cells (Ma et al. 2018). In dermal fibroblasts the A_{2A} receptor increases collagen (col) 1 and 3 production via cAMP, PKA, ERK, p38, and AKT pathways, confirming data obtained in hepatic stellate cells where collagen 1 production was influenced also by A_{2A} receptor-mediated ERK activity (Chan et al. 2006; Che et al. 2007; Shaikh and Cronstein 2016). It is known that also Wnt signaling is important in fibrosis where cAMP and Wnt pathways may converge. In this context it has been found that A_{2A} receptor increases synthesis of collagen 3 through the activation of β -catenin, suggesting a role for this subtype in dermal fibrosis and scarring (Shaikh and Cronstein 2016). In normal skin col1 is more expressed than col3 that increases in immature scars and is then replaced by col1 in mature scars, a process regulated by A_{2A} receptor and Epac2. At nanomolar levels of adenosine, the receptor via PKA induces col1 and reduces col3 production, respectively. At higher levels, the raised cAMP levels promote Epac2 signaling producing col3 (Perez-Aso et al. 2012, 2014). In mice adipose tissue, A_{2A} receptor stimulation induces an increase in p38 phosphorylation, thus resulting in improvements in glucose homeostasis and adipose tissue inflammation (DeOliveira et al. 2017). In the brain, following ischemia-reperfusion (IR) damage, a huge increase of adenosine stimulates A_{2A} receptor to potentiate neuronal injury by increasing ERK and consequently

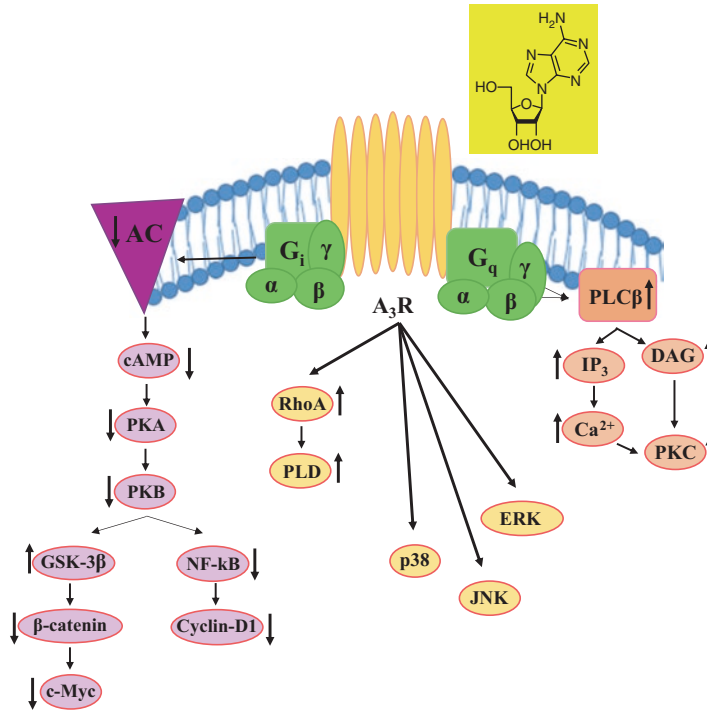


Fig. 3.2 Schematic picture of A_{2A} adenosine receptor signaling cascade. Stimulation of A_{2A}R by adenosine rises AC activity and increases cAMP levels, PKA, and CREB phosphorylation. In addition its stimulation enrolls AKT, p38, ERK1/2, and JNK1/2

stimulating microglial activation, glial tumor necrosis factor- α (TNF- α) and BDNF, glutamate, inducible nitric oxide synthase (iNOS), as well as apoptosis (Mohamed et al. 2016). In an *in vitro* model of osteoclast, differentiation occurs through activation of A_{2A} receptor activation of PKA and ERK1/2, thus inhibiting NF- κ B nuclear translocation (Mediero et al. 2013). In cancer cells, A_{2A} receptor activation stimulates proliferation phospholipase C (PLC), protein kinase C-delta (PKC- δ), ERK, JNK, and AKT (Gessi et al. 2017). Accordingly, the same effect was reached by combination of TLR2 and adenosine receptor agonists, through ERK stimulation, in oral squamous carcinoma cells (Palani et al. 2018).

