

Molecular Pharmacology and Function of the P2Y₁₄ Receptor

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Abstract
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P2Y receptors are a family of seven transmembrane spanning G protein-coupled receptors that are activated by nucleotides and nucleotide-sugars. The P2Y₁₄-R is activated by nucleotide sugars, although little is known about the physiological role(s) of this receptor. With a view toward generating pharmacological reagents for studies of P2Y₁₄-R, one goal of this dissertation was to apply a rational structure-activity relationship approach to develop novel ligands for the P2Y₁₄-R. Guided by molecular modeling studies of the P2Y₁₄-R, iterative design of synthetic ligands produced a multitude of compounds which were assessed for agonist activity at the P2Y₁₄-R. From these studies, several novel agonists were identified for the P2Y₁₄-R, including 2-thio-UDP-Glc, which exhibited greater than six-fold higher potency than UDP-Glc. Other novel agonists identified included several UDP-sugars. Using a COS-7 cell system in which recombinant P2Y₁₄-R were co-expressed with the chimeric G protein, Gαq/i, UDP was identified as a competitive antagonist at the P2Y₁₄-R. In contrast, in studies comparing the pharmacological selectivity of the rat P2Y₁₄-R to that of the human P2Y₁₄-R in the same cell system, UDP was found to be an agonist at the rat P2Y₁₄-R. Another goal of this work was to examine the signal transduction pathways downstream of P2Y₁₄-R activation, and for these studies, stable cell lines expressing P2Y₁₄-R in HEK293 and in C6 glioma cells were developed. This approach allowed study of P2Y₁₄-R coupled to native G proteins, and P2Y₁₄-R-dependent inhibition of adenylyl cyclase was observed.

P2Y₁₄-R activation also promoted pertussis toxin-sensitive phosphorylation of ERK1/2. Moreover, native P2Y₁₄-R were detected in differentiated HL-60 cells by RT-PCR, and in these cells, UDP-Glc promoted pertussis toxin-sensitive activation of ERK1/2. The work presented here provides a foundation for future development of pharmacological agents for the P2Y₁₄ receptor. Furthermore, this work establishes that the P2Y₁₄-R couples to Gi and the MAP kinase signaling pathway, and provides robust cell model systems for future studies of P2Y₁₄-R function.

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List of Abbreviations and Symbols

α , alpha

β , beta

γ , gamma

ADP, adenosine 5'-diphosphate

ATP, adenosine 5'-triphosphate

BSA, bovine serum albumin

cAMP, cyclic adenosine 3', 5'-monophosphate

DAG, diacylglycerol

DMEM, Dulbecco's Modified Eagle Medium

DMSO, dimethylsulfoxide

DTT, dithiothreitol

EC₅₀, effective concentration required to produce 50% of the maximal effect

EDTA, ethylenediaminetetraacetic acid

E-NPP, ectonucleoside pyrophosphatase/phosphodiesterase

ERK, extracellular-regulated kinase

FBS, fetal bovine serum

fMLP, formyl-methionine-leucine-phenylalanine

FPR, formyl peptide receptor

FSK, forskolin

GDI, GDP dissociation inhibitor

GDP, guanosine 5'-diphosphate

GEF, G protein exchange factor

GPCR, G protein coupled receptor

GRK, G protein coupled receptor kinase

GTP, guanosine 5'-triphosphate

HA, hemagglutinin

HBSS, Hank's Balanced Salt Solution

HEPES, N-[2-hydroxyethyl]piperazine-N'-[2-ethanesulfonic acid]

IBMX, 3-isobutyl-1-methylxanthine

IP₃, inositol trisphosphate

JNK, Jun N-terminal kinase

KO, knockout

LARG, leukemia-associated Rho GEF

LPA, lysophosphatidyl acid

MAPK, mitogen-activated protein kinase

MCMM, Monte Carlo Multiple Minimums

mRNA, messenger ribonucleic acid

NDPK, nucleoside diphosphokinase

NTPDase, nucleotide triphosphate diphosphohydrolase

PAR, protease-activated receptor

PBS, phosphate buffered saline

PI3K, phosphatidylinositol-3-kinase

PIP₂, phosphatidylinositol 4,5-bisphosphate

PKA, protein kinase A

pK_B, log dissociation constant for antagonist/receptor complex

PKC, protein kinase C

PLC, phospholipase C

PPADS, pyridoxalphosphate-6-azophenyl-2', 4'-disulphonic acid

PPi, inorganic pyrophosphate

PTX, pertussis toxin

RGS, regulator of G protein signaling

RNA, ribonucleic acid

RT-PCR, reverse transcriptase polymerase chain reaction

SAR, structure-activity relationship

SE, standard error

TCA, trichloroacetic acid

U, units

UDP, uridine 5'-diphosphate

UDP-Glc, uridine 5'-diphosphoglucose

UTP, uridine 5'-triphosphate

Chapter I. Introduction

Nucleotides are important extracellular signaling molecules that activate cell surface receptors to regulate many physiological processes such as neurotransmission, vasoconstriction/ dilation, cell differentiation, platelet aggregation, and also ion transport in epithelial cells. Previous to Burnstock's observations in the 1970's, ATP was generally accepted to function only in intracellular processes where it acts as the energy source for the cell. Burnstock originally hypothesized that ATP was released from cells and could act on cell surface receptors to contribute to second messenger signaling, based on evidence that ATP mediated responses to nerve stimulation independently from cholinergic or adrenergic nerve responses (Burnstock, 1972). We now know that ATP produces autocrine/ paracrine signaling in non-excitatory cells as well as functions as an important neurotransmitter, involved in a broad range of cellular and organ functions. Currently, ATP and ADP, as well as UTP, UDP, and UDP-glucose are well accepted as extracellular signaling molecules that act on a diverse family of nucleotide binding receptors, and extracellular concentrations of nucleotides are precisely regulated by cellular release and metabolism by ectoenzymes.

The following pages will overview the source of extracellular nucleotides and their metabolism by ectoenzymes. Subsequent to discussion of nucleotides present in the extracellular space, a general introduction to purinergic receptors will be presented. A more detailed description of members of the P2Y receptor family will follow, with an expanded focus on the P2Y₁₄-R, the topic of this dissertation.

Cellular release of nucleotides

Regulated release of ATP through exocytosis from excitatory cells is a phenomenon that has been known to occur for many decades. More recently, nucleotide release from non-excitatory cells has been established, and evidence for the release of other nucleotides including UTP and UDP-glucose has been reported. Sources for extracellular nucleotides include constitutive release from resting cells, release after hormone stimulation or mechanical stress, and cell lysis. Elucidating the mechanism(s) of release is currently the topic of investigation in many labs.

Assays for quantification of ATP have been developed using a luciferase assay, allowing spatiotemporal resolution of ATP release and hydrolysis in the medium on cultured cells (Dubyak and el-Moatassim, 1993; Taylor et al., 1998; Beigi et al., 1999). Luciferin is a substrate for luciferase, and the catalytic reaction produces luminescence in the presence of ATP. These assays are very sensitive methods for quantification of ATP in the bulk medium and have even been adapted to measure cell surface concentrations of ATP with a luciferase engineered to be anchored at the plasma membrane (Beigi et al., 1999). Sensitive assays detecting released uridine nucleotides and nucleotide-sugars from cultured cells have been developed by Lazarowski and colleagues (Lazarowski et al., 1997a; Lazarowski and Harden, 1999; Lazarowski et al., 2003). Such detection assays have informed us about circumstances of nucleotide release and also about relative rates of release versus degradation of nucleotides.

Differences in measurements of ATP with soluble luciferase compared with plasma membrane-associated luciferase suggest that measurements from the bulk medium are likely

to grossly underestimate the concentration at the receptor level (Beigi et al., 1999). One possible explanation for this may be that the microenvironment at the cell surface has a higher concentration of nucleotide than is measured in the bulk medium. That is, higher concentrations of nucleotides are retained at the surface of cells in close proximity to cell surface receptors, whereas the bulk medium contains a diffused, lower concentration of nucleotide due to ectonucleotidase activity. This may occur because the rates of release and accumulation of nucleotide at the cell surface is more rapid than the rate of diffusion throughout the bulk medium, or it is possible that hydrolyzing enzymes are localized on the cell surface or as soluble enzymes in the medium in an orientation that allows degradation of nucleotides away from the site of release and receptor expression, allowing receptors to interact with nucleotides immediately upon release before degradation of the nucleotide occurs.

Cellular release of ATP, UTP, or UDP-glucose after mechanical stimulation of cells has been well established (Gordon, 1986; Lazarowski et al., 1997a). Levels of ATP and UTP measured in the bulk medium on several types of cultured cells rise sharply within five minutes of stimulation. In contrast to the rapid rise in extracellular concentrations of other nucleotides on mechanically stimulated cells, UDP-Glc increases little. However, UDP-glucose in the medium on 1321N1 human astrocytoma cells was observed to gradually increase to a maximal concentration at 1 h after stimulation of the cells and remain at that level for a subsequent 2 h (Lazarowski et al., 2003). Extracellular UDP-glucose is apparently metabolized at a slower rate than ATP in several cell lines and furthermore, the concentration reported for UDP-glucose on resting cells was 2-6 fold higher than the ATP concentration,

suggesting that UDP-glucose is released constitutively from cells as well as upon mechanical stimulation.

In addition to constitutive release of nucleotides and after mechanical stimulation of cells, multiple reports have established that nucleotide release also occurs as a result of hormone activation of some GPCRs. Thrombin treatment of many cell types promotes ATP release (Pearson and Gordon, 1979; Joseph et al., 2003), relevant to the work described in this dissertation, thrombin promotes UDP-Glc release from astrocytoma cells (Kreda *et al.*, 2008). Bradykinin, acetylcholine, and serotonin have all been shown to induce release of ATP from several types of cells (Yang et al., 1994; Ostrom et al., 2000; Buxton et al., 2001). Hormone activation of cells leads to nucleotide release, and multiple signaling pathways may be activated in a cascade from hormone activation and subsequent activation by nucleotides.

Cell lysis due to tissue damage is another source for extracellular nucleotides. After insults such as ischemia in the brain or heart, nucleotides are released from damaged cells and are present at concentrations sufficient to activate P2 receptors (Cook and McCleskey, 2002; Melani et al., 2005). Induced ischemia in pig artery increased plasma levels of ATP and UTP, and also correlated with vasodilation (Erlinge et al., 2005). Patients with coronary heart disease were found to have higher than normal plasma levels of UTP (Wihlborg et al., 2006). Intracellular nucleotides that are released as a course of cell lysis from tissue damage are likely to activate nearby P2 receptors.

The mechanisms for regulated release of nucleotides have not been established. The proposed mechanisms for nucleotide release from epithelial cells are exocytosis of ATP-containing vesicles, release through ATP-permeable channels, or some combination of these two processes. Observations of ATP-containing vesicles in pancreatic cells support the

hypothesis that exocytosis is a mechanism for ATP release (Sorensen and Novak, 2001). Additionally, findings from several groups support exocytotic release of ATP as a result of cell swelling, and implicate the involvement of phosphatidylinositol-3-kinase (PI3K) (Merlin et al., 1996; Feranchak et al., 1999; Gatof et al., 2004). Several anion channels have been reported to be permeable to ATP under certain experimental conditions, although a selective ATP channel has not been identified (Wang et al., 1996; Roman et al., 1997; Bell et al., 2003; Okada et al., 2004).

Interest in connexin and pannexin hemichannels as potential release mechanisms is growing. Connexins and pannexins have four transmembrane domains with the amino and carboxyl termini on the intracellular side of the plasma membrane. Six subunits (connexons) assemble to form hemichannels (Shestopalov and Panchin, 2008). Connexin hemichannels are important components of gap junctions, which allow the flow of ions between cells and have even been shown to be permeable to ATP (Penuela et al., 2007). Pannexins, however, do not form gap junctions and furthermore, while they form channels that are permeable to ATP, their function has been reported to be inhibited by extracellular ATP (reviewed in Dubyak, 2009). While the exact mechanisms for cellular release of nucleotides remain to be elucidated, it seems likely that some combination of vesicular release and channel-regulated release are involved in nucleotide release from cells.

Clearly, metabolism of extracellular nucleotides regulates purinergic receptor function. The specifics of how P2 receptors and ectonucleotidases coordinate physiological functions remain largely undefined. Precise regulation of nucleotide action is likely specific to the tissue or cell type and stage of cell development. Spatiotemporal resolution of ectonucleotidase and receptor expression together with accurate measurements of nucleotide

concentrations will bring us closer to understanding the biological processes dependent on nucleotide signaling.

Ectonucleotidases

In addition to release of nucleotides from cells, extracellular concentrations of ATP, UTP, ADP, UDP, and UDP-glucose are precisely controlled by cell surface enzymes catalyzing nucleotide hydrolysis and phosphorylation (Fig. 1). Ectoenzymes remove nucleotide agonists from the cell surface, contributing an important mechanism for terminating P2Y-R signal transduction. Along with cell surface receptors, most cell types also express ecto-nucleoside triphosphate diphosphohydrolases (NTPDases) and other enzymes that metabolize nucleotides or interconvert nucleotides. In addition to ectoNTPDases, this cadre of enzymes includes ecto-nucleotide pyrophosphatase phosphodiesterase (E-NPP), alkaline phosphatase, adenylate kinase, and nucleoside diphosphate kinase (Zimmermann, 2000; Robson et al., 2006) (Fig. 2). Although some ecto-enzymes degrade nucleosides in addition to nucleotides, other enzymes that metabolize only nucleosides also are expressed on the cell surface, and these include adenosine deaminase, purine nucleoside phosphorylase (PNP), and 5'-nucleotidase, which exists as a dimer and is anchored to the cell surface through a glycosylphosphatidylinositol (GPI)-linkage, hydrolyzing $\text{AMP} \rightarrow \text{Ado} + \text{P}_i$.

NTPDases

Of the eight members of the NTPDase family, only NTPDase 1, 2, 3, and 8 are expressed at the cell surface, exhibiting an extracellular catalytic site and two transmembrane domains. These four enzymes catalyze nucleotides with a K_M in the micromolar range, and require divalent cations for their catalytic activity (Kukulski *et al.*, 2005).

NTPDase 1/ CD39 hydrolyzes both di- and triphosphate nucleotides to monophosphate nucleotides. Studies investigating the relationship between NTPDase1 and P2Y₁-R used an engineered fusion protein that expressed NTPDase1 with the P2Y₁-R as a single construct on CHO cells (Alvarado-Castillo et al., 2002). The expression of the NTPDase in tandem with the receptor caused a shift to the right in the ADP concentration effect curve, indicating that ectoenzymes can regulate concentrations of nucleotides with physiological consequences. In previous studies with the P2Y₁-R, receptor activation in the absence of added agonist was observed. Basal levels of activation of the P2Y₁-R was not observed with the fusion protein, suggesting cellular release of nucleotide was autocrinely activating receptor.

While NTPDase1 is expressed mainly in vascular smooth muscle and endothelial cells (Enjyoji *et al.*, 1999), it has also been detected in the promyeloid cell line HL-60 and increases expression with differentiation of the myeloid leukocyte (Clifford *et al.*, 1997). Studies of the NTPDase1/ CD39^{-/-} knockout mouse first implicated this enzyme as an important component of platelet biology (Enjyoji et al., 1999), and more recently of other physiological processes as well. Although the knockout mice did not exhibit any gross defects in development or viability as compared with wild-type mice, a host of disorders have been reported. Bleeding times in the NTPDase1^{-/-} mice were prolonged (Enjyoji et al., 1999), suggestive of a deficiency in platelet activation. This bleeding disorder phenotype was rescued following injection of knockout mice with the soluble potato-derived ATPDase apyrase. Likewise, platelets isolated from NTPDase1^{-/-} mice were deficient in their ability to aggregate in response to ADP, however the NTPDase1^{-/-} platelets could be activated by ADP plus serotonin, suggesting that a Gq-coupled, ADP-activated receptor was desensitized in

platelets lacking NTPDase1. Furthermore, when platelets were treated with apyrase, platelet activation in response to ADP was restored, indicating that the P2Y₁-R was desensitized with chronic agonist stimulation, and NTPDase was necessary for removal of agonist. Additional disorders reported for the NTPDase1^{-/-} mice include impaired neutrophil chemotaxis (Corriden et al., 2008), decreased insulin sensitivity (Enjyoji et al., 2008), and deficiencies in microglial migration (Farber et al., 2008), among others. The broad impact of NTPDase1 loss in mice indicated that nucleotide/nucleoside signaling has critical roles in many biological functions.

NTPDase2 is expressed on vascular smooth muscle cells as well as on stromal cells (Zimmermann, 1999). NTPDase 2 has a much higher affinity for nucleotide triphosphates over diphosphates (Fig. 2). Studies with NTPDase1 and NTPDase2 highlighted the effects of ectoenzyme isotype expression on the observed pharmacological activity of the P2Y₁-R (Alvarado-Castillo et al., 2005). When P2Y₁-R and NTPDase2 were co-expressed, the EC₅₀ of ADP was similar to that of P2Y₁-R alone. However, when NTPDase1 was coexpressed with the receptor, the ADP curve shifted to the right, likely as a function of ADP hydrolysis reducing the available agonist. In addition to illustrating how ectoenzymes may regulate extracellular nucleotide concentrations and thus altering the potency of agonist at a P2Y-R, this work also proposed the notion that ectoenzyme expression may indirectly regulate receptor expression levels, for example, by inhibiting desensitization of P2Y-R when ectoenzymes hydrolyze constitutively-released nucleotides.

NTPDases 3 and 8 prefer nucleotide triphosphates to diphosphates (Fausther *et al.*, 2007). In contrast to the membrane-bound NTPDases (1, 2, 3, and 8), NTPDase5 and NTPDase6 are expressed in golgi of monocytes and cardiocytes, respectively, and were

observed to be secreted from the cell upon heterologous expression. Both enzymes hydrolyze UDP and GDP (Chadwick and Frischauf, 1998; Ivanenkov et al., 2003). NTPDase formation of homo-oligomers has been reported, although it is unclear how oligomerization may affect catalytic activity (Grinthal and Guidotti, 2002).

E-NPPs

The E-NPP family of enzymes bear a single transmembrane domain with an extracellular C-terminus. The catalytic domain lies in the C-terminal portion of the protein, a region that also harbors an EF-hand sequence likely responsible for binding divalent cations that are necessary for catalytic activity. While there exist seven E-NPP enzymes, only three isoenzymes in this family hydrolyze nucleotides and dinucleotides. E-NPPs generally recognize a broad array of substrates, including nucleic acids, NAD, lysophospholipids, and cAMP. Furthermore, they can hydrolyze pyrophosphate bonds of nucleotide sugars (Zimmermann, 2000). E-NPP family members are also called PC-1 (E-NPP1), PDNP, and autotoxin (E-NPP2). E-NPP1 can undergo proteolysis causing the C-terminal portion of the enzyme to become soluble, a state in which it retains catalytic activity (Belli *et al.*, 1993; Clair *et al.*, 1997). The knockout mouse lacking the E-NPP1 gene develops bone abnormalities, indicating that E-NPP1 functions in bone formation biology. E-NPP2 does not have a transmembrane domain, but is secreted from the cell. E-NPP2 knockout mice are embryonic lethal (Yegutkin, 2008), suggesting a critical role in developmental processes. K_M values for ENPPs at ATP are in the 50 μ M range, similar to that of NTPDases (Zimmermann, 2000).

Phosphatases and Kinases

Other enzymes that are expressed on the cell surface also use nucleotides as substrates. Alkaline phosphatase hydrolyzes tri-, di-, and monophosphate adenine nucleotides through cleavage of the terminal phosphate, ultimately yielding nucleoside plus inorganic phosphate. Alkaline phosphatase also cleaves the phosphate group from other molecules, such as glucose-phosphate and pyrophosphate (Yegutkin, 2008). The K_M of alkaline phosphatase for nucleotides is in the millimolar range. Alkaline phosphatases can be soluble or plasma membrane-associated through a glycosylphosphatidylinositol (GPI)-linkage (Low and Saltiel, 1988; Zimmermann, 2000). Additionally, nucleoside diphosphokinase (NDPK) was identified as a transphosphorylating enzyme that uses ATP to phosphorylate UDP or GDP in a reversible reaction, and reciprocally, UTP as substrate will yield ATP + UDP (Harden et al., 1997; Lazarowski et al., 1997b; Grobben et al., 1999; Lazarowski et al., 2000). The gamma phosphate of the nucleotide triphosphate is cleaved, and subsequently used to phosphorylate a nucleotide diphosphate. Another kinase, adenylyl kinase, converts ATP + AMP into 2 ADP molecules (Yegutkin et al., 2002; Picher and Boucher, 2003).

Nucleotide concentrations on the extracellular space are a dynamic function of cellular release and nucleotide metabolism, which includes degradation, phosphorylation, and interconversion. One could imagine that the differential signaling effects regulated by nucleosides and nucleotides are dependent on the nucleotidase isotype expressed on the cell surface in addition to the P2Y-R expression. For example, distinct signal transduction pathways are activated by ATP versus ADP versus adenosine, and perhaps the relative ratios of nucleotides on the cells are just as critical to physiological homeostasis as is which P2Y-R may be expressed on a particular tissue type.

Purinergic Receptors

Purinergic signaling encompasses responses initiated by nucleosides and nucleotides. P1 receptors define the family of G protein coupled receptors that are activated by adenosine, and include the subtypes A₁, A_{2A}, A_{2B}, and A₃. P2 receptors are a class of nucleotide-activated cell surface receptors and are categorized into two families of receptors: P2X receptors and P2Y receptors.