3.4.3 A_{2B} Adenosine Receptors

The G_s-coupled A_{2B} adenosine receptor activates AC, causing phosphorylation of PKA and recruitment of various effectors like guanine nucleotide exchange factor 2 (Epac), directly stimulated by cAMP. However it has been recently reported that a complex constituted by A_{2B} receptor stimulates AC5 bound to D-AKAP2 to generate cAMP, activating two other tethered proteins named Epac2 and PDE3B

(Guinzberg et al. 2017). Epac activation by A_{2B} receptor stimulation has been previously reported to affect cell proliferation in human umbilical vascular endothelial cells and to induce early gene expression decreasing cell proliferation in human coronary artery smooth muscle cells (Fang and Olah 2007; Mayer et al. 2011). In addition, by enrolling Gq proteins, it triggers PLC activation, thus determining Ca^{2+} increase, and through $\beta\gamma$ subunits modulates ion channels. Furthermore, A_{2B} adenosine receptor presents numerous binding actors that influence its responses and effects such as netrin-1, E3KARP-ezrin-PKA, SNARE, NF- κ B / P105, and α -actinin-1. Specifically, netrin-1 is a neuron protein hypoxia-dependent, which by binding to A_{2B} adenosine receptor reduces neutrophil migration and consequent inflammation (Rosenberger et al. 2009). SNARE protein is responsible for the translocation of the receptor from the cytoplasm to the cell membrane in the presence of an agonist through a mechanism involving (Wang et al. 2004) a structure composed by E3KARP (NHERF2) and ezrin which fixes A_{2B} adenosine receptor at cell surface (Sitaraman et al. 2002). In particular, A_{2A} and A_{2B} receptor dimerization is induced by α -actinin-1 promoting expression of the A_{2B} subtype on the cell surface (Moriyama and Sitkovsky 2010). In addition, it interacts with P105 then blocking NF- κ B inflammatory effects (Sun et al. 2012). MAPK and AKT are target also for A_{2B} receptor in different cells thus regulating numerous pathophysiological functions (Sun and Huang 2016) (Fig. 3.3). In cardiac fibroblasts its stimulation reduced fibroblast proliferation and α -SMA expression generated by endothelin or angiotensin II, through a pathway dependent on cAMP, Epac, PI3K, and AKT signaling, thus contrasting cardiac fibrosis (Phosri et al. 2017, 2018). In bone A_{2B} subtype stimulation decreases ERK1/2, p38, and NF- κ B induced by RANKL, thus contributing to the reduction of osteoclastogenesis (Kim et al. 2017). In human coronary artery smooth muscle cells, the A_{2B} adenosine receptor, cAMP, and PKA signaling decrease cell growth by inhibiting ERK1/2, AKT, and Skp2 stimulators of the cell cycle regulator cyclin D (Dubey et al. 2015). In the placenta A_{2B} receptor activation depresses trophoblast migration through MAPK signaling inhibition and lower proMMP-2 levels, suggesting a role for it in placenta formation and preeclampsia (Darashchonak et al. 2014). In glioblastoma cells prostatic acid phosphatase increases proliferation in a HIF-2 α -dependent manner, requiring activation of A_{2B} receptors AKT and ERK pathways, suggesting this receptor subtype as a target for antiglioblastoma therapies (Liu et al. 2014). In microglia A_{2B} receptor increases IL-10 through p38 phosphorylation as well as IL-6 secretion and cell proliferation, through PLC, PKC- ϵ , PKC- δ , and p38 pathways, thus indicating their role in microglial activation and neuroinflammation (Koscsó et al. 2012; Merighi et al. 2017). In enterochromaffin cells this subtype increases serotonin hypoxic synthesis and release through MAPK, CREB, and tryptophan hydroxylase-1 stimulation, a signaling having relevance in inflammatory bowel disease (Chin et al. 2012; Dammen et al. 2013). In HEK293 cells and in cardiomyocytes, A_{2B} receptor inhibited superoxide generation from mitochondrial complex I via Gi/o protein, ERK, PI3K, and NOS signaling having a role in ischemic preconditioning (Yang et al. 2011). In foam cells it accumulates HIF-1 α through involvement of ERK, p38, and AKT and induces VEGF and IL-8 secretion, playing a role in atherosclerosis development (Gessi et al. 2010a).