P2X receptors are ligand-gated ion channels, and all are activated by ATP. The seven receptors in the P2X family are: P2X₁, P2X₂, P2X₃, P2X₄, P2X₅, P2X₆, and P2X₇. P2X receptors are comprised of three subunits and can exist as homomeric or heteromeric receptor assemblies. When ATP binds, the channel opens, allowing cations to pass through to the intracellular space. P2X_{1-5,7} are permeable to Na⁺, K⁺, and Ca²⁺ ions. P2X₆ cannot form a homomeric receptor, but can form a functional heteromeric receptor with other P2X subunits (Ralevic and Burnstock, 1998; Abbracchio et al., 2006).

P2Y receptors are metabotropic receptors that couple to heterotrimeric G-proteins. There are eight identified P2Y receptors: P2Y₁, P2Y₂, P2Y₄, P2Y₆, P2Y₁₁, P2Y₁₂, P2Y₁₃, and P2Y₁₄. The nomenclature assigned includes numbers up to fourteen, reflecting a repeated problem in the field of P2Y receptor research. The missing P2Y receptor numbers are due to receptors that were mistakenly included in this family of receptors. The receptors that were erroneously assigned P2Y numbers have since been re-classified as either non-mammalian P2Y orthologs, or belonging to other receptor families, including leukotriene receptors and lysophosphatidic acid (LPA) receptors (Yokomizo et al., 1997; Li et al., 1998; Noguchi et al., 2003).

G Protein Signal Transduction

P2Y receptors, like other G protein-coupled receptors, couple to heterotrimeric G proteins comprised of α , β , and γ subunits. When agonist binds the cell-surface receptor, conformational changes in the receptor coordinate subsequent conformational rearrangements in the G protein. Guanosine 5'-triphosphate (GTP) then replaces guanosine 5'-diphosphate (GDP) on the $G\alpha$ subunit and the result is disengagement of the $\beta\gamma$ dimer from the α subunit. The GTP-bound $G\alpha$ is the activated form, and so initiates downstream signaling events. The $G\beta\gamma$ dimer also activates downstream signaling targets such as phospholipases, adenylyl cyclases, phosphatidylinositol-3-kinase γ , and ion channels. Additional proteins and pathways may also be regulated by $G\beta\gamma$ -dependent signaling, as evidenced by the number of $G\beta\gamma$ -binding proteins that have been identified (Smrcka 2008). G protein-induced signaling ceases when the intrinsic GTPase activity of the $G\alpha$ subunit causes hydrolysis of GTP to GDP, and the heterotrimeric G protein reassembles.

The main signaling pathways activated by GPCRs are represented by at least four families of heterotrimeric G proteins: Gq, Gs, Gi, and G12. The Gq family of G proteins includes $G\alpha_q$, $G\alpha_{11}$, $G\alpha_{15}$, and $G\alpha_{16}$, and these subunits activate phospholipase C- β , which hydrolyzes phosphatidylinositol 4, 5-bisphosphate (PIP₂) into inositol 1, 4, 5-triphosphate (IP₃) and diacylglycerol (DAG). IP₃ acts on receptors at the endoplasmic reticulum to release from its intracellular calcium stores. DAG activates protein kinase C (PKC). Gq also has been shown to bind to the regulator of G protein signaling (RGS) domain of G protein receptor kinase-2 (GRK2) (Carman et al., 1999), and evidence shows that GRK2 is an important hub of signaling for the Gq signal transduction pathway, as it binds a number of elements in the cascade (Tesmer et al., 2005). Additionally, guanine nucleotide exchange

factors (GEFs) for Rho family proteins interact with Gq. Rho family proteins are small G protein GTPases that control myriad cellular functions such as contraction, motility, and proliferation. At least three Rho GEFs, p63-RhoGEF, Trio, and PDZ-RhoGEF, are known to interact with GTP-bound Gq and lead to RhoA activation (Lutz et al., 2005; Rojas et al., 2007), establishing a link between heterotrimeric G protein signaling and Rho signaling pathways.

The Gs family includes $G\alpha_s$ and the related olfactory system expressed $G\alpha_{olf}$. Gs family proteins activate adenylyl cyclase, which generates cyclic adenosine 5'-monophosphate (cAMP) from ATP. Protein kinase A (PKA) is downstream of adenylyl cyclase and is activated by intracellular cAMP. Conversely, Gi proteins inhibit some isoforms of adenylyl cyclase (I, III, V, VI, and VIII) and also regulate ion channels (Gilman, 1987; Birnbaumer, 1992; Clapham and Neer, 1997), which appears to be through released $G\beta\gamma$ subunits. The Gi family is comprised of $G\alpha_{i1}$, $G\alpha_{i2}$, $G\alpha_{i3}$, $G\alpha_o$, $G\alpha_t$, $G\alpha_z$, and $G\alpha_{gust}$. Tissue-specific expression was established for $G\alpha_t$ in the retina, $G\alpha_{gust}$ in the gustatory system, and $G\alpha_z$ in platelets and brain.

G12 family proteins ($G\alpha_{12}$, $G\alpha_{13}$) are ubiquitously expressed. G12 proteins activate guanine nucleotide exchange factors (GEFs) for RhoA family members such as PDZ-RhoGEF, p115RhoGEF, and leukemia-associated RhoGEF (LARG) (Kozasa et al., 1998; Suzuki et al., 2003). G12 G proteins may also interact with other signaling molecules such as cadherins, protein phosphatases, and non-receptor tyrosine kinases to modulate other signaling pathways. Studies of mouse models suggest that the functions of $G\alpha_{12}$ and $G\alpha_{13}$ are distinct. $G\alpha_{13}^{-/-}$ mice do not survive more than a few days, while $G\alpha_{12}^{-/-}$ mice survive into

adulthood, suggesting differential roles for G12 proteins in developmental processes (Offermanns et al., 1997).

Termination of agonist-promoted GPCR signaling occurs when G protein receptor kinases (GRK) phosphorylate residues on intracellular domains of the receptor. This acts as a signal for β -arrestin recruitment to the plasma membrane, where it uncouples GPCR from G proteins. Arrestins also mediate internalization of some GPCRs, acting as a scaffold for the receptor with endocytosis machinery. Endocytosed receptors may be either recycled to the plasma membrane, or degraded via the lysosome (Krupnick and Benovic, 1998).

P2Y Receptors

P2Y receptors are grouped into two categories based on amino acid sequence homology and proposed G-protein coupling selectivity (Fig. 3). The P2Y₁-R subgroup includes P2Y₁, P2Y₂, P2Y₄, P2Y₆, and P2Y₁₁, all of which couple to G α_q and lead to activation of PLC. The P2Y₁₁ receptor also couples to G α_s to increase intracellular cAMP. The P2Y₁₂-R subgroup is comprised of P2Y₁₂, P2Y₁₃, and P2Y₁₄, all of which are proposed to couple to G α_i to inhibit formation of cAMP (Abbracchio *et al.*, 2006). GPR87, an orphan receptor, exhibits high amino acid sequence homology to the P2Y₁₄-R, (Schoneberg *et al.*, 2007), suggesting that GPR87 likely shares a common ancestor with the P2Y₁₂-like P2Y-R. However, GPR87 was recently reported to be activated by lysophosphatidic acid (LPA) (Tabata et al., 2007).

The P2Y₁ receptor is activated by ADP. The P2Y₂ receptor is activated by UTP and ATP, while the human P2Y₄ receptor is activated only by UTP. The only receptor known to be activated by UDP is the P2Y₆ receptor. The P2Y₁₁ receptor is activated by ATP. In the

P2Y₁₂-R subgroup, both P2Y₁₂ and P2Y₁₃ receptors are activated by ADP, and the P2Y₁₄ receptor is activated by UDP-glucose and other nucleotide-sugars.

While the lack of selective, high affinity antagonists has impeded research on P2Y receptors, several labs have ongoing studies to identify competitive antagonists at each of the P2Y receptors, and progress has been greatest for the P2Y₁-R and P2Y₁₂-R. In fact, a prodrug, clopidogrel, that metabolizes into a P2Y₁₂-R antagonist, is used therapeutically to prevent thrombosis (Foster et al., 2001; Hollopeter et al., 2001). Antagonists for the P2Y₂, P2Y₆, P2Y₁₁, and P2Y₁₃ receptors have been described and can be used as templates for the development of high affinity compounds that will be useful for pharmacological studies of P2Y receptors (Jacobson *et al.*, 2008). Although ATP is an antagonist at the human P2Y₄-R (Herold *et al.*, 2004), no selective antagonists have been identified for the P2Y₄ and P2Y₁₄ receptors. Several non-selective acting antagonists for P2Y receptors have been identified. These include PPADS, suramin, and reactive blue 2 (Ralevic and Burnstock, 1998; Brown and Brown, 2002).

P2Y₁-like Receptors

P2Y₁-R

The P2Y₁ and P2Y₁₂ receptors have a well established function in platelet biology (Dubyak et al., 1993; Savi et al., 1998; Hechler et al., 1998a; Leon et al., 1999; Fabre et al., 1999). The role of ADP in platelet aggregation involves both the Gq-activating P2Y₁-R as well as the Gi-activating P2Y₁₂-R. Knockout mice for P2Y₁-R exhibited increased bleeding time after tail amputation as compared with wild-type mice. Platelets from these mice lost the ability to undergo shape change in response to ADP. However, platelets treated with ADP retained the capacity to inhibit adenylyl cyclase (Fabre et al., 1999). Although the

P2Y₁-R is one element of the platelet clotting response to injury, the P2Y₁₂-R governs the aggregation component of platelet activation only after Gq-dependent shape change has occurred (Enjyoji et al., 1999; Bourdon et al., 2006). Pharmacological studies using P2Y₁-R-selective ligands in human platelets revealed that the P2Y₁-R undergoes rapid desensitization upon activation (Bourdon et al., 2006).

P2Y₂-R

The P2Y₂-R has been reported to have an important role in ion secretion and absorption in airway epithelial cells. Upon activation of P2Y₂-R by UTP or ATP, Cl⁻ secretion increases and Na⁺ absorption is inhibited. Improvement of mucociliary clearance in cystic fibrosis patients was demonstrated after treatment with inhaled P2Y₂ receptor agonists (Kellerman et al., 2002). In the P2Y₂-R knockout mouse, the effect of UTP on inositol phosphate levels and calcium mobilization in tracheal and nasal epithelial cells was abrogated. Likewise, UTP- and ATP-dependent Cl⁻ transport was disrupted in trachea from the P2Y₂-R^{-/-} mouse (Cressman et al., 1999; Homolya et al., 1999). Additionally, multiple studies have identified P2Y₂-R mRNA in immune cells, where ATP and UTP effects have been reported (Chen et al., 2006; Myrtek and Idzko, 2007). Moreover, the P2Y₂-R is implicated in atherosclerosis (Seye et al., 2002), suggesting that P2Y₂-R may have a role in inflammation processes. In rats overexpressing the P2Y₂-R, lesions were observed on their lacrimal glands, which regulate fluid secretion to the eyes, and also on the kidney by 3 months of age (Agca et al., 2008), supporting the notion that P2Y₂-R also regulates fluid secretion in the eye and kidney.

P2Y₄-R

The P2Y₄-R is activated by UTP. ATP acts as an antagonist at the human P2Y₄-R, and it was determined also to be an agonist at the rat ortholog receptor (Kennedy et al., 2000). In humans, P2Y₄-R are expressed in brain, intestine, lung, liver, and placenta (Communi et al., 1995). Chloride secretion in the epithelium of the small and large intestines is dependent on P2Y₄-R activation, as determined by studies with P2Y₄-R knockout mice (Robaye et al., 2003; Ghanem et al., 2005). Just as the P2Y₂-R is important for chloride secretion in lung, the P2Y₄-R is likely the primary P2Y-R involved in chloride secretion in intestine.

P2Y₆-R

UDP-activated P2Y₆-R are expressed throughout the body, specifically in heart, lung, spleen, and intestine, as well as in monocyte-derived immune cells (Communi et al., 1996). Recently, cooperative signal transduction of the P2Y₆-R with the cysteinyl leukotriene receptor CysLT₁R was reported in human mast cells, such that when one receptor was inhibited via shRNA technology or with the use of a selective antagonist, the other receptor also lost its function (Jiang et al., 2009). Although the relevance of such an effect is unknown, the overlapping receptor expression distribution and the possibility that the two signal transduction pathways are linked suggest that the P2Y₆-R may have an important role in innate immune responses. While the physiological function of P2Y₆-R is unknown, reports of UDP-dependent phagocytosis in rat microglia and upregulation of P2Y₆-R mRNA 72 h after neuronal damage suggest an immunoprotective role for P2Y₆-R (Koizumi et al., 2007). A recently developed knockout mouse for the P2Y₆-R strongly supports the role of P2Y₆-R in immune responses (Bar et al., 2008). While no obvious abnormalities were

observed on the P2Y₆-R^{-/-} mouse, macrophages isolated from the mouse lacked UDP-promoted signal transduction and cytokine production. Additional studies with the P2Y₆-R knockout mouse suggested that P2Y₆-R may regulate vasoconstriction in aorta in response to UDP treatment. The P2Y₆-R was recently reported to be involved in the induction of cardiac fibrosis through G_{12/13} signaling to Rho in mice (Nishida et al., 2008), prompting further investigation of the P2Y₆-R as a potential therapeutic target for heart disease.

P2Y₁₁-R

P2Y₁₁-R mRNA has been detected in placenta, brain, and lymphocytes (Communi et al., 1997; Moore et al., 2001). Unique among the P2Y receptors, the P2Y₁₁-R gene has several introns (Communi et al., 2001b). Another distinctive characteristic of the P2Y₁₁-R is that it couples to both G_q to activate PLC as well as to G_s to activate adenylyl cyclase (Qi et al., 2001). Additionally, species-specific pharmacological differences have been identified for the P2Y₁₁-R. While ADP may be a weak partial agonist at the human P2Y₁₁-R, ADP acts as a potent full agonist at the canine P2Y₁₁-R (Qi et al., 2001). ATP was reported to induce differentiation of HL-60 cells into neutrophil-like cells, and conventional inducers of differentiation such as DMSO and dibutyryl-cAMP increased the mRNA expression of P2Y₁₁-R. The P2Y₁₁-R has been implicated for involvement in maturation and migration of dendritic cells (Wilkin et al., 2001; Marteau et al., 2004; Idzko et al., 2007). Taken together, it appears that the P2Y₁₁-R may be involved in hematopoiesis.

P2Y₁₂-like receptors

The three P2Y receptors in the P2Y₁₂-R subgroup share amino acid sequence homology of approximately 44%. The P2Y₁₂-like receptor genes are clustered on chromosome 3, at 3q24-25 (Nomura *et al.*, 1994). Evolution of the P2Y₁₂-R family has been

fairly conserved across species. The P2Y₁₂-like receptors are found in almost all vertebrate classes, and have not been identified in non-vertebrates (Schoneberg *et al.*, 2007). In some fishes and amphibians, orthologous receptors share close homology to two receptors from the P2Y₁₂-like subgroup. For example, one ortholog is related to P2Y_{12/13} and another is related to P2Y₁₄/GPR87, suggesting a point of evolutionary distinction for these receptors.

P2Y₁₂-R

The P2Y₁₂-R is the most investigated of the subgroup due to its clinical relevance in anti-blood clotting therapeutics. Evidence for a critical physiological role of the P2Y₁₂-R in aggregation of platelets is well-accepted. Knockout mice lacking the P2Y₁₂-R exhibited prolonged bleeding times (Foster *et al.*, 2001). Platelets from P2Y₁₂-R^{-/-} mice responded to ADP with shape change as did the platelets from wild-type mice. However, platelets lacking P2Y₁₂-R did not aggregate and further analysis revealed they did not inhibit adenylyl cyclase in response to ADP. Studies with the knockout mouse underscore the role of the P2Y₁₂-R as a critical component in platelet biology. Antithrombotic therapeutics successfully interrupt platelet aggregation in response to P2Y-R signaling, as evidenced by the widely-prescribed drug clopidogrel, an active metabolite of which acts as an irreversible P2Y₁₂-R antagonist (Quinn and Fitzgerald, 1999; Gachet, 2005; Savi and Herbert, 2005).

In addition to platelets, P2Y₁₂-R are expressed throughout brain and in smooth muscle cells (Burnstock and Knight, 2004). The importance of the P2Y₁₂-R in microglial response to tissue injury was highlighted by a study comparing wild-type mice to P2Y₁₂-R^{-/-} mice (Haynes *et al.*, 2006). The P2Y₁₂-R was detected at the protein and RNA levels expressed on microglia. Wild-type microglial cultures, but not those from P2Y₁₂-R^{-/-} mice, responded to ADP with lamellipodial extensions. Furthermore, chemotaxis of P2Y₁₂-R-

expressing cells toward an ADP gradient was demonstrated with microglial cultures, and process extension and migration of microglia were observed in response to laser-induced tissue damage in living mice, but were significantly delayed in P2Y₁₂-R^{-/-} mice. This study and others define the P2Y₁₂-R as a crucial element in microglial development and response to injury (Davalos et al., 2005).

P2Y₁₃-R

The P2Y₁₃-R is similar to the P2Y₁₂-R in amino acid sequence, in G protein coupling, and in agonist profile. The P2Y₁₃-R also couples to ERK1/2 activation in CHO-K1 cells. In contrast to the P2Y₁₂-R, expression of the P2Y₁₃-R is reported in spleen, small intestine, liver, kidney, brain, and on peripheral immune cells (Communi et al., 2001a; Fumagalli et al., 2004; Wang et al., 2004), but the physiological significance of the P2Y₁₃-R has not yet been examined. An analogue of PPADS, MRS2211, recently has been described as a selective, competitive antagonist at the P2Y₁₃-R (Wirkner et al., 2004; Kim et al., 2005).

P2Y₁₄-R

The P2Y₁₄-R is the eighth member of the P2Y receptor family. It shares 44% amino acid sequence homology to the P2Y₁₂-R and P2Y₁₃-R, compared to only 22% with the P2Y₁-R; it is accordingly grouped into the P2Y₁₂-like receptor sub-family. The intronless P2Y₁₄-R gene encodes 338 amino acids (Fig. 5). While the P2Y₁₄-R was first cloned from the human myeloid cell line KG-1 (Nomura *et al.*, 1994) and relatively high levels of P2Y₁₄-R mRNA have been detected in neutrophils, expression of the P2Y₁₄-R has also been reported in the brain, lung, stomach, heart, placenta, and adipose tissue (Moore *et al.*, 2003). Although a functional role for the P2Y₁₄-R has not yet been identified, evidence suggests that one function of the receptor may be contributing to immune system homeostasis.

P2Y₁₄-R Tissue Distribution

There have been several antibodies generated to recognize the P2Y₁₄-R, although none has been fully characterized. For example, a commercially available antibody is reported to recognize the second extracellular loop of the receptor, a region that is conserved in mouse and rat sequences (Alomone, Jerusalem, Israel). This antibody was used to detect expression of glycosylated P2Y₁₄-R in glioma C6 cells (Krzeminski *et al.*, 2008), and the authors reported that non-glycosylated receptor became predominantly expressed upon serum starvation of the cells. However, results discussed in Chapter 4 of this dissertation contradicts the expression of P2Y₁₄-R in C6 glioma cells. Another P2Y₁₄-R antibody was generated against the first extracellular loop of the receptor (Lee *et al.*, 2003) and was used to detect expression of the P2Y₁₄-R on human fetal bone marrow cells. Additionally, an antibody against the C-terminus of the P2Y₁₄-R was generated for immunohistochemical studies in which P2Y₁₄-R expression was reported throughout the brain, but only in sub-populations of glial cells (Moore *et al.*, 2003). The specificity of these antibodies is unknown because results for recognition of other P2Y-R or of non-specific immunoreactivity in each experimental system were not reported. Until the usefulness of these antibodies has been validated, we still lack reliable means for detecting P2Y₁₄-R directly.

In their report of glial P2Y₁₄-R expression, Moore and colleagues also used RT-PCR to demonstrate the presence of P2Y₁₄-R transcripts in neutrophils, lymphocytes, and also in the leukocyte cell lines M-07e and UT7-Epo, as well as in HEK293 cells (Moore *et al.*, 2003). The P2Y₁₄-R message has been detected in platelets (Moore *et al.*, 2003; Dovlatova *et al.*, 2008). However, the receptor has not been shown to be functional in such cells. Other reports of tissue distribution based on RT-PCR studies include highest levels in placental and

adipose tissue, and also in stomach, intestine, lung, and heart (Chambers *et al.*, 2000).

Reports of P2Y₁₄-R mRNA upregulation in mouse uterus after estradiol treatment for seven days (Crabtree *et al.*, 2006; Crabtree *et al.*, 2008) suggest that P2Y₁₄-R expression may be regulated by circulating hormone levels.

Other reports of P2Y₁₄-R expression include microglia and astrocytes (Charlton *et al.*, 1997), non-neuronal spinal cord cells (Kobayashi *et al.*, 2006), and synoviocytes from human patients suffering from rheumatoid arthritis (Caporali *et al.*, 2008), which together may indicate a neuroprotective role for the P2Y₁₄-R.

Regulation of the P2Y₁₄-R

Expression and function of GPCRs are dynamically regulated through several mechanisms, from post-translational modifications, cellular localization and cell-stage-dependent expression to signaling events and internalization regulated by motifs and domains harbored within the receptor's sequence. Although little is known about the regulation of the P2Y₁₄-R, we can surmise that it has many potential mechanisms for regulation based on what is known of other GPCRs and shared sequence characteristics of the P2Y₁₄-R.