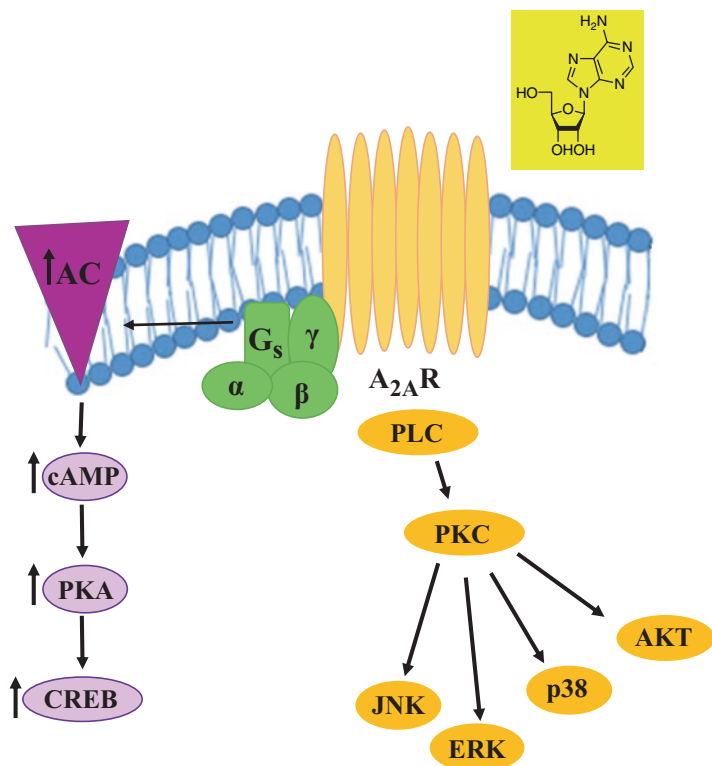


Fig. 3.3 Schematic picture of A_{2B} adenosine receptor signaling cascade. Activation of A_{2B}R stimulates AC activity, increase of cAMP, and PKA phosphorylation. A_{2B}R triggers PLC-β and increases Ca²⁺. Other effectors activated by A_{2B}R include p38, ERK1/2, and JNK1/2

3.4.4 A₃ Adenosine Receptors

The G_i-coupled A₃ adenosine receptor inhibits AC, thus reducing cAMP accumulation, while through G_q coupling stimulates PLC, thereby increasing Ca²⁺ release from intracellular stores in different cellular models (Gessi et al. 2008; Borea et al. 2015). Other signal transducers coupled to this receptor subtype include the monomeric G protein RhoA and phospholipase D as well as sarcolemmal K_{ATP} channels, to produce cardioprotection (Borea et al. 2015). In addition a role for PKC has been reported in both early and delayed preconditioning (Borea et al. 2016). Specifically, in cardiac mast cells, A_{2B}/A₃ receptor stimulation leads to activation of aldehyde dehydrogenase type 2, via PKC-ε, thus reducing renin release and the activation of renin-angiotensin system (Koda et al. 2010). Concerning delayed preconditioning, A₃ receptor activation exerts a protective role through PKC-δ (Zhao and Kukreja 2003). A pro-survival intracellular cascade involving ERK, PI3K, and AKT is enrolled by it to decrease caspase-3 activity and apoptosis (Hussain et al. 2014). Another relevant effect induced by A₃ receptor activation is neuroprotection through

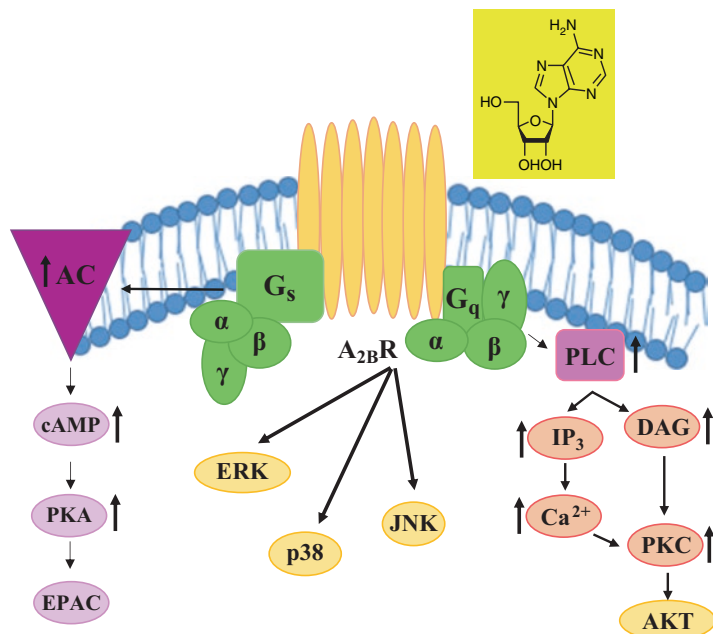


Fig. 3.4 Schematic picture of A₃ adenosine receptor signaling cascade. Interaction of adenosine with A₃R reduces AC activity and cAMP levels and stimulates GSK-3 β with consequent reduction of β -catenin, cyclin D1, and c-Myc. Stimulation of A₃R activates PLC- β and Ca²⁺, RhoA, and PLD. p38, ERK1/2, and JNK1/2 are phosphorylated through A₃R activation