Like other GPCRs, the P2Y₁₄-R exhibits several distinctive amino acid sequence characteristics. At the intracellular region of transmembrane 3, the sequence includes the residues aspartate-arginine-tyrosine. This “DRY motif” is highly conserved among seven transmembrane GPCRs. In other GPCRs, these residues are suspected to interact with acidic residues in the third intracellular loop and such interactions are thought to regulate receptor activation (Ballesteros *et al.*, 2001). However, the P2Y₁₄-R does not have any acidic residues in the third intracellular loop, and 30% of seven transmembrane GPCRs, including all of the known chemokine receptors, do not exhibit an acidic residue at the expected point of

interaction. In fact, the P2Y₁₄-R sequence in the third intracellular loop is rich in positively charged residues, so the significance of the DRY motif in this receptor may be different from other GPCRs. Additionally, GPCRs are known to exhibit two conserved cysteine residues in the extracellular domains that form disulfide bonds for stabilizing the receptor's tertiary structure. Indeed, the P2Y₁₄-R has a cysteine residue in each of the four extracellular domains. The P2Y₁₄-R also exhibits potential consensus sequences for phosphorylation by protein kinase A (PKA) and protein kinase C (PKC) in its third intracellular loop, but there is no evidence available that either of these protein kinases interact with this receptor.

Similar to all other P2Y-R, potential N-glycosylation sites occur on extracellular domains of the P2Y₁₄-R. Glycosylation of the receptor was reported to modulate its function (Krzeminski *et al.*, 2008). Indeed, the glycosylation state of the P2Y₁₂-R has also been reported to bear functional consequences (Zhong *et al.*, 2004). While glycosylation of GPCRs is thought to be important for insertion into the lipid bilayer, it is possible that the glycosylation state has an impact on receptor expression or otherwise promotes a conformational orientation of the receptor that compromises ligand binding or G-protein coupling or activation. However, it remains to be determined whether glycosylation is an important mechanism for regulating the P2Y₁₄-R.

Cellular localization of the receptor may also be an important means for regulating receptor function. Confocal microscopy studies of HA-epitope tagged P2Y₁₄-R suggest that the receptor localizes to the basolateral membrane of polarized epithelial cells (Wolff *et al.*, 2005). In light of the reported P2Y₁₄-R expression in lung and in immune cells, it is possible that the P2Y₁₄-R has a specific function related to its basolateral localization in cells. The P2Y₂-R, for example, exhibits apical localization in lung epithelial cell lines (Qi *et al.*,

2005; Wolff *et al.*, 2005), and has been demonstrated to be important in mucociliary clearance (Cressman *et al.*, 1999; Donaldson *et al.*, 2000).

Desensitization is an important mechanism for GPCRs to terminate receptor signaling in the presence of chronic agonist exposure. Because it has been demonstrated that UDP-Glc is released from cells constitutively as well as after mechanical and pharmacological stimulation, it is likely that UDP-Glc is constantly present in the extracellular space. Therefore, the question arises whether the P2Y₁₄-R desensitizes and how this may impact UDP-Glc-dependent signal transduction. Other P2Y-R are regulated by desensitization, and exhibit various rates of desensitization upon agonist stimulation. The P2Y₆-R, for example is reported to desensitize after prolonged agonist stimulation (Brinson and Harden, 2001), while the P2Y₁-R and P2Y₁₂-R desensitize quickly in platelets after agonist activation leads to shape change and aggregation (Hardy *et al.*, 2005; Bourdon *et al.*, 2006). Future studies will determine whether desensitization plays a role in P2Y₁₄-R-dependent processes.

As we gain insight into the functional role of the P2Y₁₄-R, we will undoubtedly learn more about how this receptor is regulated. Myriad mechanisms have been demonstrated for regulation of other P2Y receptor functions, and the significance of amino acid sequence signals, post-translational modifications and desensitization on P2Y₁₄-R function will await further investigation.

Pharmacology and Signal Transduction

UDP-Glc has long been known as a compound that is concentrated in the ER/Golgi apparatus and is a component of the protein synthesis quality control machinery (Parodi, 2000). With the discovery that the P2Y₁₄-R is activated by UDP-Glc and three other UDP-sugars (Fig. 5), the notion of nucleotide-sugars as extracellular signaling molecules was

introduced. The rank order of potency of P2Y₁₄-R agonists has been reported as follows:
UDP-glucose \geq UDP-galactose \geq UDP-glucuronic acid > UDP-N-acetylglucosamine
(Chambers *et al.*, 2000). While UDP-Glc is considered the endogenous agonist, the other
UDP-sugars have been reported to have varying degrees of efficacy at the P2Y₁₄ receptor.
There have not been any reports of antagonists for this receptor.

UDP-Glc promoted GTP γ S binding on HEK293 membranes expressing recombinant
P2Y₁₄-R. Additionally, UDP-Glc promoted calcium mobilization when the P2Y₁₄-R was co-
expressed with the promiscuous G α 16 (Chambers *et al.*, 2000). The P2Y₁₄-R also couples to
the chimeric G $\alpha_{q/i}$ (Lazarowski *et al.*, 2003; Moore *et al.*, 2003). This chimeric G protein is a
Gq that has been engineered to couple Gi-coupled receptors to PLC (Coward *et al.*, 1999).
The P2Y₁₄-R is expected to couple to G α_i leading to inhibition of adenylyl cyclase, but this
has yet to be shown.

In some experimental systems, investigators have observed UDP-Glc-dependent Ca²⁺
mobilization, indicating that the P2Y₁₄-R may couple to PLC β isoforms, likely through
release of G $\beta\gamma$ upon activation of Gi. UDP-glucose- and UDP-galactose-dependent increases
in Ca²⁺ in rat cortical astrocytes were reported (Fumagalli *et al.*, 2003). UDP-Glc-dependent
increases in Ca²⁺ were also observed in human immature dendritic cells (Skelton *et al.*,
2003).

Physiological Significance

While the physiological role of the P2Y₁₄-R remains unclear, the reportedly high
expression levels in leukocytes in conjunction with several reports of UDP-Glc-dependent
activity in immune response assays suggests that there may be a potential role for the P2Y₁₄-
R in immune system homeostasis. P2Y₁₄-R mRNA was demonstrated to be upregulated in

rat brain after immunologic challenge with lipopolysaccharide (Moore *et al.*, 2003), suggesting that the P2Y₁₄-R may be involved in immune responses to bacterial insult, as LPS treatment has been shown to modulate release of cytokines and upregulate expression of chemokine receptors (Palin *et al.*, 2001; Banisadr *et al.*, 2002). P2Y₁₄-R mRNA has also been detected in immature human dendritic cells, which are immune cells that mature and migrate to a site of inflammation in response to insult or injury (Skelton *et al.*, 2003). UDP-Glc affected a calcium response in immature dendritic cells, suggesting that the P2Y₁₄-R may have a role in induction of maturation of dendritic cells in response to high concentrations of ligand released from injured tissues. Furthermore, Scrivens and Dickenson (2005, 2006) reported P2Y₁₄-R expression in T-lymphocytes from mice and in human neutrophils, and reported UDP-Glc-, but not other UDP-sugar-dependent inhibition of adenylyl cyclase stimulation in both cell types (Scrivens and Dickenson, 2005; Scrivens and Dickenson, 2006). In T-lymphocytes, the authors reported that all four UDP-sugar agonists partially inhibited IL-2- and anti-CD3-induced cell proliferation, suggesting that perhaps the P2Y₁₄-R is involved in T-lymphocyte biology. The authors observed no P2Y₁₄-R-dependent effect on elastase release, which is an assay for neutrophil degranulation. While it seems likely there will be a role for the P2Y₁₄-R in immune response physiology, it is too early to speculate on details related to which cell processes may be modulated by P2Y₁₄-R function.

Aims of this dissertation

The work presented in the following pages addresses specific aims of research regarding molecular pharmacology and signal transduction of the P2Y₁₄-R. In Chapter 2, studies to develop novel ligands for the P2Y₁₄-R will be discussed. Rhodopsin-based homology modeling was used to simulate theoretical interactions of known P2Y₁₄-R agonists

with the receptor. Analyses revealed the putative involvement of several residues interacting with the hexose moiety, suggesting that the glucose structure may be an important part of the molecule for receptor activation. For these studies, a cellular assay system was developed that employs the chimera $G\alpha_{q/i}$ and over-expressed $P2Y_{14}$ -R in COS-7 cells. Novel, selective ligands for the $P2Y_{14}$ -R have been developed based on structure-activity relationships, and we are continuing in this endeavor to identify high affinity agonists and antagonists that can be used as templates to propel the development of pharmacological research tools for the $P2Y_{14}$ -R. A specifically acting ligand will augment the currently available methods for studying the $P2Y_{14}$ -R and distinguishing its individual physiological role relative to other $P2Y$ receptors.

In Chapter 3, the identification of a competitive antagonist for the $P2Y_{14}$ -R in a heterologous system is reported. Few selective antagonists are available for any of the $P2Y$ receptors, causing difficulties in conclusive establishment of a physiological role for individual receptor subtypes. The lack of selective antagonists for the $P2Y_{14}$ -R has impeded investigation into the signaling properties and tissue distribution of this receptor. The identification of UDP as an antagonist at the $P2Y_{14}$ -R contributes to our knowledge of $P2Y_{14}$ -R pharmacology and will further our work toward developing a high affinity, non-hydrolyzable competitive antagonist for the receptor.

An additional element of Chapter 3 includes an investigation into the molecular pharmacology of the rat ortholog of the $P2Y_{14}$ -R, and a comparison of known ligands to determine whether the rat $P2Y_{14}$ -R functions similarly to the human receptor. Precedence for divergent pharmacological activation profiles among species orthologs has been reported for the $P2Y_4$ -R and for the $P2Y_{11}$ -R. The studies presented in Chapter 3 reveal differences in the

pharmacological profile between the human and rat P2Y₁₄-R and will be necessary criteria for assessing studies of the P2Y₁₄-R in murine model systems.

Chapter 4 details the findings that the P2Y₁₄-R couples to inhibition of adenylyl cyclase and activates ERK1/2. One goal of these studies was to generate stable cell lines for examining P2Y₁₄-R signal transduction through its natively coupling G protein. Studies performed in HEK293 epithelial cells and in C6 rat glioma cells have established that the P2Y₁₄-R couples to the Gi family of G proteins. Furthermore, the identification of a functional P2Y₁₄-R endogenously expressed in differentiated HL-60 cells provides a system for examining this receptor at expression levels and with signal transduction pathways that are likely to be similar to its native physiological activity. While P2Y₁₄-R expression has been reported in various tissues and brain regions, we are still far from understanding the physiological role of this receptor, and have barely begun to uncover the signaling networks downstream of receptor activation. With no explicit pathophysiologies in mouse or man to hint at potential functions for this receptor, model cell systems will be critical for furthering our knowledge of signal transduction and biological responses from P2Y₁₄-R activation.

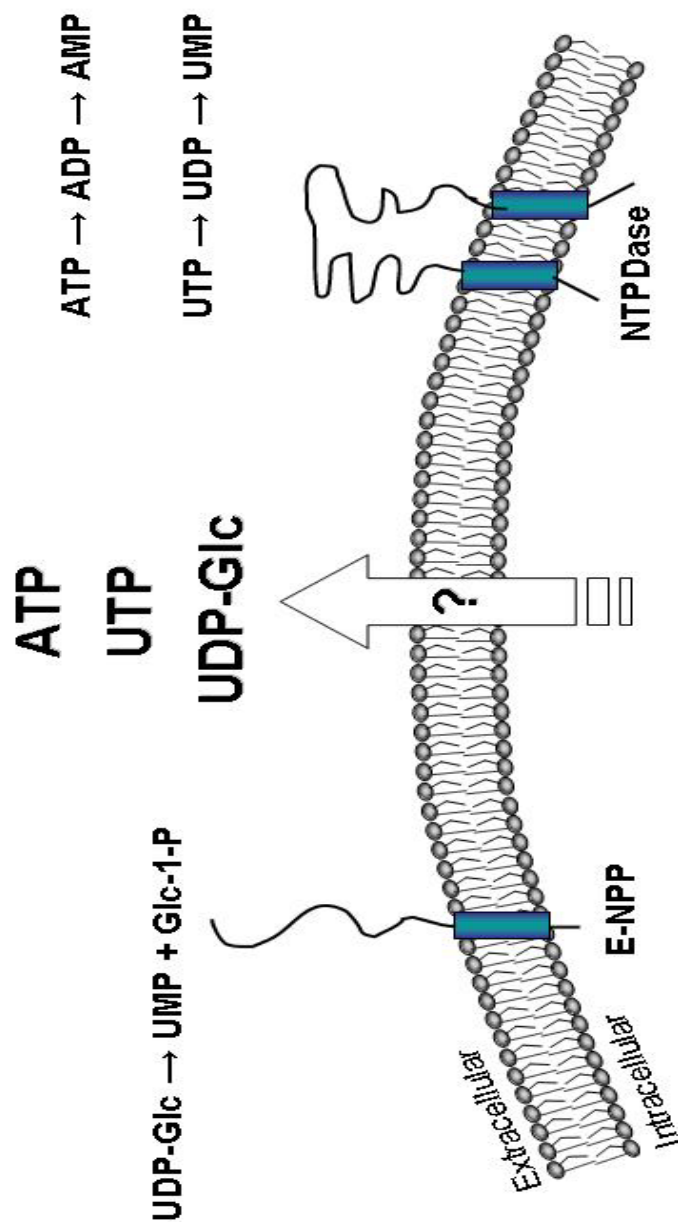
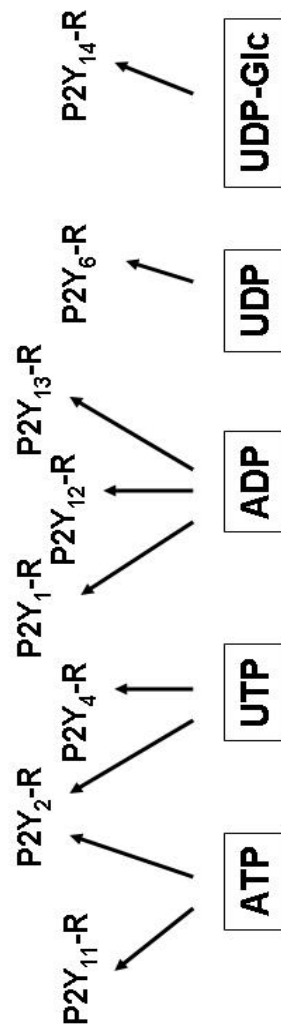


Figure 1. Nucleotides are released from cells and are metabolized by ectoenzymes. ATP, UTP, and UDP-Glc undergo regulated release from cells via an unknown mechanism. Extracellular nucleotides and nucleotide-sugars are metabolized by plasma membrane-anchored enzymes such as E-NPPs and NTPDases. Nucleotide triphosphates are degraded into nucleotide diphosphates, and subsequently into nucleotide monophosphates. UDP-Glc is metabolized by E-NPP family of ectoenzymes, resulting in UMP and glucose-1-P.



NTPDase1:	NTP → NMP + 2Pi	NDP → NMP + Pi
NTPDase2:	NTP → NDP + Pi	
NTPDase3:	NTP → NMP + 2Pi	NDP → NMP + Pi
NTPDase5:		NDP → NMP + Pi
NTPDase8:	NTP → NDP + Pi	NDP → NMP + Pi
E-NPPs (1-3):	NTP → NMP + PPi	NDP → NMP + Pi
Alkaline phosphatase:	ATP → ADP + Pi	ADP → AMP + Pi
NDPK:		NDP + N ₁ TP ↔ NTP + N ₁ DP
Adenylyl kinase:	ATP + AMP ↔ 2ADP	

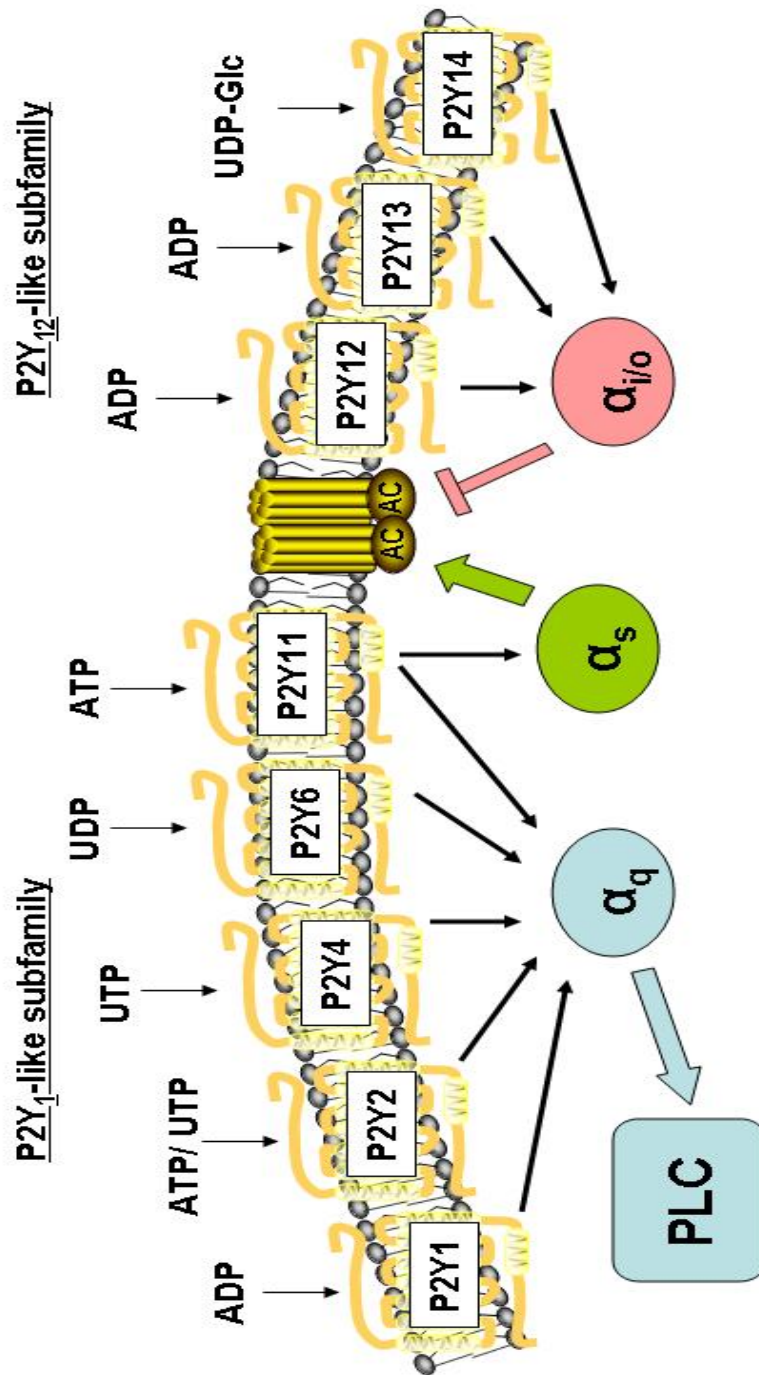


Figure 3. P2Y-R agonists and G protein coupling schematic. The metabotropic P2Y receptor family is comprised of eight members and is divided into two subfamilies, P2Y₁-like and P2Y₁₂-like, based on amino acid sequence homology and proposed G-protein coupling. P2Y₁-R, P2Y₂-R, P2Y₄-R, P2Y₆-R, and P2Y₁₁-R activate G_q, and P2Y₁₁-R also activates G_s. P2Y₁₂-R, P2Y₁₃-R, and P2Y₁₄-R activate G_i. P2Y-R are activated by nucleotides and nucleotide sugars.

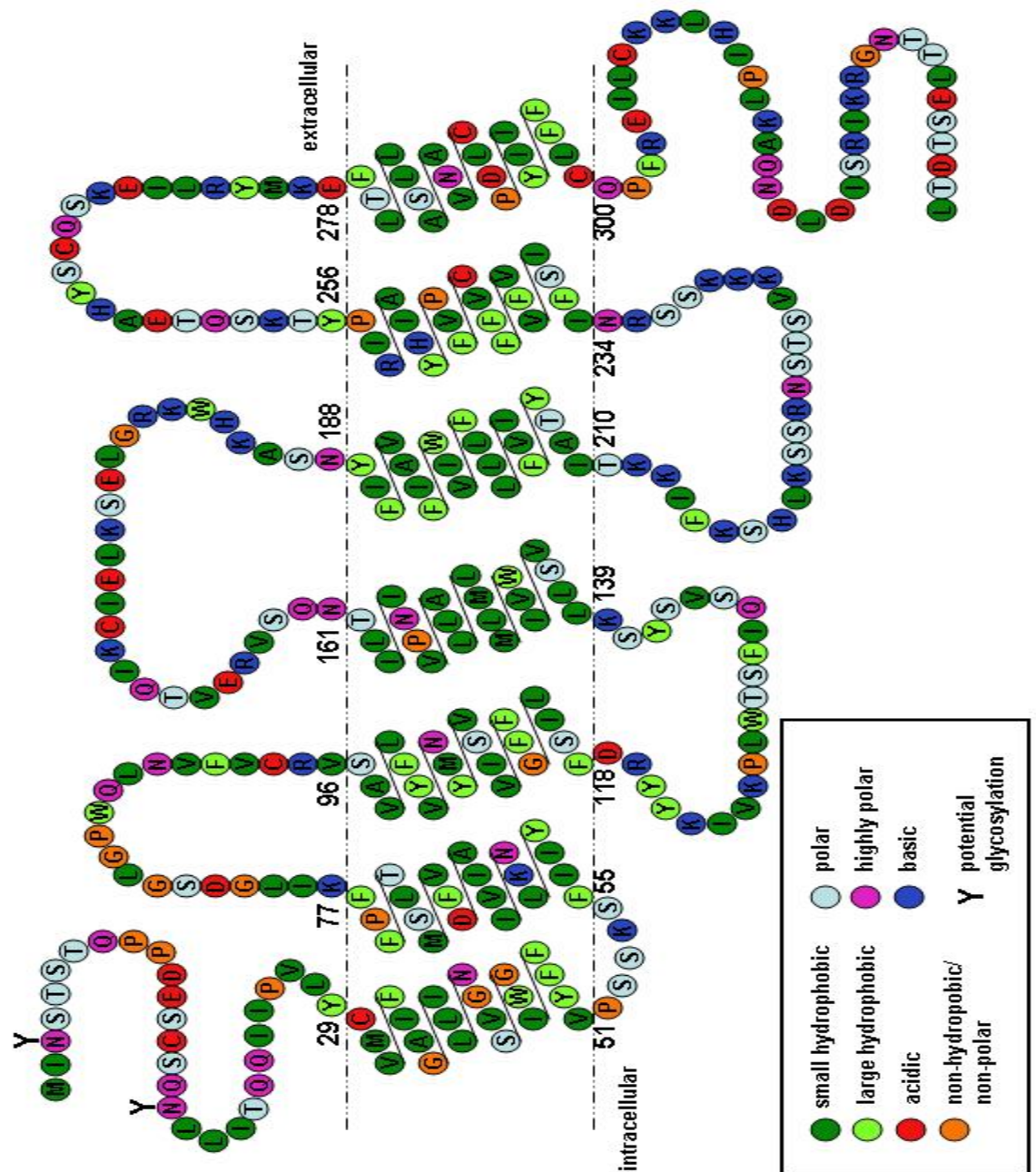


Figure 4. P2Y₁₄-R serpentine model. The P2Y₁₄-R has 338 amino acids with seven predicted transmembrane domains. The P2Y₁₄-R exhibits protein sequence features common to other P2Y-R, such as potential N-glycosylation sites at the amino-terminal region, four extracellular cysteine residues that are predicted to form 2 disulfide bridges, and aspartate118-arginine119-tyrosine120 form a “DRY motif” at the intracellular cusp of transmembrane 3.

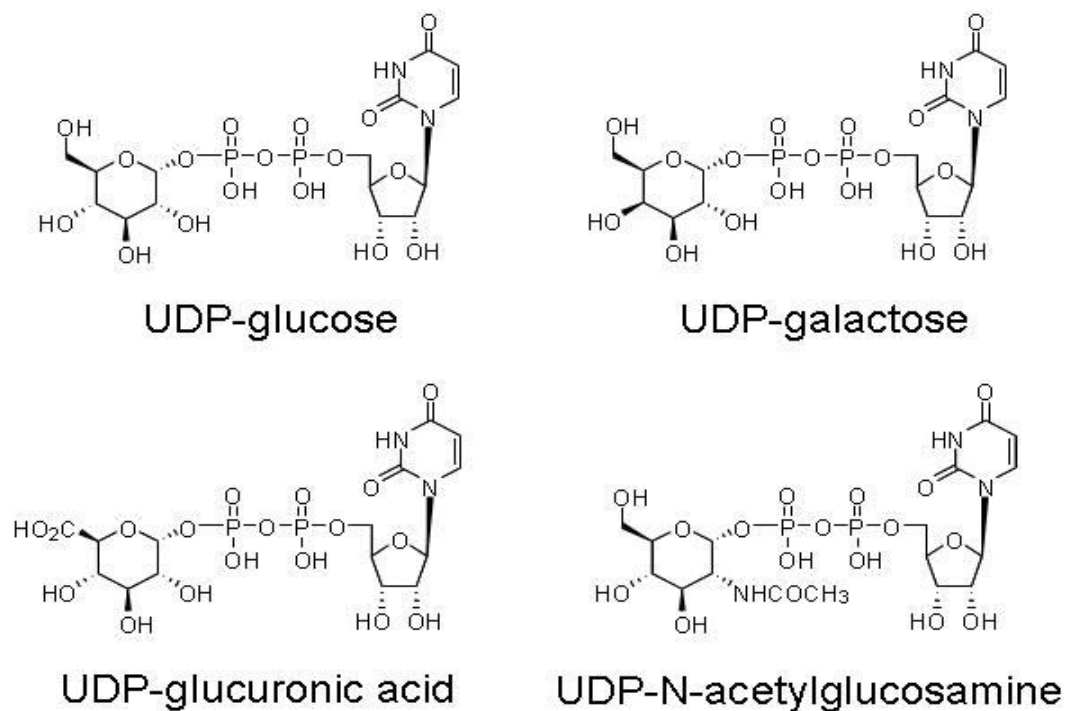


Figure 5. The P2Y₁₄-R is activated by UDP-sugars. Four agonists possessing similar chemical structures have been identified. Compared with UDP-glucose, UDP-galactose has an inverted chirality of the hydroxyl group at position 4 of the hexose ring. UDP-glucuronic acid has a carboxylic acid substituted for the hydroxyl group in UDP-glucose at position 6 of the hexose ring. UDP-N-acetylglucosamine exhibits a bulky acetamide group at position 2 of the hexose ring in comparison with the hydroxyl group of UDP-glucose.

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Chapter II. Identification of P2Y₁₄-R ligands using structure-activity relationships and molecular modeling

Introduction

The diverse family of P2Y-R are widely distributed and have emerged as therapeutic targets for several pathophysiologies (Volonte et al., 2006). The P2Y₁-R and P2Y₁₂-R play a vital role in platelet activation, and a metabolite of the drug clopidogrel, clinically used as an antithrombotic, is an irreversible antagonist at the P2Y₁₂-R (Foster et al., 2001; Hollopeter et al., 2001). Also, the P2Y₂-R is an essential regulator of chloride transport in lung and other tissues. In cystic fibrosis patients, the P2Y₂-R is a therapeutic target for improvement of mucociliary clearance (Kellerman et al., 2002). Although evidence for P2Y-R involvement in a number of physiological processes is robust, research on this receptor family has been impeded by the lack of selectively acting pharmacological agents. Further complicated by cellular release of nucleotides and the metabolism of extracellular nucleotides, characterization of P2Y-R has relied primarily on studies of recombinant receptors and detection of receptor mRNA in tissues.

Detection of P2Y receptors has been primarily based on quantification of mRNA due to the lack of reliable radioligand binding assays. Because levels of mRNA expression do not always equate to levels of expressed protein, studies attributing receptor function to presence of mRNA must be interpreted cautiously. Additionally, reports of species-specific pharmacological profiles for P2Y-R underscore the necessity to validate findings from

animal models in human tissues as well. For example, ATP was demonstrated to be an antagonist at the human P2Y₄-R and an agonist at the rat P2Y₄-R (Kennedy et al., 2000).

Ectonucleotidases are expressed on the cell surface, and they metabolize agonist for some P2Y-R subtypes even while generating agonist for another. Extracellular nucleotide concentrations are dependent on expression of ectonucleotidases, thus impacting the potency for a particular nucleotide at a given receptor. The expression of different types of ectoenzymes on the cell surface may selectively permit the activation of a subset of P2Y-R due to the availability of each nucleotide. Another inherent challenge to studies of P2Y receptors is that nucleotides are released from cells upon mechanical stimulation, with changes in the pH of cell growth medium, after hormone stimulation of cells, and upon cell lysis (Fitz, 2007).

Commercial preparations of nucleotides with a high level of purity are sometimes difficult to obtain. ATP that is contaminated with UTP, for example, would produce confounding results in studies of multiple P2Y receptors. When uridine nucleotide receptors were first cloned, the selectivities of the agonists were only clarified when contaminating UTP was converted to UDP with the use of hexokinase (Nicholas et al., 1996). Likewise, ATP that has degraded into ADP would complicate studies of receptors targeted by ATP, or mislead the investigator to believe that ATP has an effect at ADP-activated receptors. A study investigating P2Y₁₄-R function in N9 microglial cells describes different effects of UDP-Glc depending on the source of the material, underscoring potential technical complications that may occur due to contaminated compounds purchased commercially (Brautigam *et al.*, 2008).

Novel P2Y receptor ligands exhibiting high affinity and receptor selectivity have been developed with the use of high throughput screens, receptor mutagenesis studies, structure-activity relationships (SAR), and molecular modeling (Jacobson et al., 2008). High throughput screening has been limited in its usefulness for identifying P2Y receptor ligands, but in contrast, molecular modeling has recently become an effective method in conjunction with activity studies to guide development of new structural compounds.

Ligand development studies have identified novel agonists and antagonists for the P2Y₂-R, P2Y₆-R, and the P2Y₁₂-R. Greatest progress has been realized, however, with ligand development for the P2Y₁-R. The finding that the adenosine bisphosphate molecules (A3P5PS) and (A3P5P) are competitive antagonists at the P2Y₁-R was the impetus for launching a series of studies to develop high affinity antagonists for the P2Y₁-R (Boyer et al., 1996). These compounds were used in studies to delineate the role of the P2Y₁-R in platelet biology and also to distinguish the effects of the P2Y₁₂-R from those of the P2Y₁-R in signal transduction leading to platelet activation (Hechler et al., 1998; Jin et al., 1998). These bisphosphate molecules were not ideal P2Y-R ligands because of their low affinity for the P2Y₁-R and their structure was easily metabolized by ectoenzymes, so molecular modeling of the P2Y₁-R in conjunction with SAR studies produced synthetic ligands with more desirable properties, using A3P5P as a template. A selective and higher affinity antagonist, N⁶-methyl 2'-deoxyadenosine 3',5'-bisphosphate (N6MABP), also known as MRS2179, was developed subsequently, although it also was vulnerable to hydrolysis (Boyer et al., 1998). MRS2179 was widely used in studies characterizing the P2Y₁-R in platelets and in astrocytes. [³³P]MRS2179 was used for quantifying P2Y₁-R in platelets, verifying P2Y₁-R

function in platelets, and MRS2179 also was assessed for its effects on platelet aggregation when systemically administered to mice (Baurand et al., 2001).

Following success with MRS2179, ligand development studies for the P2Y₁-R became focused on non-hydrolyzable ligands that retained selectivity and high affinity at the receptor. A constrained bicyclo-hexane ring moiety was introduced in place of the ribose, and through molecular modeling studies, the Northern (N) conformation of the ring was found to be tolerated at the P2Y₁-R. One of the molecules that emerged from these studies, 2-chloro-N⁶-methyl-(N)-methanocarpa-2'-deoxyadenosine 3',5'-bis-phosphate, also called MRS2279, was the first non-nucleotide competitive antagonist at the P2Y₁-R that was widely used for characterization of the P2Y₁-R without agonist degradation (Boyer et al., 2002). [³H]MRS2279 was used in radioligand binding assays to quantify P2Y₁-R expression on various types of cells (Waldo et al., 2002). An analogous molecule with a 2-iodo substitution, MRS2500, exhibited an affinity at the P2Y₁-R of 1 nM, ten-fold higher than that of MRS2279 (Kim et al., 2003). With the development of [³²P]MRS2500, distribution of the P2Y₁-R was quantified in rat tissues and also in human platelets (Houston et al., 2006).

In addition to the development of high affinity competitive antagonists, development of high affinity selective agonists for the P2Y₁-R has also met with success. Upon determination of the high affinity and hydrolysis-resistant properties conferred by the (N)-methanocarpa modification in antagonists, (N)-methanocarpa-2-methylthio-ADP (MRS2365) was developed as a high affinity non-nucleotide agonist for the P2Y₁-R that was inactive at the ADP-activated P2Y₁₂-R and P2Y₁₃-R (Chhatriwala et al., 2004). These newest synthetic ligands for the P2Y₁-R will prove useful in further studies of P2Y₁-R function not only in platelets, but also in other tissues expressing functional P2Y₁-R.

Propelled by successes with ligand development for the P2Y₁-R, we have applied a similar rational SAR approach to discovery of high affinity ligands for the P2Y₁₄-R. Characterization of the P2Y₁₄-R has been primarily based on RNA-level receptor expression and also with studies reporting biological consequences of extracellular UDP-Glc treatment on cultured cells, but has been impaired by the lack of high affinity agonists and competitive antagonists. What we know of P2Y₁₄-R function and tissue expression in native tissues is limited, and could benefit from the development of non-hydrolyzable, selective, high affinity ligands.

The P2Y₁₄-R was first described as a UDP-glucose receptor after the receptor was cloned and expressed in a heterologous cell system, and screened against multiple potential agonists (Chambers et al., 2000). In addition to UDP-glucose, three other UDP-sugars were identified as agonists at the P2Y₁₄-R: UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine. This initial discovery provided the framework for a series of studies in a collaboration between our lab and the lab of Dr. Kenneth A. Jacobson at the National Institutes of Health. The goal of this work is to develop selective, high affinity agonists and antagonists for the P2Y₁₄-R. Molecular modeling studies have guided syntheses of UDP-Glc analogues examined for agonist action at the P2Y₁₄-R. These studies have been published (Ivanov et al., 2007; Ko et al., 2007; Ko et al., 2009), and will be reviewed herein.

Methods

Cell Culture. COS-7 cells were grown on 12-well culture dishes and maintained in DMEM supplemented with 10% FBS and 4 mM L-glutamine at 37°C in a 10% CO₂ environment. Cells were transfected 48 h prior to assay with pcDNA3.1 expression vectors encoding the human P2Y₁₄ receptor. Transfections also included a pcDNA3.1-Gα_{q/i}, a vector that directs

expression of a chimera of Gq containing the last five amino acids of Gi. This chimeric G protein promotes activation of phospholipase C through Gi-coupled receptors (Coward et al., 1999). The levels of basal inositol phosphates increase markedly in COS-7 cells upon expression of human P2Y₁₄-R and G $\alpha_{q/i}$. Since we have previously shown that this activity is dependent on release of cellular UDP-sugars (Lazarowski et al., 2003), in some experiments pcDNA3.1 expressing ectonucleotide pyrophosphatase/ phosphodiesterase-1 (ENPP1) was co-transfected with the goal of lowering basal inositol phosphate signaling and therefore increasing fold response to the agonist. FuGENE 6 (Roche Applied Science, Indianapolis, IN) was used as the transfection reagent following the manufacturer's protocol.

Inositol Phosphate Accumulation Assay. Cells were labeled 18 h prior to assay with 1 μ Ci/well [³H]-*myo*-inositol (American Radiolabeled Chemicals, St. Louis, MO) in inositol-free and serum-free DMEM. The assay was started with the addition of 10 mM LiCl with or without drugs and cells were incubated for 45 min at 37°C. The reaction was stopped by aspiration of medium and addition of ice-cold 50 mM formic acid. After neutralization with 150 mM ammonium hydroxide, [³H]inositol phosphates were isolated by Dowex column chromatography as described previously (Nakahata and Harden, 1987).

Summary of Results

The P2Y₁₄-R was subjected to rhodopsin-based homology modeling to estimate an overall structure for the receptor, and UDP-Glc was modeled into the putative binding pocket of the P2Y₁₄-R to predict points of contact in the ligand-receptor complex. From these studies, extrapolations regarding regions of the pharmacophore that would tolerate modifications as well as enhance potency at the receptor were made. Structural analogs of UDP-Glc were synthesized and pharmacologically assessed at recombinant P2Y₁₄-R. The

receptor was co-expressed with a chimeric Gq/i in COS-7 cells. Gq/i is an engineered chimeric construct that replaces the five carboxyl terminal residues of Gq with those of Gi (Coward et al., 1999). Thus, P2Y₁₄-R were artificially coupled to PLC activation, and measurement of P2Y₁₄-R function was accomplished by quantifying accumulated [³H]inositol phosphates.

Structure of the P2Y₁₄-R by molecular modeling

When all of the P2Y receptors were modeled to rhodopsin, general interpretations were made regarding similarities and differences among P2Y receptors. All of the P2Y receptors, including P2Y₁₄-R have intermolecular hydrogen bonds among the transmembrane regions that help to stabilize the protein: TM1 – TM7; TM3 – TM6, TM7; TM2 – TM4. Specific differences in the binding sites between P2Y₁-like and P2Y₁₂-like receptors were also identified (Costanzi et al., 2004).

The initial modeling study of the P2Y-R used rhodopsin as a template and built a homology model of the P2Y₁₄-R (Costanzi et al., 2004). Homology modeling is a useful tool to estimate the three dimensional orientation of a protein, and can provide information about intermolecular interactions and putative ligand binding sites. The modeling study of the P2Y₁₄-R was refined by molecular dynamics simulation, and furthermore, UDP-Glc was used in studies to identify the ligand binding site on the P2Y₁₄-R by automatic molecular docking to the P2Y₁₄-R model and then Monte Carlo Multiple Minimum (MCMM) analyses were performed (Ivanov et al., 2007; Ko et al., 2007).

The molecular dynamic simulation revealed that the first extracellular loop and the third intracellular loop exhibited the greatest flexibility in the molecule, while the second extracellular loop exhibited virtually no movement. The constrained nature of the second

extracellular loop was verified with the identification of multiple interactions among residues in that region of the protein. Hydrogen bonds can form between Arg165 and Glu166, and also between Arg165 and Lys176. Arg165 is also in proximity to Glu12 in the N-terminal region, suggesting a potential interaction between these two residues. Other potential interactions between EL2 residues and other regions of the receptor include hydrogen bonds between Glu174 and Arg253, and also between Glu166 and Lys277.

When UDP-Glc was docked into the putative binding site of the P2Y₁₄-R model, multiple potential points of interaction between ligand and receptor were identified (Fig. 6). The two possible conformations of the ribose ring (Northern versus Southern) of UDP-Glc were compared to determine which may be favored. In modeling studies of other P2Y-R-ligand complexes, the Northern (N) conformation of the ribose ring was preferred, with the exception of the P2Y₆-R (Kim et al., 2002). The 3'-hydroxyl group of the ribose ring of UDP-Glc did not form hydrogen bonds with the receptor in either (N)-UDP-Glc or (S)-UDP-Glc. The 2'-hydroxyl group, however, formed hydrogen bonds with different residues in each of the conformations. With (N)-UDP-Glc, the 2'-hydroxyl group formed a hydrogen bond with Asn104. In contrast, the 2'-hydroxyl group of (S)-UDP-Glc formed a hydrogen bond with Asn287. The modeling studies indicated that either of the conformations of UDP-Glc may be tolerated, and this hypothesis was probed experimentally with UDP-Glc containing a carbocyclic analogue of the ribose, a methanocarpa ring, and results of which will be discussed below.

The uracil ring of UDP-Glc was in close proximity to several residues, suggesting potential interactions between ligand and receptor at these points (Fig. 6). Tyr29 is a highly conserved residue among P2Y receptors, and has been identified as a residue that may

interact with the uracil moiety in other P2Y-R (Costanzi et al., 2004). Likewise, it may also be important in ligand binding at the P2Y₁₄-R, as the oxygen atom at position 4 of the uracil ring in UDP-Glc was close to Tyr29 in the P2Y₁₄-R model. Additional interactions are predicted to occur between the oxygen atom at position 2 of the uracil ring with Asn287 and/or Val288. Other potentially important interactions for receptor binding to the uracil moiety may be between the 3-NH group of uracil and Val32 and Val288.

The phosphate groups of UDP-Glc were also analyzed for potential interactions with the P2Y₁₄-R (Fig. 6). The α -phosphate of UDP-Glc associated with the hydroxyl groups of Ser284 and with residue Thr280, which is highly conserved among P2Y-R. Another proposed receptor interaction with the phosphate chain of UDP-Glc is with Lys171, which is located in the second extracellular loop of the P2Y₁₄-R. Other P2Y₁₂-like receptors also have been proposed to interact with the ligand phosphate chain at an EL2 lysine. However, other proposed interactions between the phosphate chain and residues in TM6 and TM7 in the P2Y₁₂-like receptors do not appear to be critical for phosphate group interactions with the P2Y₁₄-R. The hexose moiety of UDP-Glc is predicted to form many hydrogen bonds with residues in the P2Y₁₄-R, most of which are located in the second extracellular loop and transmembrane regions (Fig. 6). Hydroxyl groups on the hexose ring likely form hydrogen bonds with one or more of the following residues when the P2Y₁₄-R binds UDP-Glc: Arg253 (TM6), Lys277 (TM7), Lys171 (EL2), Glu174 (EL2), and Glu166 (EL2).

Other UDP-sugars that are known agonists were used in modeling studies of the P2Y₁₄-R (Ko et al., 2009). UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine are all similar in structure to UDP-glucose except at the sugar moiety (Table 1). UDP-galactose has a hydroxyl group at position 4 of the hexose ring like UDP-

glucose, but the hydroxyl group has an inverted chirality. UDP-glucuronic acid is like UDP-glucose except that there is a carboxylic acid group at position 6 of the hexose, while UDP-glucose has only a hydroxyl group at that position. UDP-N-acetylglucosamine is the least like the other UDP-sugars. At the 2 position of the hexose ring, UDP-Glc has a hydroxyl group, but UDP-N-acetylglucosamine has a bulky acetamide group. UDP-N-acetylglucosamine has been observed to exhibit the least potency of the four UDP-sugars at the P2Y₁₄-R (Table 1), and molecular modeling may give us an idea as to why that may be true. When each of the UDP-sugars was docked into the P2Y₁₄-R model, they all assumed a relatively similar position to UDP-Glc in the putative binding site and were proposed to maintain most of the hydrogen bonds observed for UDP-Glc. However, in the case of UDP-N-acetylglucosamine, the bulky acetamide group did not appear to form any interactions with the receptor and caused a slight shift in the orientation of the receptor in that region. While it is not clear whether an altered receptor orientation is responsible for the lower potency of UDP-N-acetylglucosamine at the P2Y₁₄-R, it is likely that the acetamide group at position 2 of the hexose ring is responsible for steric occlusion of the receptor binding site. Further docking studies substituted other sugar moieties for glucose in an attempt to guide design of novel agonists at the P2Y₁₄-R.