PLC, PKC, or intracellular Ca²⁺ sequestration giving synaptic depression following oxygen-glucose deprivation as well as a reduction in AMPA receptors on hippocampal neurons (Dennis et al. 2011). It is well known that A₃ receptor intracellular transduction occurs through modulation of MAPKs in numerous cellular models (Merighi et al. 2010; Jacobson et al. 2018) (Fig. 3.4). This receptor induced ERK1/2 and cell proliferation in human fetal astrocytes, CHO cells expressing the human A₃AR (CHO-hA₃), microglia, colon carcinoma, glioblastoma, melanoma, and foam cells (Neary et al. 1998; Schulte and Fredholm 2000, 2002; Hammarberg et al. 2003; Merighi et al. 2006, 2007a, b; Gessi et al. 2010a, b; Soares et al. 2014). In contrast, a decrease of ERK activation has been reported in melanoma, prostate cancer, and glioma cells, reducing proliferation as well as decreasing TNF- α release in RAW 264.7 cells (Madi et al. 2003; Martin et al. 2006; Jajoo et al. 2009; Kim et al. 2012). A₃ receptor activation modulates also p38 in several cell types such as CHO-hA₃, human synoviocytes, melanoma, glioblastoma, and colon carcinoma (Merighi et al. 2005b, 2006, 2007b; Varani et al. 2010). In addition it regulates JNK, in microglia and glioblastoma cells, to increase cell migration and matrix metalloproteinase-9 (MMP-9) secretion, respectively (Gessi et al. 2010b; Ohsawa et al. 2012). Interestingly, A₃ receptor increases chemoresistance induced by multiple resistance-associated protein-1 (MRP1) transporter through a pathway involving PI3K/AKT and MEK/ERK1/2 (Torres et al. 2016; Uribe et al. 2017). Another

effect induced by this subtype through AKT phosphorylation was protection from apoptosis in RBL-2H3 and stimulation of MMP-9 in glioblastoma cells (Gao et al. 2001; Merighi et al. 2005a, 2007a; Gessi et al. 2010b). In melanoma the same pathway modulated by A₃ receptor decreased proliferation and increased pigmentation (Madi et al. 2013). Anti-inflammatory effects are produced by its modulation of PI3K/AKT and NF- κ B transduction systems in BV2 microglial cells, monocytes, arthritis, and mesothelioma (Haskó et al. 1998; la Sala et al. 2005; Fishman et al. 2006; Lee et al. 2006, 2011; Madi et al. 2007; Varani et al. 2011). Instead reduction of AKT has been reported in murine astrocytes to decrease HIF-1 α accumulation (Gessi et al. 2013). Accordingly, A₃ receptor inhibits angiogenesis in endothelial cells through PI3K/AKT/mammalian target of rapamycin (mTOR) signaling decrease (Kim et al. 2013). Finally, the inhibition of PKA mediated by A₃ receptor stimulation raised glycogen synthase kinase-3 β (GSK-3 β), inducing beta-catenin reduction; decrease of its transcriptional gene products, such as cyclin D1 and c-Myc; as well as reduction of NF- κ B DNA-binding capacity in melanoma, hepatocellular carcinoma, and synoviocytes from RA patients and in adjuvant-induced arthritis rats (Fishman et al. 2002, 2004; Bar-Yehuda et al. 2008; Ochaion et al. 2008). Accordingly, following a reduction of A₃ receptor expression in colon cells after ulcerative colitis due to miR-206 activity, increased NF- κ B, and related cytokines in the mouse colon, has been observed resulting in a proinflammatory event (Wu et al. 2016).

3.5 Conclusion

Adenosine receptors are important targets for drug development in several pathologies spanning from ischemic brain and heart injury, pain, neurodegenerative diseases, cancer, and inflammation, and for this reason there is a big interest in the development of novel selective and potent molecules targeting this system. This issue today may be better afforded, thanks to the improvement in the knowledge about the structure of receptor subtypes, which are the targets of new drugs. During the last 10 years, the crystallization approach has dramatically revealed the biological structure of GPCRs, and the A_{2A} receptor has been the pioneer in this process, followed by the A₁ subtype. In the next future, continued energy to reveal the structures of all four adenosine receptor subtypes in the three distinct activation states is fundamental to better improve the rational drug design process to develop novel molecules. From the extensive literature mentioned in this chapter, it is evident that adenosine modulates different intracellular signaling pathways involving MAPK and AKT to produce its pathophysiological effects. The regulation of these cascades is not univocal meaning that stimulation or inhibition of specific kinases may occur differentially depending on the receptor subtype involved and the cell system investigated. It is auspicious that future drugs coming from the adenosinergic field could exploit separated signaling pathway linked to a specific adenosine subtype, thus avoiding or limiting side effects.

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