Molecular modeling studies of the P2Y₁₄-R were informative with regard to identifying the putative ligand binding site of the receptor and assisted in predictions of receptor conformation within the lipid bilayer and potential intermolecular interactions. These studies revealed that the hexose moiety of UDP-Glc appears to be the most flexible region of the molecule for purposes of synthesizing novel ligands for the P2Y₁₄-R, and this prediction is well supported by results from biological assays as described below.

a. Uracil and Ribose Modifications

Most of the modifications made to UDP-glucose on the uracil or ribose rings yielded an inactive molecule at the P2Y₁₄-R (Table 2). Specifically, substitution of the uracil moiety with the other bases cytidine, guanine, or adenine produced a compound with no effect. Modifications at the 5-position of the uracil ring (iodo-, azido-, amino-) of UDP-Glc abolished agonist activity. Two uracil modifications were tolerated. A 4-thio substitution on the uracil ring retained agonist activity and 4-thio-UDP-Glc was equipotent to UDP-Glc (Fig. 7A). A methylated thio group at the same position was not tolerated, resulting in a compound with no effect. A thio substitution at the 2 position, 2-thio-UDP-Glc, resulted in a compound that exhibited at least six-fold greater potency than UDP-Glc (Fig. 7B).

More than a dozen ribose-modified compounds were synthesized. These modifications included 2'- and 3'-deoxy compounds, substitutions at varying positions on the ring, and replacement of the ribose with a rigid methanocarba moiety, in either the Southern or Northern conformation. All of the ribose modified compounds had no effect at the P2Y₁₄-R (Table 2), indicating that this part of the molecule is important for maintaining stability of the ligand-receptor complex. Additionally, UMP, UDP, UTP, and several dinucleotides were tested for agonist activity, and no effect of any of these compounds was observed. From these results we have determined that modifications to the ribose moiety of UDP-Glc are not tolerated, and while more permissive, few modifications to the uracil ring are tolerated that retain agonist activity at the P2Y₁₄-R. This restrictive SAR of the P2Y₁₄-R is in sharp contrast to that of other P2Y receptors, since modifications to the base or ribose moieties were mostly tolerated and retained efficacy, although not necessarily potency.

b. Hexose Modifications

Informed by molecular modeling studies of the P2Y₁₄-R in complex with various potential ligands, compounds with substitutions at the glucose ring were synthesized and tested as novel ligands. Generally, substitutions of other sugars for glucose were well tolerated (Table 3). UDP-fructose, UDP-mannose, and UDP-inositol were identified as novel agonists at the P2Y₁₄-R with potencies similar to that of UDP-Glc. Additional sugar substitutions were made to synthesize UDP-arabinose, UDP-fucose, and UDP-ribose, which all retained activity at the P2Y₁₄-R. Thus, it appears that most simple sugar substitutions are tolerated in place of the hexose position and exhibit agonist action at the P2Y₁₄-R.

It is clear that chirality of the hydroxyl groups on the hexose ring is critical in ligand recognition. UDP-galactose is structurally similar to UDP-Glc. However, the inverted chirality of the hydroxyl group at position 4 slightly reduces the potency of UDP-galactose at the P2Y₁₄-R (Table 1). Similarly, while a chiral inversion at position 1 of the hexose ring, UDP- β -glucose, decreased the potency of UDP-Glc at the P2Y₁₄-R only two-fold, an inverted chirality of the hydroxyl group at position 2 resulted in UDP-mannose, a compound with three-fold lower potency than UDP-Glc (Table 3).

More in depth studies were undertaken to probe the pharmacophore with particular consideration to the hexose moiety. Fluoro-substitutions for the hydroxyl moieties at each of the hexose ring positions revealed reduced potencies upon fluoro substitution at the 2' and 6' positions, likely destabilizing the receptor-ligand complex due to the loss of a hydrogen bond. The importance of the hydrogen bond at the 2' position was further demonstrated by the observations that inversion of the 2'-hydroxyl chirality reduced the potency of UDP-Glc at the P2Y₁₄-R, and 2'-deoxy-UDP-Glc exhibited greatly reduced efficacy (Table 3).

To explore the possibility of attaching a bulky chain onto a P2Y₁₄-R ligand, a functional congener approach was employed (Li et al., 1999). An amide-linked chain was attached to the carboxylic acid moiety of UDP-glucuronic acid. As was predicted from modeling studies, these UDP-glucuronic acid analogues exhibited agonist activity at the P2Y₁₄-R with similar potencies compared to UDP-glucuronic acid (Table 3). We concluded that position 6 of the hexose moiety is a tractable portion of the pharmacophore, and thus, it may be possible to conjugate large molecules to a P2Y₁₄-R agonist through a carefully-placed functional group without losing affinity for the receptor. These findings provide an opportunity to synthesize new P2Y₁₄-R ligands with bulky chemical groups, compounds which may be utilized in pharmacological studies. Fluorophore-conjugated ligands that are selective for the P2Y₁₄-R would be useful in characterizing receptor expression in tissues and cells. Likewise, attachment of probes that increase affinity or selectivity for the receptor would provide a useful tool for quantifying and further characterizing the P2Y₁₄-R in various tissues.

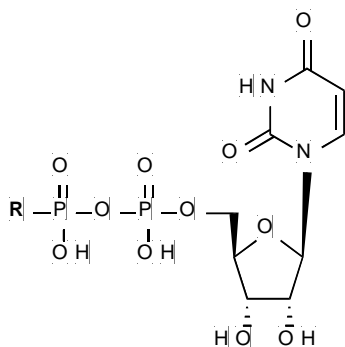
Conclusions

Molecular modeling functions as a rational starting point to guide objectives of ligand structure-activity relationship studies for the purpose of developing novel ligands for the P2Y₁₄-R. Molecular modeling has predicted UDP-Glc contact sites at the uracil, phosphate, and hexose moieties. The SAR studies, however, expanded our understanding of the nature of those interactions with regard to the role of each putative contact point in stabilizing the receptor-ligand complex. Furthermore, studies of UDP-Glc analogues informed us about how modifications at each part of the molecule impacts potency at the receptor. The second extracellular loop of the P2Y₁₄-R appears to play an important role in stabilizing the hexose

moiety of the UDP-Glc molecule, and transmembrane domains three, six, and seven also harbor contact points for the phosphate and uracil moieties.

Agonist binding pockets of other P2Y receptors have also been predicted to form among residues in the TM3, TM6, TM7, and the EL2 (Costanzi et al., 2004), although different orientations of agonist in each receptor's binding pocket dictates the particular residues that are important for agonist binding for each receptor. Evidence from comparisons modeling ADP in the binding sites of the P2Y₁-R or the P2Y₁₂-R suggests that the same agonist uses non-correlative residues in each of the distinctive binding pockets. While 44% shared sequence homology between the P2Y₁₄-R and the P2Y₁₂-R may ostensibly indicate closely aligned binding sites, differences in ligand selectivity undoubtedly make differences in binding modes necessary. Comparisons to previous modeling studies with the P2Y₁₂-R and P2Y₁₃-R suggest that the P2Y₁₄-R uses some analogous residues – an arginine in TM6, a lysine in TM7, and another lysine in EL2 - in forming a binding pocket. These studies are ongoing, and as we learn more about the structure of the P2Y₁₄-R and its ligand selectivity, we can pursue further the development of high affinity ligands for use in characterizing P2Y₁₄-R function and expression.

Table 1. P2Y₁₄-R agonists. Table of P2Y₁₄-R agonists previously identified with corresponding EC₅₀ values measured by phosphatidylinositol hydrolysis assays in COS-7 cells. *Left*, structure of UDP-sugars, and R denotes the sugar substitution shown in the table.



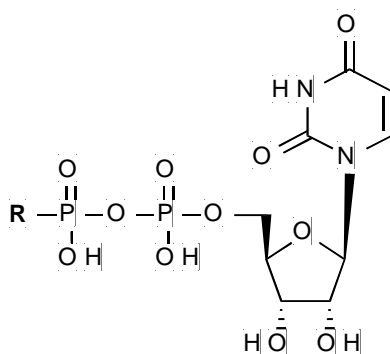
Agonist	R	EC ₅₀ , $\mu\text{M} \pm \text{SE}$
[UDP-glucose]		0.261 ± 0.053
[UDP-galactose]		0.670 ± 0.090
[UDP-N-Ac-glucosamine]		4.38 ± 1.05
[UDP-glucuronic acid]		0.370 ± 0.070

Table 2. Ribose and uracil modifications on UDP-Glc are largely inactive at the P2Y₁₄-R. Compounds assessed for agonist activity at the P2Y₁₄-R include ribose-modified, base-modified, ribose- and base-modified UDP-Glc analogues, and also dinucleotides. EC₅₀ values reported are derived from phosphatidylinositol hydrolysis assays in COS-7 cells transiently expressing the P2Y₁₄-R and G_{q/i} as described in Methods. (NE= no effect at 10 μM)

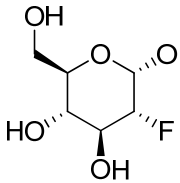
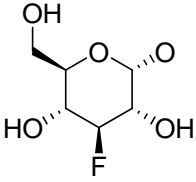
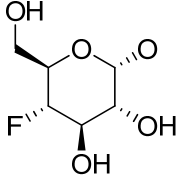
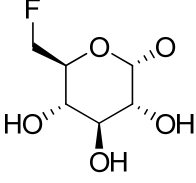
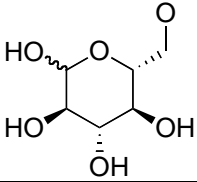
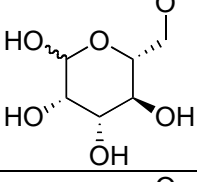
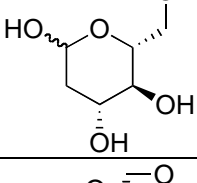
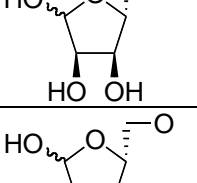
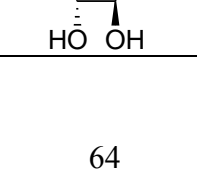
Modification	EC ₅₀ at hP2Y ₁₄ receptor, μM ± SE
Ribose modified	
2'-deoxy	NE
2'-deoxy-2'-azido	NE
2'-deoxy-2'-amino	NE
cyclic-2'- deoxy-2'-aminocarbonyl-3'-O	NE
3'-deoxy	NE
2',3'-dideoxy-2'-methoxy-carbonyl	NE
2'-fluoro-2'-deoxyara	NE
(S)-methanocarba	NE
(N)-methanocarba	NE
(S)-mc-2'-deoxy	NE
carbocyclic	NE
Base-modified	
4-thio	0.29 ± 0.16
4-methylthio	>10
2-thio	0.049 ± 0.02
5-iodo	NE
5-azido	NE
5-amino	NE

Base = C	NE
Base = A	NE
Base = G	NE
<i>N</i> ⁴ -methoxy-CDP-glucose	<50% max at 10 μM
Ribose- and Base-modified	
2'-deoxy-C	NE
2'-deoxy-T	NE
2'-deoxy- 5-F-U	NE
Dinucleotides	
Up ₂ U	NE
Cp ₂ C	NE

Table 3. Modifications at the hexose moiety of UDP-Glc are largely tolerated as agonists at the P2Y₁₄-R. All of the simple sugars substituted for the glucose moiety retain agonist activity at the P2Y₁₄-R, most with similar potency as UDP-Glc. EC₅₀ values were determined from phosphatidylinositol assays in COS-7 cells transiently expressing the P2Y₁₄-R. 2'-Substitutions or deletion of the hydroxyl group reduce potency or efficacy. Functional congener substitutions are the last two compounds in the table. *Inset*, structure of UDP-sugar, and R denotes the hexose substitution shown in the table.



Modification	Structure R =	EC ₅₀ at hP2Y ₁₄ receptor, $\mu\text{M} \pm \text{SE}$
UDP- β -[1]glucose		0.588 ± 0.130
UDP-[1]mannose		0.910 ± 0.150
UDP-[1]fucose		0.562 ± 0.173
UDP-N-Ac-galactosamine		0.810 ± 0.090

UDP-2'-F-[1]glucose		2.5 ± 0.9
UDP-3'-F-[1]glucose		0.361 ± 0.094
UDP-4'-F-[1]glucose		0.567 ± 0.156
UDP-6'-F-[1]glucose		0.905 ± 0.429
UDP-[6]glucose		0.373 ± 0.073
UDP-[6]mannose		0.658 ± 0.022
UDP-[6]2'-deoxyglucose		<50% max at 10 μ M
UDP-[5]ribose		0.238 ± 0.084
UDP-[5]arabinose		0.460 ± 0.057

UDP-[1]fructose		0.880 ± 0.210
UDP-[6]fructose		0.323 ± 0.069
UDP-inositol		1.88 ± 1.10
UDP-[2-(acetylamino)-2-deoxy α -D-glucopyranosyl] methyl phosphonyl uridine 5'yl phosphate		<50% max at 10 μ M
UDP-glucuronyl-ED-Ac		0.496 ± 0.067
UDP-glucuronyl-ED-Boc		0.951 ± 0.277

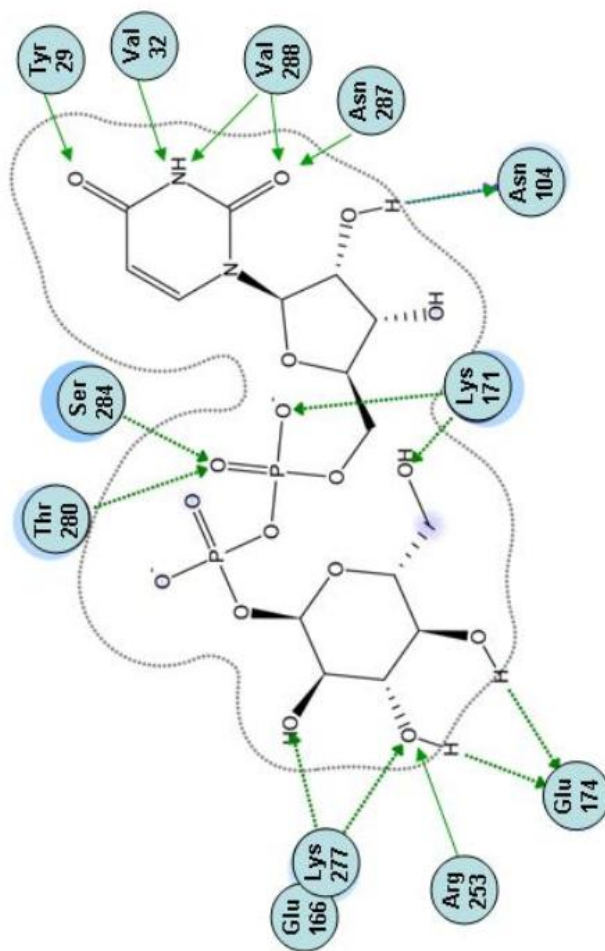


Figure 6. Potential points of interaction between UDP-Glc and the P2Y₁₄-R. Diagram of putative binding site for UDP-Glc depicting amino acid side chains that may form bonds with various atoms on the UDP-Glc molecule. Tyr29 and Val32 lie in the amino terminal end; Asn104 is in TM3; Arg253 is in TM6; Thr280, Ser284, Asn287, and Val288 are in TM7; Glu166, Lys171 and Glu174 are in EL2; Lys277 is in EL3. |

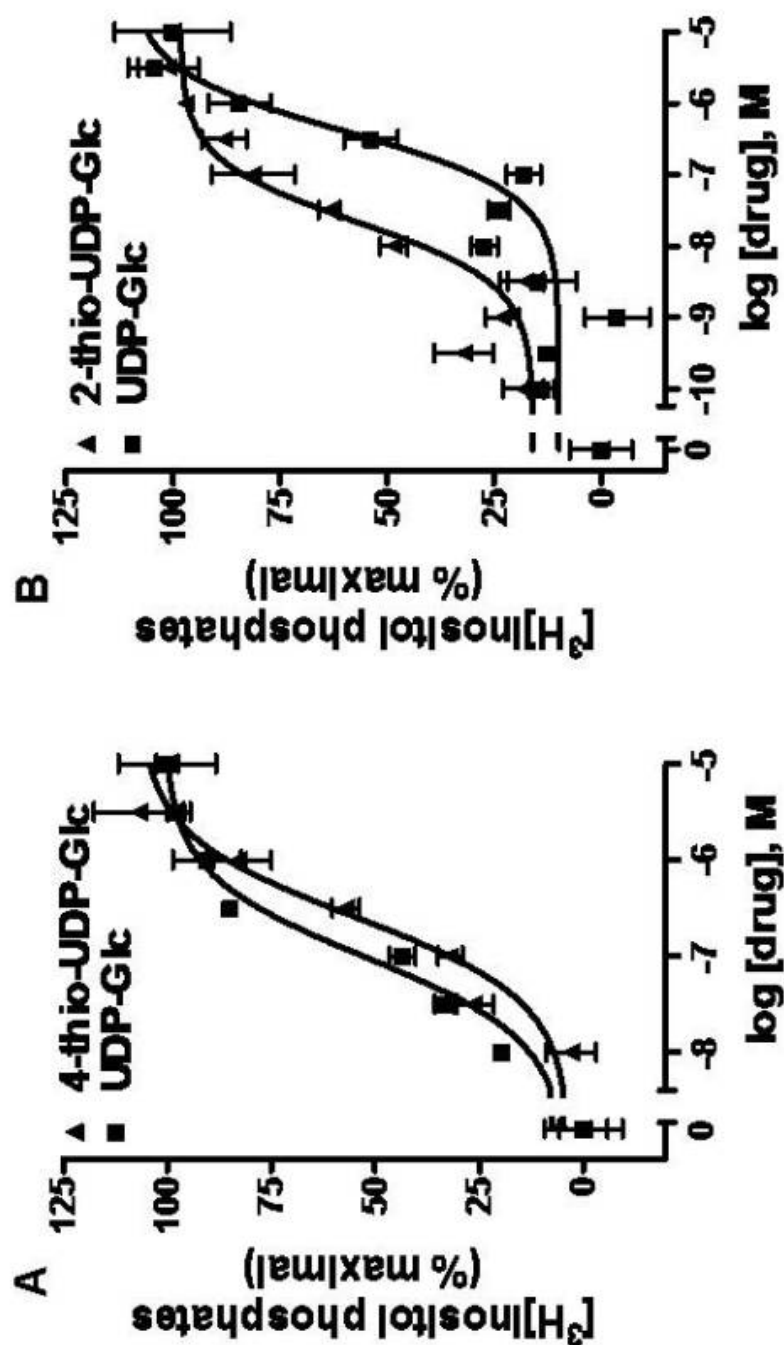


Figure 7. UDP-Glc analogues with 4'- and 2'-uracil ring modifications are novel agonists at the P2Y₁₄-R. COS-7 cells expressing P2Y₁₄-R and Gq/i were radiolabeled with [³H]inositol, and incubated with varying concentrations of indicated compound for 45 min. A, 4-thio-UDP-Glc is equipotent to UDP-Glc. B, 2-thio-UDP-Glc is >6X more potent than UDP-Glc at the P2Y₁₄-R.

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Chapter III. UDP is a competitive antagonist at the human P2Y₁₄ receptor

Abstract

G-protein coupled P2Y receptors (P2Y-R) are activated by adenine and uridine nucleotides. The P2Y₁₄ receptor (P2Y₁₄-R) is activated by at least four naturally occurring UDP-sugars, with UDP-glucose (UDP-Glc) being the most potent agonist. With the goal of identifying a competitive antagonist for the P2Y₁₄-R, UDP was examined for antagonist activity in COS-7 cells transiently expressing the human P2Y₁₄-R and a chimeric G protein that couples Gi-coupled receptors to stimulation of phosphoinositide hydrolysis. UDP antagonized the agonist action of UDP-Glc, and Schild analysis confirmed the antagonism was competitive ($pK_B = 7.28$). UDP β S also antagonized the hP2Y₁₄-R with an apparent affinity similar to that of UDP. In contrast, no antagonist activity was observed with ADP, CDP, or GDP, and other uracil analogues also failed to exhibit antagonist activity. Antagonist activity of UDP was not observed at other human P2Y receptors. In contrast to its antagonist action at the human P2Y₁₄-R, UDP was a potent agonist ($EC_{50} = 0.35 \mu M$) at the rat P2Y₁₄-R. These results identify the first competitive antagonist of the P2Y₁₄-R and demonstrate pharmacological differences between receptor orthologs.

Introduction

P2Y receptors are members of the superfamily of G-protein coupled receptors and are activated by adenine and uridine nucleotides and nucleotide-sugars. At least eight receptors comprise the P2Y-R family. P2Y₁, P2Y₂, P2Y₄, and P2Y₆ receptors are coupled to Gq and

activate phospholipase C, while P2Y₁₂, P2Y₁₃, and P2Y₁₄ receptors couple to Gi, leading to the inhibition of adenylyl cyclase and activation of ion channels (Burnstock, 2006). The P2Y₁₁-R uniquely couples both to Gq to activate phospholipase C and to Gs to stimulate adenylyl cyclase (Communi et al., 1997; Qi et al., 2001).

The human P2Y₁₄-R was identified as the eighth legitimate member of the P2Y receptor family (Chambers et al., 2000). UDP-glucose (UDP-Glc) was proposed to be the endogenous agonist for the P2Y₁₄-R, with UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine acting as less potent P2Y₁₄-R agonists. P2Y₁₄-R mRNA was detected in a broad range of human tissues including placenta, stomach, intestine, adipose, brain, lung, spleen and heart, and also in specialized cells such as circulating neutrophils (Chambers et al., 2000; Scrivens and Dickenson, 2006). The rat and mouse P2Y₁₄-R exhibit 80% and 83% amino acid identity to the human receptor, and both rodent orthologs are activated by known agonists with a similar profile to that of the human P2Y₁₄-R (Freeman et al., 2001).

Cellular UDP-Glc is released in a constitutive manner into the medium of a broad range of cell types. While most extracellular nucleotides are metabolized quickly, UDP-Glc accumulates in the medium of several cell lines (Lazarowski et al., 2003). The mechanisms of UDP-Glc release and extracellular metabolism remain unclear. Observations of UDP-Glc-promoted signaling were reported in multiple types of immune cells (Fumagalli et al., 2003; Skelton et al., 2003; Scrivens and Dickenson, 2005; Muller et al., 2005), suggesting that the P2Y₁₄-R may have a yet to be defined role in the regulation of immune system homeostasis.

Characterization of the P2Y₁₄-R has been slowed by the lack of a selective competitive antagonist. We have identified and developed novel, selective ligands for several P2Y receptors that have proven useful for pharmacological resolution of molecularly

defined P2Y-R in cells and tissues (Boyer et al., 1996; Jacobson et al., 2006; Houston et al., 2006; Houston et al., 2007). Accordingly, we are interested in identifying a selective antagonist for the P2Y₁₄-R.

Ault and Broach (2006) recently used a yeast model system in which various nucleotides and nucleotide-sugars were examined for their ability to stimulate growth of mutant P2Y₁₄-R-expressing yeast cells in studies focused on identification of mutant P2Y₁₄ receptors with differential agonist sensitivities. Studies performed using one of these mutant receptors revealed that UDP antagonized UDP-Glc-promoted receptor activation in a concentration-dependent manner (Ault and Broach, 2006). We hypothesized that UDP acts as a competitive antagonist at the wild-type P2Y₁₄-R, and therefore, used a transfected COS-7 cell system to investigate UDP activity at the human and rat P2Y₁₄-R. Here we show that UDP is a selective and competitive antagonist of the human P2Y₁₄-R. Thus, signals emanating from extracellular UDP apparently occur as a consequence of activation of the P2Y₆-R as well as through antagonism of the P2Y₁₄-R. Surprisingly, UDP is a potent full agonist at the rat P2Y₁₄-R.

Methods

Materials

UDP-Glc, UDP, ADP, CDP, GDP, and 2-methyl-thio-ADP were purchased from SigmaAldrich (St. Louis, MO). UP₃U was synthesized according to Methods detailed in Pendergast et al (2001). The source of UP₄U was as previously reported (Ivanov et al 2007). ATP and UTP were purchased from GE Healthcare (Piscataway, NJ). [³²P]PPi was synthesized as described previously (Lazarowski et al., 2003). UDPβS as well as a

mammalian expression vector for ENPP1 were generous gifts from Dr. José Boyer of Inspire Pharmaceuticals, Durham, NC.

Cell Culture and Transfection

COS-7 cells were grown on 12-well culture dishes and maintained in DMEM supplemented with 10% FBS and 4 mM L-glutamine at 37°C in a 10% CO₂ environment. Cells were transfected 48 h prior to assay with pcDNA3.1 expression vectors encoding either the human or rat P2Y₁₄ receptor with an N-terminal Hemagglutinin epitope. The expression vector for the hP2Y₁₄-R was obtained as previously reported (Lazarowski et al 2003). Transfections also included pcDNA3.1-Gα_{q/i}, a vector that directs expression of a chimera of Gα_q containing the last five amino acids of Gα_i. This chimeric G protein promotes activation of phospholipase C through Gα_i-coupled receptors (Coward et al., 1999). The levels of basal inositol phosphates increased markedly in COS-7 cells upon expression of human or rat P2Y₁₄-R and Gα_{q/i}. Since we previously illustrated that UDP-sugars are basally released by various cell types (Lazarowski et al., 2003), in some experiments pcDNA3.1 expressing ENPP1 was co-transfected with the goal of hydrolyzing extracellular nucleotide sugars and potentially decreasing inositol phosphate accumulation in the absence of added P2Y₁₄-R agonists. FuGENE 6 (Roche Applied Science, Indianapolis, IN) was used as the transfection reagent following the manufacturer's protocol.

Inositol Phosphate Accumulation Assay

Cells were labeled 8-18 h prior to assay with 0.5-3 μCi/ well [³H]-*myo*-inositol (American Radiolabeled Chemicals, St. Louis, MO) in inositol-free and serum-free DMEM. Assays were initiated with the addition of 10 mM LiCl with or without drugs, and incubations continued for 45 min at 37°C. Reactions were stopped by aspiration of medium and addition

of ice-cold 50 mM formic acid. After neutralization with 150 mM ammonium hydroxide, [^3H]inositol phosphates were isolated by Dowex column chromatography as described previously (Nakahata and Harden, 1987). Stable cell lines for P2Y₁, P2Y₂, P2Y₄, P2Y₆, or P2Y₁₁ receptors were generated in 1321N1 human astrocytoma cells as previously described (Nicholas et al., 1996; Kennedy et al., 2000). Experiments testing the potential activity of UDP at the P2Y₂-R and P2Y₄-R included hexokinase to eliminate contaminating UTP as described previously in Nicholas et al. (1996). Briefly, UDP was treated with 10 U/mL hexokinase in the presence of 22 mM glucose for 1 h at 37°C, and 1 U/mL hexokinase was included in the assay buffer for the duration of the incubation. Variability in cpm of [^3H]inositol phosphate accumulation across experiments occurred due to differences in the amount of [^3H]inositol utilized for labeling and/or the duration of the prelabeling period.

Measurement of UDP-Glc in the cell medium

Quantification of UDP-Glc was performed as previously described (Lazarowski et al. 2003). Briefly, incubations were in a final volume of 150 μl containing known or unknown amounts of UDP-glucose, 25 mM HEPES, pH 7.4, and 0.5 U/ml UDP-glucose pyrophosphorylase from baker's yeast (Sigma), and 100 nM [^{32}P]PPi (200,000 cpm). Incubations were terminated by addition of 0.3 mM PPi and immediate heating of samples for 2 min at 95°C, and formation of [^{32}P]UTP was quantified by high performance liquid chromatography as described (Lazarowski et al. 2003).

Quantification of P2Y₁₄-R expression

Cells were seeded in 12-well plates at 5×10^4 cells/well 3 days prior to assay and transfected with mammalian expression vectors as described above. Cells were fixed with 0.4 ml of 4% paraformaldehyde for 30 min at room temperature, washed twice with 1 ml of HBSS plus $\text{Ca}^{2+}/\text{Mg}^{2+}$, and incubated for 30 min at room temperature with 0.4 ml of DMEM plus 50 mM HEPES, pH 7.1, and 10% fetal bovine serum. Cells were incubated with mouse HA.11 monoclonal antibody at a 1:1000 dilution in 0.4 ml of medium for 1 h at room temperature. Following two washes with 1 ml of HBSS plus $\text{Ca}^{2+}/\text{Mg}^{2+}$, cells were incubated with [^{125}I]rabbit anti-mouse IgG antibody diluted to 1:500 in 0.4 ml of medium for 2 h at room temperature. Following another series of washing steps, cells were solubilized in 0.4 ml of 1 M NaOH overnight and transferred to glass tubes for quantification of radioactivity in a gamma counter.

Rat P2Y₁₄-R subcloning

The rat homolog of the P2Y₁₄-R (rP2Y₁₄-R) was amplified from rat genomic DNA using Pfu polymerase with the following primers: (5'-GAGACGCGTCCGACAACACAACAACCACAGAAC-3') and (5'-AGACTCGAGTTACAAAGTATCTGTGCTTTCC-3'). The primers contained either a MluI (upstream primer) or a XhoI (downstream primer) restriction site, respectively (sites are underlined) to facilitate cloning. The amplification conditions were 94°C for 5 min; 35 cycles of 94°C for 45 s, 55°C for 45 s, 72°C for 90 s; and a final extension for 4 min at 72°C. The amplified rP2Y₁₄-R fragment was digested with MluI and XhoI, purified, and ligated into a similarly digested, modified pcDNA3 expression vector, which fuses an HA-epitope to Asp-2 at the N-terminus of the receptor. An individual clone encoding the

receptor was sequenced and found to be identical to the published sequence (Freeman et al., 2001).

Data Analyses

The results from each experiment are expressed as mean \pm S.E. from triplicate samples, and were analyzed using GraphPad Prism 4.0 software. All experiments were repeated at least three times with similar results. Schild analysis was performed using EC50 values from the concentration effect curves for UDP-Glc generated in the absence and presence of increasing concentrations of UDP. The pK_B was calculated using the equation: $\log ([A']/[A] - 1) = \log [B] - \log pK_B$ (Arunlakshana and Schild, 1959), where $[A']$ is the concentration of UDP-Glc necessary to produce fifty percent of the maximal effect in the presence of antagonist $[B]$ and $[A]$ is the concentration of agonist necessary to produce fifty percent of the maximal effect in the absence of antagonist. Drug response data presented in Figs 3A, 5A-D, and 7B are normalized as a percentage of the response observed with a maximally effective concentration (usually 10 μ M) of UDP-Glc. Statistics were carried out using Student's t test.

Results

Agonist activity of UDP-Glc at the hP2Y₁₄-R.

To assay the functional activity of the hP2Y₁₄-R, we utilized COS-7 cells transiently co-expressing the hP2Y₁₄-R and a $G\alpha_{q/i}$ chimera. The $G\alpha_{q/i}$ chimera is a $G\alpha_q$ protein in which the last five amino acids at the carboxyl terminus have been substituted with those of $G\alpha_i$. This chimeric $G\alpha$ subunit is activated by GPCRs that couple to the $G\alpha_i$ family of G-proteins and signal through downstream $G\alpha_q$ effectors such as phospholipase C (Coward et al., 1999). Expression of the hP2Y₁₄-R or the $G\alpha_{q/i}$ chimera alone in COS-7 cells resulted in levels of [³H]inositol phosphate accumulation similar to that observed in cells expressing

empty vector alone. [^3H]Inositol phosphate accumulation was not changed by the addition of 100 μM UDP-Glc to cells expressing empty vector, the hP2Y₁₄-R, or G $\alpha_{q/i}$ (Fig. 1). Co-expression of the hP2Y₁₄-R and G $\alpha_{q/i}$ resulted in increased [^3H]inositol phosphate accumulation in the presence of buffer alone as we previously reported (Lazarowski et al., 2003). Addition of 100 μM UDP-Glc to cells co-expressing the hP2Y₁₄-R and G $\alpha_{q/i}$ resulted in a two-fold increase in inositol phosphate accumulation, consistent with agonist-promoted activation of phospholipase C (Fig. 8).

To investigate the nature of the hP2Y₁₄-R-dependent [^3H]inositol phosphate accumulation in the absence of added agonist, we co-expressed ENPP1 with the hP2Y₁₄-R and G $\alpha_{q/i}$ in COS-7 cells with the goal of removing any released nucleotide/nucleotide-sugar potentially present in the medium. UDP-Glc levels (3.6 ± 1.9 nM) in the bulk medium from COS-7 cells expressing hP2Y₁₄-R and G $\alpha_{q/i}$ were similar to that of control cells (3.3 ± 0.3 nM). In contrast, co-expression of ENPP1 in cells also expressing hP2Y₁₄-R and G $\alpha_{q/i}$ resulted in an approximately 78 % reduction in UDP-Glc levels (0.8 ± 0.5 nM) compared to control. Although expression of ENPP1 alone had no effect on basal [^3H]inositol phosphate accumulation, expression of ENPP1 with hP2Y₁₄-R and G $\alpha_{q/i}$ resulted in an approximately 40% decrease ($p < 0.01$) in basal [^3H]inositol phosphate levels compared to cells expressing receptor and G protein alone (Fig. 9A). Expression of ENPP1 had no effect on surface expression of the hP2Y₁₄-R as quantified with an immunoassay (data not shown; see Methods), and did not notably change the concentration effect curve for added UDP-Glc (Fig. 9B). Thus, we conclude that the hP2Y₁₄-R-dependent elevation of [^3H]inositol phosphate levels in the absence of added agonist occurs largely because of autocrine/paracrine release of P2Y₁₄-R agonist. However, these results do not entirely rule

out the possibility that the overexpressed P2Y₁₄-R exhibits constitutive activity in this test system.

Antagonist Effect of UDP at the hP2Y₁₄-R.

Four UDP-sugars were identified as agonists at the hP2Y₁₄-R, and neither UTP nor UDP exhibited agonist activity (Chambers et al., 2000). To determine whether UDP is an antagonist at the wild-type hP2Y₁₄-R, we generated a series of concentration-effect curves for UDP-Glc-promoted stimulation of phospholipase C in the presence of increasing concentrations of UDP (Fig. 10A). UDP caused a parallel rightward shift of the UDP-Glc concentration-effect curve, and Schild analysis (Fig. 10B) confirmed that the antagonism produced by UDP was competitive (slope = 1.15 ± 0.06 , $n = 3$). The pK_B of UDP for antagonism of the hP2Y₁₄-R was 7.28 ± 0.04 .

We also assessed whether UDP exhibited antagonist activity at other P2Y-R stably expressed in 1321N1 human astrocytoma cells. P2Y₁-R was maximally activated by 1 μ M 2MeSADP (Fig. 11A), P2Y₂-R and P2Y₄-R were each activated by 3 μ M UTP (Fig. 11B, C), and P2Y₁₁-R was activated by 100 μ M ATP (Fig. 11D). Although 10 μ M UDP completely blocked a near-maximal concentration of UDP-Glc at the hP2Y₁₄-R (Fig. 10), UDP had no effect at any other P2Y receptors tested. Thus, we conclude that UDP is a selective antagonist at the hP2Y₁₄-R.

To determine whether the antagonist effect of UDP at the hP2Y₁₄-R is specific to the uracil structure, we also tested other nucleotides and nucleotide derivatives as antagonists at the hP2Y₁₄-R. In contrast to the action of UDP, other nucleoside diphosphates including ADP, CDP, and GDP, at concentrations of 10 μ M or 100 μ M did not inhibit UDP-Glc (3 μ M)-promoted [³H]inositol phosphate formation (Fig. 12). We also tested whether other

uridine-based molecules would antagonize activation of the hP2Y₁₄-R by UDP-Glc. Neither UTP, UP₃U, nor UP₄U inhibited UDP-Glc activation of the receptor, although each of these nucleotides, when tested alone, produced a stimulatory effect in untransfected COS-7 cells (data not shown). The discovery of antagonist activity of UDP at the hP2Y₁₄-R was also supported by the observation that the UDP analogue, UDPβS, inhibited activation of this receptor by UDP-Glc (Fig. 13). The IC₅₀ value observed for UDPβS was similar to that determined for UDP under the same assay conditions. From these results, we conclude that UDP appears to be unique among naturally-occurring nucleotides in its capacity to inhibit UDP-Glc-dependent activation of the hP2Y₁₄-R.

Effects of UDP at the rP2Y₁₄-R.

Since pharmacological studies often are carried out with rat or mouse tissues, it is important to assess whether receptor orthologs exhibit pharmacological selectivity similar to those of human P2Y-R. Based on the precedent that ATP acts as an antagonist at the human P2Y₄-R but is an agonist at the rat P2Y₄-R (Bogdanov et al. 1998; Kennedy et al. 2000), we compared the action of UDP at the rP2Y₁₄-R with its action at the hP2Y₁₄-R. The rat P2Y₁₄-R, which exhibits approximately 80% amino acid sequence identity to the hP2Y₁₄-R, and almost 90% identity in the transmembrane regions alone, was reported to display a similar UDP-sugar selectivity to that of the hP2Y₁₄-R (Freeman et al., 2001), but the actions of other uridine nucleotides on the rP2Y₁₄-R have not been reported.

Expression of either the rP2Y₁₄-R or Gα_{q/i} in COS-7 cells had no effect on [³H]inositol phosphate accumulation as compared to untransfected cells, but co-expression of receptor and Gα_{q/i} resulted in markedly increased basal accumulation (Fig. 14A). Consistent with other reports (Freeman et al., 2001), UDP-Glc was a potent agonist at the rP2Y₁₄-R

(Fig. 14B). Whereas UDP had no effect on inositol phosphate accumulation in wild-type COS-7 cells, in cells expressing $G\alpha_{q/i}$ alone, or in cells expressing the rP2Y₁₄-R alone (data not shown), concentration of UDP-dependent increases in formation of [³H]inositol phosphates occurred in COS-7 cells co-expressing the rat P2Y₁₄-R with $G\alpha_{q/i}$ (Fig 14B). The maximal stimulatory effect observed with UDP was similar to that observed with UDP-Glc as were the EC₅₀ values of UDP ($0.35 \mu\text{M} \pm 0.17$) and UDP-Glc ($\text{EC}_{50} = 0.28 \mu\text{M} \pm 0.05$). No additivity was observed between UDP and UDP-Glc on rP2Y₁₄-R-promoted [³H]inositol phosphate formation (Fig. 14C).

Discussion

In this study, we show that UDP is a competitive antagonist at the human P2Y₁₄-R, and this action is receptor-selective since UDP does not inhibit agonist-promoted activation of other hP2Y receptors. Moreover, the activity of UDP at the P2Y₁₄-R is species-dependent since we observed that UDP is a potent, and apparently full, agonist at the rat P2Y₁₄-R.

Chambers et al. (2000) reported in their initial study of the hP2Y₁₄-R that UDP has no agonist activity, and we observed similar results in the studies reported here. Using a reporter system in yeast, Ault and Broach (2006) generated a mutant hP2Y₁₄-R displaying a mutation in intracellular loop 1 and various mutations in several of the transmembrane regions. This mutant, selected for its ability to support growth of yeast at lower concentrations of UDP-Glc than the wild-type receptor, exhibited an enhanced UDP-Glc-stimulated response that was inhibited by UDP, and a K_B in the micromolar range was reported. The >20-fold higher potency of UDP observed in our studies likely reflects large differences in the assay systems employed. For example, whereas incubations with nucleotide were for minutes in the current study they were for hours in assays measuring

P2Y₁₄-R mediated regulation of growth of yeast. Our results illustrate that UDP is a potent competitive antagonist of the wild-type hP2Y₁₄-R.

Demonstration of antagonist action at the hP2Y₁₄-R suggests that UDP may have broader physiological importance as an extracellular signaling molecule than has been previously appreciated. Both UDP and UDP-glucose are known to be released from cells, although the mechanisms of their release remain unclear. UDP is the most potent and selective agonist of the hP2Y₆-R (Lazarowski and Harden, 1994; Communi et al., 1996), and physiological responses attributed to UDP-initiated P2Y₆-R-promoted signaling include modulation of IL-8 production in monocytes (Warny et al., 2001) and human mature dendritic cells (Idzko et al., 2004). Additionally, UDP was observed to induce a positive inotropic effect in mouse cardiomyocytes (Wihlborg et al. 2006) and to promote ion transport in human placental cytotrophoblast cells (Roberts et al., 2006). Our data indicate that potential contributions of the P2Y₁₄-R to responses associated with UDP must be considered. While reported distribution of P2Y₆-R mRNA overlaps with that of P2Y₁₄-R mRNA in many cells and tissues, such as lung, heart, placenta, and neutrophils (Communi et al., 1996; Moore et al., 2001), it remains unclear whether the two receptor types are co-expressed in the same cells or in different cells that share the same extracellular space.

The actions of extracellular neurotransmitters and hormones are highly regulated by their release, metabolism, and reuptake. The possibility that direct antagonism of GPCR activation occurs by extracellular signaling molecules has been suggested by observations that ATP is a competitive antagonist of the hP2Y₁₂-R (Cusack and Hourani, 1982; Bodor et al., 2003) and of the hP2Y₄-R (Bogdanov et al., 1998; Kennedy et al., 2000). The physiological relevance of UDP antagonism at the hP2Y₁₄-R will be important to investigate,

as will the idea that UDP simultaneously activates the hP2Y₆-R while inhibiting the hP2Y₁₄-R.

Our finding that UDP has agonist activity at the rP2Y₁₄-R was surprising. Study of the rat and human receptors under identical conditions rules out trivial explanations of this observation. These data do not unambiguously rule out the possibility that UDP is a partial agonist at the human receptor under some conditions. However, the agonist versus antagonist action of the nucleotide at the rat versus human P2Y₁₄-R has been observed over a broad range of expression levels of these two receptors. Our activity data suggest that the binding affinity of UDP for the human and rat receptors in fact are quite similar, but development of a radioligand binding assay will be necessary to fully assess this assertion. The fact that the maximal agonist activity of UDP was similar to that of UDP-Glc over a broad range of P2Y₁₄-R expression levels (data not shown) suggests that the intrinsic efficacy of UDP at the rat P2Y₁₄-R is similar to that of UDP-Glc.

The differential activity of UDP observed between the rat and human orthologs of the P2Y₁₄-R shares similarities to the actions of ATP at the P2Y₄-R. Kennedy et al. (2000) compared the ligand selectivities of the rat and human P2Y₄ receptors under conditions that minimize effects of released nucleotides and of extracellular bioconversion of nucleotides and observed that ATP is an agonist at the rat P2Y₄-R and a competitive antagonist at the human P2Y₄-R. Residues in the second extracellular loop of the P2Y₄ receptor are the primary determinants for the agonist versus antagonist activity of ATP between the two species orthologs (Herold et al., 2004). Like the P2Y₄-R, the P2Y₁₄-R shares approximately 80% amino acid sequence identity between the rat and human orthologs, with 90% identity when analysis is restricted to transmembrane regions only. Recent work by Ko et al. (2007)

defines the human P2Y₁₄ receptor through structure-activity studies in conjunction with molecular modeling studies. Residues in the second extracellular loop of the hP2Y₁₄-R are predicted to interact with the diphosphate moiety and hydroxyl groups on the hexose ring of UDP-Glc. Comparative modeling of the rat P2Y₁₄-R and receptor mutagenesis directed from these predictions may identify key domains responsible for agonist efficacy at the hP2Y₁₄-R.

The mouse P2Y₁₄-R has been cloned and is reported to be activated by the same UDP-sugar agonists as the human and rat receptors (Freeman et al., 2001). The rat and mouse P2Y₁₄-R share 89% overall amino acid sequence identity and are essentially identical in their transmembrane spanning domains and the second extracellular loop. Thus, we anticipate that the agonist action of UDP observed with the rat receptor will be similarly observed at the mouse P2Y₁₄-R.

The finding that UDP acts as a competitive antagonist at the hP2Y₁₄-R provides an excellent template for rational synthesis of antagonist analogues that exhibit high affinity at the hP2Y₁₄-R. Our structure-activity studies of UDP analogues at the hP2Y₆-R (Besada et al., 2006) also provide potential avenues for development of P2Y₁₄-R antagonists that do not act as ligands for the P2Y₆-R. Synthesis of a hydrolysis-resistant competitive antagonist for the P2Y₁₄-R is an obvious goal, as is a high affinity radiolabeled antagonist.

UDP-glucose, UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine previously were identified as full or partial agonists at human and rodent P2Y₁₄-R (Chambers et al., 2000; Freeman et al., 2001). The pharmacological selectivity for the P2Y₁₄-R is now broadened with the finding that UDP also acts at this receptor. The identification of UDP as a competitive antagonist for the hP2Y₁₄-R provides new insight into the physiological

regulation of this receptor, and should be of pharmacological importance in delineating the functional roles subserved by this signaling protein.

Acknowledgments

We appreciate the excellent technical assistance of Sonia de Castro for the synthesis of UP₃U.

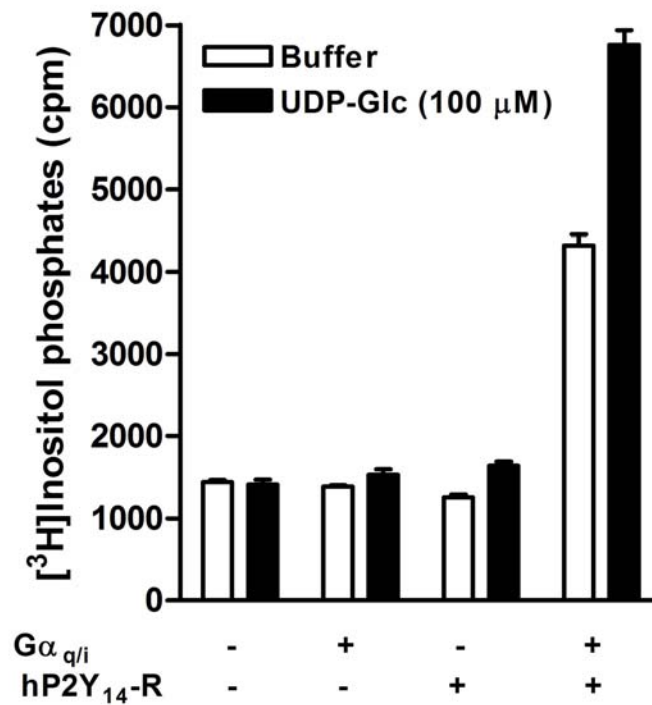


Figure 8. hP2Y₁₄-R- and $G\alpha_{q/i}$ -dependent increases in [³H]inositol phosphate accumulation. COS-7 cells were transfected with empty vector or expression vectors for hP2Y₁₄-R and/or $G\alpha_{q/i}$ as described in Methods. Cells were labeled with [³H]inositol for 18 h prior to assay. LiCl (10 mM) buffer was added to the cells to inhibit inositol monophosphatase, and the cells were simultaneously incubated in the absence or presence of 10 μ M UDP-Glc for 45 min. [³H]inositol phosphates were isolated as described in Methods. Data shown are means \pm S.E. calculated from triplicate samples and are representative of results obtained in three independent experiments.

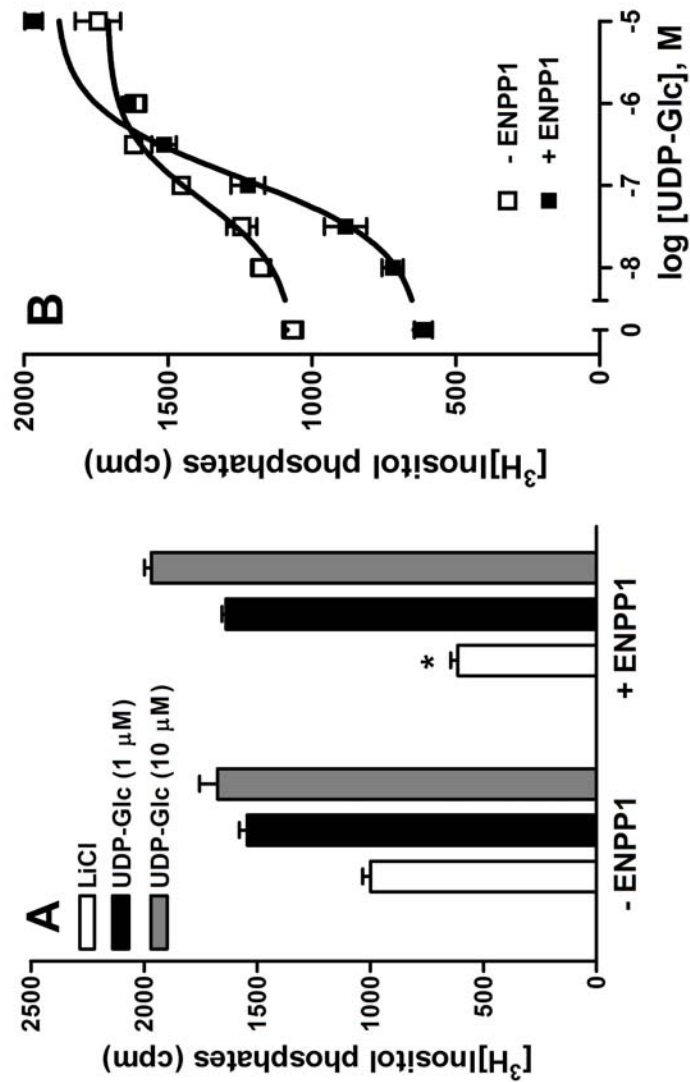


Figure 9. Co-expression of ENPP1 reduces the basal activation of the hP2Y₁₄-R. COS-7 cells were co-transfected with expression vectors for hP2Y₁₄-R and Gα_{q/i} with (+) or without (-) an expression vector for ENPP1. A) [³H]Inositol-labeled cells were incubated with 10 mM LiCl in the absence or presence of UDP-Glc. * p<0.01 B) [³H]Inositol-labeled cells were incubated with 10 mM LiCl in the absence or presence of UDP-Glc at the indicated concentrations. Data shown are means ± S.E. calculated from triplicate determinations.

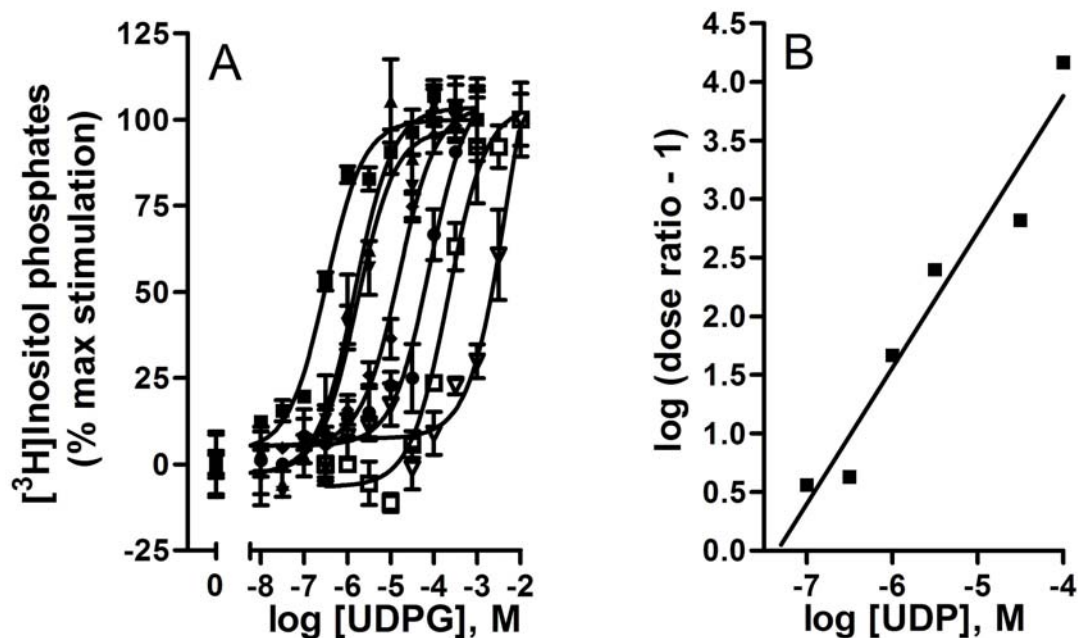


Figure 10. UDP is a competitive antagonist at the hP2Y₁₄-R. A) [³H]Inositol-labeled COS-7 cells co-expressing hP2Y₁₄-R and Gα_{q/i} were incubated with LiCl (10 mM) and increasing concentrations of UDP-glucose in the absence or presence of the indicated concentrations of UDP: ■, Buffer; ▲, 0.1 μM; ▼, 0.3 μM; ◆, 1 μM; ●, 3 μM; □, 30 μM; ▽, 100 μM. Data shown are means ± S.E. calculated from triplicate samples and are representative of results obtained in three independent experiments. B) EC₅₀ values from the concentration-effect curves in (A) were used for Schild regression analysis. The data shown are results from a representative experiment repeated three times to yield a mean pK_B of 7.28 ± 0.04 and a slope of 1.15 ± 0.06.

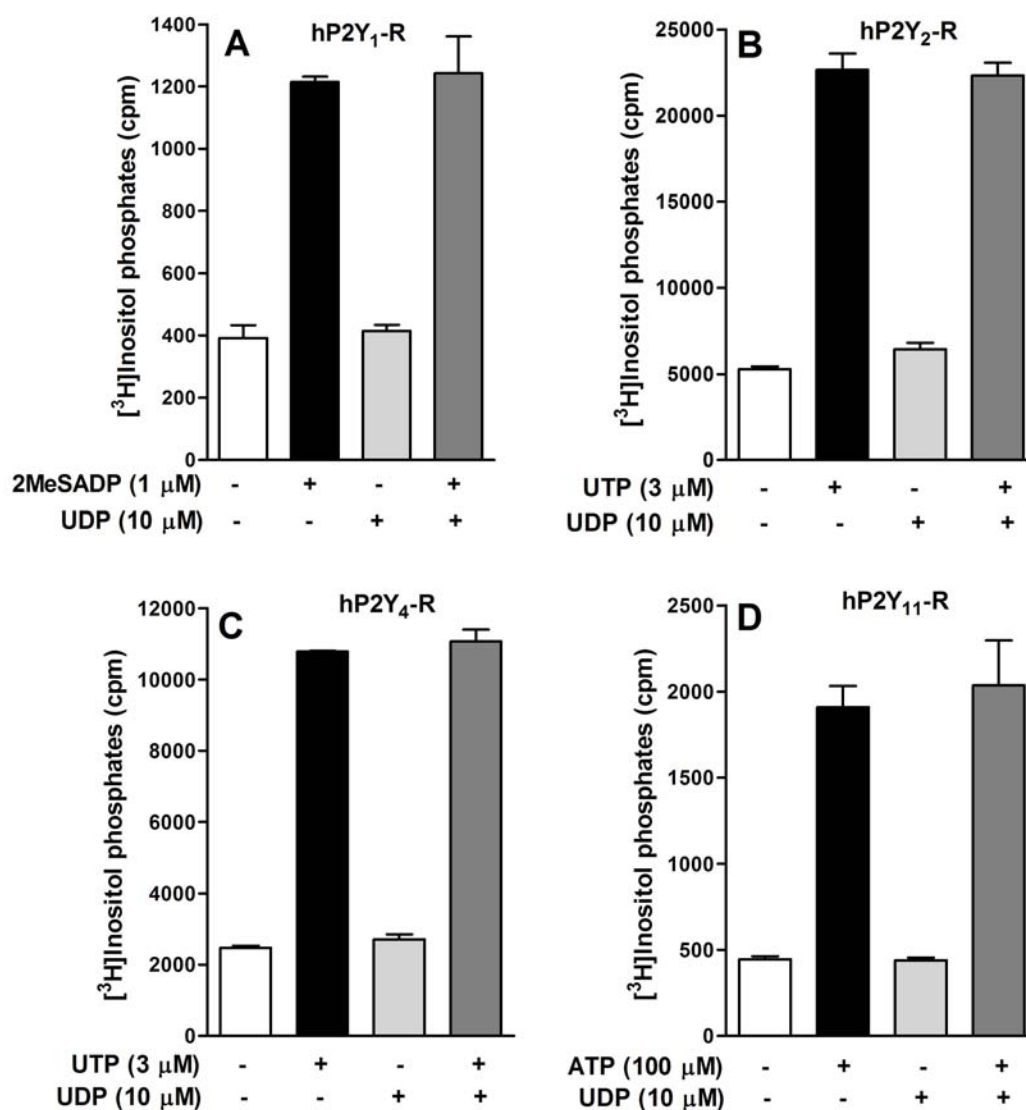


Figure 11. UDP is a selective antagonist at the hP2Y₁₄-R. [³H]Inositol-labeled 1321N1 human astrocytoma cells stably expressing either the A) human P2Y₁-R, B) human P2Y₂-R, C) human P2Y₄-R, or D) human P2Y₁₁-R were incubated for 30 min with 10 mM LiCl with the cognate agonist (indicated), or 10 μ M UDP, or both agonist and UDP, and inositol phosphate accumulation was quantified as described in Methods. Data shown are means \pm S.E. calculated from triplicate samples and are representative results obtained in three or more independent experiments.

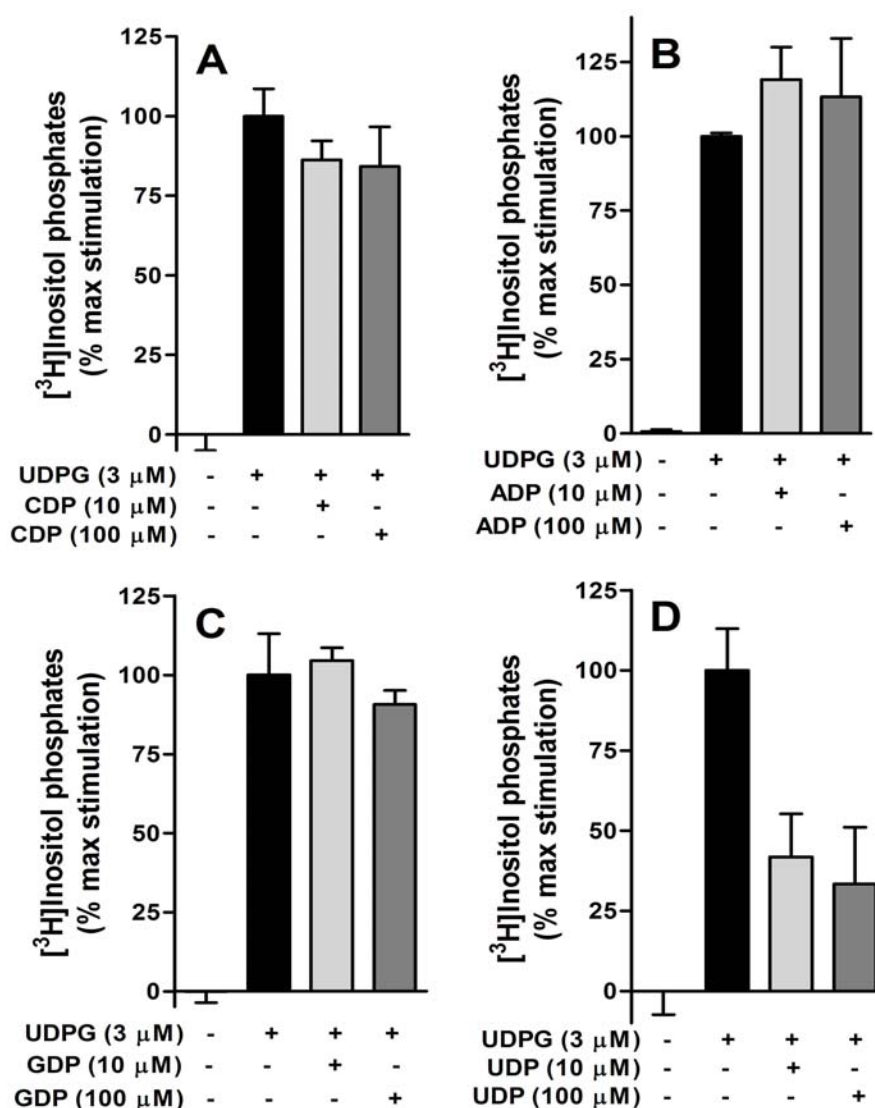


Figure 12. UDP is unique among nucleotide diphosphates for its antagonist effect at the hP2Y₁₄-R. A) CDP, B) ADP, C) GDP, or D) UDP (10 μ M or 100 μ M) and LiCl (10 mM) were applied simultaneously with 3 μ M UDP-Glc to [3 H]inositol-labeled COS-7 cells transiently expressing hP2Y₁₄-R and G $\alpha_{q/i}$. Data were normalized to values from maximal activation of hP2Y₁₄-R by UDP-Glc alone, and the LiCl alone value was subtracted from each data point. The data shown in (A), (C), and (D) are results from a representative experiment repeated three times. The data shown in (B) is the average of results from four experiments.

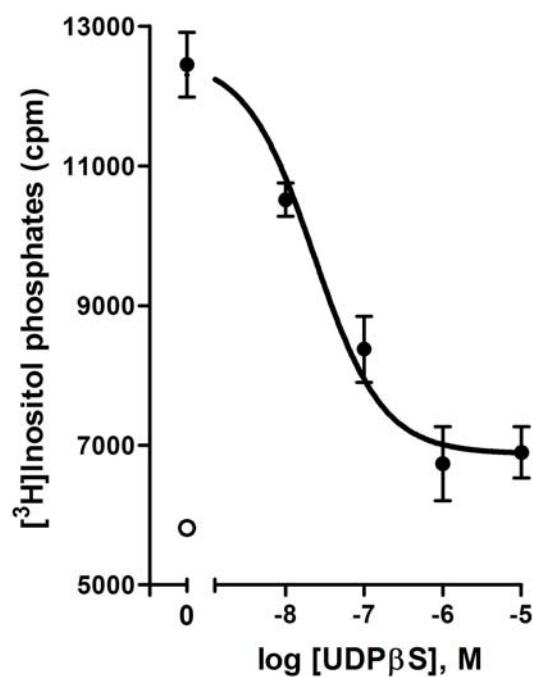


Figure 13. Antagonist effect of UDPβS at the hP2Y₁₄-R. [³H]inositol-labeled COS-7 cells transiently expressing hP2Y₁₄-R and Gα_{q/i} were incubated with 10 mM LiCl in the absence (○) or presence (●) of 1 μM UDP-Glc in the presence of the indicated concentrations of UDPβS for 30 min. The data shown are means ± S.E. of triplicate determinations, and the results are representative of those obtained in three experiments.

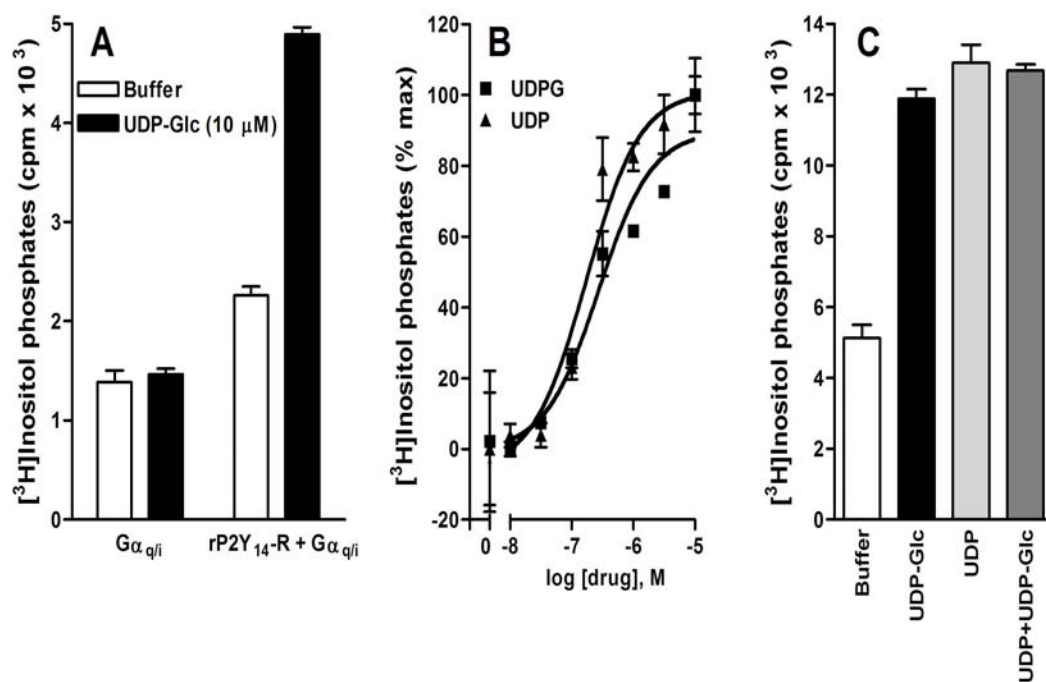


Figure 14. Agonist effect of UDP-Glc and UDP at the rP2Y₁₄-R. A) COS-7 cells transfected with an expression vector for G α_{qi} and with empty vector and/or rP2Y₁₄-R were [³H]inositol-labeled and incubated with 10 mM LiCl in the absence or presence of 10 μM UDP-Glc. B) [³H]Inositol-labeled COS-7 cells transiently expressing the rP2Y₁₄-R and G α_{qi} were incubated with 10 mM LiCl and UDP-Glc or UDP at the indicated concentrations, and [³H]inositol phosphate accumulation was quantified as described in Methods. Data shown are means \pm S.E. calculated from triplicate samples and are results from a representative experiment repeated three times, yielding an EC₅₀ of 0.28 μM \pm 0.05 for UDP-Glc, and 0.35 μM \pm 0.17 for UDP. Data were normalized to the maximal activation of rP2Y₁₄-R by UDP-Glc. C) Cells incubated with UDP-Glc (10 μM) + UDP (100 μM) exhibited no difference in [³H]inositol phosphate accumulation compared to accumulation in the presence of either agonist alone. Data shown are means \pm S.E. calculated from triplicate samples and are representative of results obtained in three independent experiments.

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Chapter IV. Gi-dependent cell signaling responses of the human P2Y₁₄-receptor in model cell systems

Abstract

Eight G protein-coupled receptors comprise the P2Y receptor family of cell signaling proteins. The goal of the current study was to define native cell signaling pathways regulated by the uridine nucleotide sugar-activated P2Y₁₄ receptor (P2Y₁₄-R). The P2Y₁₄-R was stably expressed in HEK293 and C6 rat glioma cells by retroviral infection. Nucleotide sugar-dependent P2Y₁₄-R activation was examined by measuring inhibition of forskolin-stimulated cyclic AMP accumulation. The effect of P2Y₁₄-R activation on mitogen activated protein kinase (MAPK) signaling also was studied in P2Y₁₄-R-HEK293 cells and in differentiated HL-60 human myeloid leukemia cells. UDP-glucose, UDP-galactose, UDP-glucuronic acid and UDP-N-acetylglucosamine promoted inhibition of forskolin-stimulated cyclic AMP accumulation in P2Y₁₄-R-HEK293 and P2Y₁₄-R-C6 cells, and this signaling effect was abolished by pretreatment of cells with pertussis toxin. Inhibition of cyclic AMP formation by nucleotide sugars also was observed in direct assays of adenylyl cyclase activity in membranes prepared from P2Y₁₄-R-C6 cells. UDP-glucose promoted concentration-dependent and pertussis toxin-sensitive extracellular regulated kinase (ERK) 1/2 phosphorylation in P2Y₁₄-R-HEK293 cells. P2Y₁₄-R mRNA was not observed in wild type HL-60 cells, but was readily detected in DMSO-differentiated cells. Consistent with this observation, no effect of UDP-glucose was observed in wild type HL-60 cells, but UDP-glucose-promoted pertussis-sensitive activation of ERK1/2 occurred after differentiation. These results illustrate that the human P2Y₁₄-R signals through Gi to inhibit adenylyl

cyclase, and P2Y₁₄-R activation also leads to ERK1/2 activation. This work also identifies two stable P2Y₁₄-R-expressing cell lines and differentiated HL-60 cells as model systems for the study of P2Y₁₄-R-dependent signal transduction.

Introduction

The P2Y₁₄-R is a seven-transmembrane-spanning G-protein coupled receptor that is activated by UDP-glucose (UDP-Glc) and other UDP-sugars (Chambers *et al.*, 2000). P2Y₁₄-R mRNA is expressed in stomach, intestine, placental and adipose tissues, lung, heart, and throughout the brain, as well as in many types of immune cells (Lee *et al.*, 2003; Moore *et al.*, 2003; Skelton *et al.*, 2003; Scrivens and Dickenson, 2006). Consistent with its prominent immune cell expression, the P2Y₁₄-R has been implicated in several immune cell functions. Moore and colleagues (2003) reported that P2Y₁₄-R mRNA is upregulated in several brain regions after immunological challenge of mice with lipopolysaccharide. Additionally, UDP-Glc was reported to promote chemotaxis of bone marrow-derived hematopoietic stem cells (Lee *et al.*, 2003).

The P2Y₁₄-R is a member of a subgroup of P2Y receptors, which includes the P2Y₁₂ and P2Y₁₃ receptors thought primarily to activate heterotrimeric G proteins of the Gi family, but a comprehensive understanding of the signal transduction pathways activated by the P2Y₁₄-R is not available. Nonetheless, several reports are consistent with the idea that the P2Y₁₄-R couples to Gi. For example, Chambers and his colleagues illustrated in their initial study of the cloned human P2Y₁₄-R that UDP-glucose promotes pertussis toxin-sensitive binding of radiolabeled GTPγS to membranes prepared from HEK293 cells expressing this receptor. Modest UDP-glucose-promoted inhibition of cyclic AMP accumulation also has been reported for murine T-lymphocytes (Scrivens and Dickenson, 2005), human neutrophils

(Scrivens and Dickenson, 2006), and C6 glioma cells (Krzeminski *et al.*, 2008), although the effects were not shown unambiguously to involve the P2Y₁₄-R. Other pharmacological studies of the P2Y₁₄-R have relied on coexpression with the promiscuous G protein, Gα16 (Chambers *et al.*, 2000), or with a chimeric Gq (Moore *et al.*, 2003; Fricks *et al.*, 2008) engineered to couple Gi-activating receptors to activation of phosphoinositide hydrolysis and Ca²⁺ mobilization (Coward *et al.*, 1999).

Studies of the P2Y₁₄-R have been limited by inability to detect and quantify receptor expression directly through the use of antibodies or radioligand binding assays, and also by the absence of high affinity, non-hydrolyzable, selective agonists and competitive antagonists to verify receptor-specific signal transduction. It is critical that we understand the cell signaling processes engaged in response to P2Y₁₄-R activation, and with this goal in mind, we generated two different cell lines that stably express the human P2Y₁₄-R. Robust P2Y₁₄-R-dependent inhibition of adenylyl cyclase was observed in both cell lines, and P2Y₁₄-R-dependent MAP kinase signaling was studied in P2Y₁₄-R-HEK293 cells. We also discovered that expression of native P2Y₁₄-R is induced during differentiation of HL-60 myeloid leukemia cells, and that UDP-glucose promotes activation of MAP kinase signaling in these cells. The model cell systems reported here should provide useful platforms for investigation of the P2Y₁₄-R at the cellular and biochemical level.

Methods

Cell Culture

HEK293 cells were grown in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% fetal bovine serum (FBS) at 37°C in a 10% CO₂ environment. C6 rat glioma cells were cultured in DMEM supplemented with 5% FBS in a 5% CO₂ environment. HL-60 cells

were maintained in Iscove's medium supplemented with 10% FBS. Differentiation of HL-60 cells was achieved by inclusion of 1.3% DMSO in the culture medium for 5 days (Servant *et al.*, 2000).

P2Y₁₄-R Expression

Human P2Y₁₄-R cDNA was amplified and ligated into the retroviral expression vector pLXSN as described previously (Wolff *et al.*, 2005). Retrovirus encoding the P2Y₁₄-R was produced in PA317 cells according to the method of Johnson and colleagues (Johnson *et al.*, 1998) and was used to infect HEK293 cells or C6 glioma cells. Geneticin-resistant cells were selected for two weeks in medium containing 0.4 mg/ml G418. Clonal HEK293 cells stably expressing the hP2Y₁₄-R were obtained by performing serial dilutions of cells in 96-well plates, and growing clonal populations from a single cell under selection medium.

Membrane Preparation

Membranes were prepared as described previously (Smith and Harden, 1985). Briefly, P2Y₁₄-R-C6 rat glioma cells were grown on 150 mm dishes until confluent. Cells were washed gently with PBS and then lysed with ice-cold 1 mM Tris, pH 7.4. Cells were harvested by scraping dishes and homogenized with a glass homogenizer for ten strokes. Lysates were centrifuged at 40,000 x g for 10 min. Membranes were resuspended in 10 mM Tris, pH 7.4, containing 1 mM EDTA and centrifuged again at 40,000 x g for 10 min. Washed membranes were resuspended in assay buffer (25 mM HEPES, pH 7.4, 5 mM MgCl₂, 150 mM NaCl, 1 mM EDTA) and used immediately.

Cyclic AMP Accumulation

Cells were grown in 24-well plates and incubated with 1 μ Ci [³H]adenine/well in serum-free DMEM for 2 h prior to assay. Assays were initiated by the addition of HEPES-buffered,

serum-free DMEM containing 500 μ M 3-isobutyl-1-methyl-xanthine (IBMX), with or without drugs, and incubation continued for 12 min at 37°C. Incubations were terminated by aspiration of medium and addition of 450 μ L ice-cold 5% trichloroacetic acid. [3 H]Cyclic AMP was isolated by sequential Dowex and alumina chromatography (Salomon *et al.*, 1974) and quantified by liquid scintillation counting.

Adenylyl Cyclase Activity

Quantification of adenylyl cyclase activity was carried out according to the procedure described previously (Harden *et al.*, 1982). Briefly, assay tubes on ice contained drug or vehicle and a reaction mix of assay buffer containing, at final assay concentrations, 0.01 mM [α - 32 P]ATP (10-15 cpm/pmol), 0.5 mM [3 H]cyclic AMP (10,000 cpm/assay), 8 mM creatine phosphate, creatine phosphokinase (6 U/assay), 0.01 mM GTP, 0.5 mM IBMX, 25 mM HEPES (pH 7.5), 5 mM MgSO₄, 2 mM EDTA, and 150 mM NaCl. Assays were initiated by the addition of 100 μ g of membrane protein, and the incubations were carried out for 12 min at 30°C. The reaction was terminated with addition of 0.85 mL of ice-cold 5% trichloroacetic acid. [32 P]Cyclic AMP was isolated by sequential Dowex and alumina chromatography and quantified by liquid scintillation counting. Recovery of [3 H]cyclic AMP over columns averaged 50-60 %.

MAP Kinase Activation Assays

HEK293 cells were grown on 12-well plates until 70-90% confluent. Cells were serum-starved 24 h prior to assay. Drugs were added to cells for the indicated times, and the assay was terminated by aspiration of medium. The cells were washed once with PBS, and Laemmli buffer containing 60 μ M dithiothreitol (DTT) was added to each well. The resultant cell lysates were passed through a 27G needle ten times, heated to 95°C for five

min, and proteins resolved by electrophoresis on a 12.5% polyacrylamide gel. Proteins were transferred to a nitrocellulose membrane, blocked with 5% BSA, washed with TBST (20 mM Tris, pH 7.4, 120 mM NaCl, 0.1% Tween20), and then incubated with antibody for phospho-ERK1/2, phospho-p38, or phospho-JNK, according to the manufacturer's directions. After washing with TBST, membranes were incubated with horseradish peroxidase-conjugated goat-anti-mouse (phospho-ERK1/2, phospho-JNK) or goat-anti-rabbit (phospho-p38) antibody, membranes were washed, then incubated with chemiluminescent substrate (Pico West system, Thermo Fisher Scientific, Waltham, MA) and exposed to film. Membranes were stripped with 200 mM glycine, pH 2.6, for 1 h at 25°C, then re-probed with a primary antibody against total MAP kinase to verify equal loading of lanes. HL-60 cells were serum-starved 24 h prior to the assay, and resuspended in Hanks Buffered Salt Solution for the assay at a density of 5×10^6 cells/mL, 0.2 mL/assay. Drugs were added for the indicated times, and the cells were lysed by adding one volume of Laemmli buffer containing 60 μ M DTT to the cells. Lysates were analyzed as described above.

Data Analysis

EC₅₀ values were determined using Prism software (GraphPad, San Diego, CA) and are presented as mean \pm SE. Statistical significance was determined by Analysis of Variance (ANOVA), and $p < 0.02$ was considered statistically significant. All experiments were repeated at least three times.

Materials

IBMX, creatine phosphate, creatine phosphokinase, forskolin, formyl-Met-Leu-Phe (fMLP), and GTP were purchased from SigmaAldrich (St. Louis, MO). UDP-glucose, UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine were all from FLUKA,

purchased through SigmaAldrich. HPLC analysis of the UDP-Glc used in the current experiments revealed >98% purity. ATP was purchased from GE Healthcare (Piscataway, NJ). Pertussis toxin was purchased from List Biologicals (Campbell, CA). [³H]Adenine and [³H]cyclic AMP were purchased from American Radiolabeled Chemicals (St. Louis, MO). [α -³²P]ATP was purchased from PerkinElmer (Waltham, MA). Antibodies for P-ERK1/2, ERK1/2, P-p38, p38, P-JNK, and JNK were purchased from Cell Signaling Technologies (Beverly, MA). All cell culture medium and serum was from Gibco (Invitrogen, Carlsbad, CA). PAR agonist peptide SLIGKV was a generous gift from Dr. Joann Trejo. Anisomysin and sorbitol were kind gifts from Dr. Gary Johnson.

Results

UDP-sugars promote inhibition of forskolin-stimulated cyclic AMP formation in cells stably expressing the human P2Y₁₄-R

To examine potential regulation of adenylyl cyclase activity downstream of the human P2Y₁₄-R, we stably expressed this receptor in HEK293 cells. UDP-Glc promoted concentration-dependent inhibition of forskolin-stimulated accumulation of cyclic AMP in P2Y₁₄-R-expressing HEK293 cells. An EC₅₀ value of 82 ± 11 nM ($n = 3$) was observed for UDP-Glc, and the maximal inhibition of forskolin-stimulated cyclic AMP accumulation ranged from 60-80% (Fig. 15). In contrast, no effect of UDP-Glc was observed on basal or forskolin-stimulated cyclic AMP accumulation in HEK293 cells infected with vector alone. Pre-incubation of P2Y₁₄-HEK293 cells with pertussis toxin resulted in complete loss of UDP-Glc-dependent inhibition of cyclic AMP accumulation, indicating that the P2Y₁₄-R signals through G α -subunits of the Gi family.

While UDP-Glc is reported to be a full agonist at the P2Y₁₄-R, several studies of the P2Y₁₄-R have reported variable effects of other nucleotide-sugars (Chambers et al., 2000; Scrivens and Dickenson, 2006). Therefore, we tested the capacity of UDP-sugars to activate the P2Y₁₄-R in P2Y₁₄-HEK293 cells. UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine all promoted inhibition of cyclic AMP accumulation and the maximal inhibition observed was similar to that of UDP-Glc. The potencies of UDP-galactose and UDP-glucuronic acid were similar to that of UDP-Glc, while UDP-N-acetylglucosamine exhibited an approximately 10-fold higher EC₅₀ value (Fig. 16 and Table 4).

We concluded it important to stably express the P2Y₁₄-R in several cell backgrounds. Previous studies by our and other labs revealed robust inhibition of adenylyl cyclase in C6 rat glioma cells expressing several different G protein-coupled receptors (Schachter et al., 1997; Thomas et al., 2000; Castillo et al., 2007). Therefore, we also infected C6 cells with recombinant pLXSN virus harboring the hP2Y₁₄-R coding sequence. Again, whereas UDP-Glc had no effect on cyclic AMP accumulation in C6 cells expressing empty vector alone, robust inhibitory effects were observed with UDP-Glc in P2Y₁₄-R-expressing C6 cells. An EC₅₀ value of 107 ± 68 nM was determined and up to 90% inhibition of forskolin-stimulated accumulation of cyclic AMP occurred in the presence of a maximally effective concentration of UDP-Glc. The action of UDP-Glc in P2Y₁₄-R-C6 cells was completely blocked by pre-treatment of the cells with pertussis toxin (Fig. 17). The concentration-dependent inhibition of cyclic AMP formation with other UDP-sugars also was established, and the EC₅₀ values are reported in Table 4.

Effects of UDP-sugars on adenylyl cyclase activity in membranes from P2Y₁₄-R-expressing C6 cells

Based on the robust P2Y₁₄-R-dependent inhibition of cyclic AMP accumulation observed in C6 glioma cells, we also isolated plasma membrane-enriched fractions to determine whether UDP-Glc- and P2Y₁₄-R-dependent inhibition of adenylyl cyclase activity could be observed in a cell-free system. While no effect of UDP-Glc was observed in membranes from control cells, approximately 50% inhibition of forskolin-stimulated adenylyl cyclase activity was observed in the presence of 10 μ M UDP-Glc in membranes isolated from P2Y₁₄-R-C6 glioma cells (Fig. 18). This UDP-Glc-promoted response did not occur in membranes from P2Y₁₄-R-C6 cells pretreated with pertussis toxin.

MAP kinase activation by UDP-glucose in P2Y₁₄-R-HEK293 cells

Many important biological processes are regulated by MAP kinase signaling pathways. To assess the capacity of the P2Y₁₄-R to activate MAP kinase signaling cascades, P2Y₁₄-R-HEK293 cells were treated with UDP-Glc and cell lysates were analyzed for phosphorylated ERK1/2 by Western blotting. Whereas no effect was observed in mock-infected cells, UDP-Glc-dependent ERK1/2 phosphorylation occurred in P2Y₁₄-R-HEK293 cells (Fig. 19A).

The time course for UDP-Glc activation of ERK1/2 was compared to that occurring as a consequence of activation of the protease activated receptor-2 (PAR2), which is natively expressed in HEK293 cells (Amadesi *et al.*, 2004; Dai *et al.*, 2007). Incubation of cells with the PAR2 agonist peptide SLIGKV (100 μ M) resulted in marked phosphorylation of ERK1/2 within 5 min, but phosphorylation quickly diminished thereafter. In contrast, UDP-Glc-dependent activation of ERK1/2 was not maximal until at least 15 min of incubation and was retained for at least 30 min. The effects of UDP-Glc on ERK1/2 phosphorylation were concentration-dependent, and the EC₅₀ (30 nM) observed was similar to that obtained in

studies of inhibition of cyclic AMP accumulation in these cells (Fig 19C). As was observed in the studies of adenylyl cyclase activity, P2Y₁₄-R-regulated ERK1/2 phosphorylation was not observed in cells preincubated with pertussis toxin (Fig. 19B).

The capacity of the P2Y₁₄-R to activate p38 and Jun-N terminal kinase (JNK) also was examined. Although p38 was phosphorylated with a peak response observed within 5 min after treatment of cells with sorbitol, no UDP-Glc-dependent activation of p38 was observed at any time point up to 60 min (Fig 19D). In contrast to a robust activation observed in the presence of anisomycin, we also observed no effects of UDP-Glc on JNK phosphorylation (Fig. 19D).

Functional P2Y₁₄-R are endogenously expressed in differentiated HL-60 cells

With the goal of identifying a cell line that natively expresses the P2Y₁₄-R, we tested by RT-PCR several candidate cell lines previously reported to express P2Y₁₄-R mRNA, as well as other cell lines derived from tissues reported to express this receptor (Chambers *et al.*, 2000; Moore *et al.*, 2003; Skelton *et al.*, 2003). Although no P2Y₁₄-R mRNA was detected in undifferentiated HL-60 cells, differentiation of these cells with 1.3% DMSO to a neutrophil-like cell resulted in a marked increase in expression of P2Y₁₄-R mRNA (data not shown).

We also investigated the cell signaling responses discussed above to determine whether functional P2Y₁₄-R could be observed in differentiated HL-60 cells. In multiple experiments, 100 μ M UDP-Glc exhibited no effect on cyclic AMP accumulation promoted by either forskolin, amthamine, an agonist for the Gs-coupled H₂ histamine receptor, or forskolin + amthamine (data not shown). Although a formyl peptide receptor (FPR) is

natively expressed by HL-60 cells (Boulay *et al.*, 1990; Klinker *et al.*, 1996), we also failed to observe effects of 1 μ M fMLP on cyclic AMP accumulation in these cells.

Potential activation of the MAP kinase signaling pathway also was studied in HL-60 cells. Whereas no effect of UDP-Glc was observed in wild type cells, time-dependent activation of ERK1/2 by UDP-Glc was observed after differentiation of the cells. This effect was apparent within 5 min and peaked within 30 min (Fig. 20A). In contrast to the time course of the phosphorylation response to UDP-Glc, cells treated with 1 μ M fMLP exhibited a robust ERK1/2 activation at 5 min that quickly diminished thereafter (Fig. 20B). Neither UDP-Glc- nor fMLP-dependent ERK1/2 activation was observed in cells pre-incubated with pertussis toxin (Fig 20C), consistent with the notion that the UDP-Glc-promoted ERK1/2 activation in differentiated HL-60 cells occurs through a mechanism involving Gi in differentiated HL-60 cells.

Discussion

In this report, we demonstrate that the human P2Y₁₄-R couples to inhibition of adenylyl cyclase in a pertussis toxin-sensitive manner in HEK293 and C6 cells stably expressing this receptor. This work provides the first unequivocal demonstration of P2Y₁₄-R-dependent inhibition of adenylyl cyclase in a membrane preparation. Robust stimulation of MAP kinase signaling also occurs with activation of the P2Y₁₄-R. This was the predominant activity observed with native P2Y₁₄-R in differentiated HL-60 human myeloid leukemia cells.

UDP-Glc is released from many cell types. This phenomenon was initially demonstrated by Lazarowski and colleagues who illustrated both basal and mechanically-induced release of UDP-Glc from multiple mammalian cell types (Lazarowski *et al.*, 2003).

Constitutive release of UDP-Glc also occurs in yeast (Esther *et al.*, 2008). Although the mechanism(s) underlying UDP-Glc release is not well-established, calcium-dependent release of UDP-Glc was demonstrated in Calu-3 cells (Kreda *et al.*, 2007), and UDP-Glc release occurred downstream of thrombin receptor-promoted signaling pathways in human astrocytoma 1321N1 cells (Kreda *et al.*, 2008).

UDP-sugars in addition to UDP-Glc are predictably present in the extracellular space. UDP-glucose, UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine all were previously reported as potent agonists of the P2Y₁₄-R in test systems that involved coexpression of the receptor with a phospholipase C-activating G protein (Chambers *et al.*, 2000; Freeman *et al.*, 2001). Our results measuring responses of a native signaling pathway also indicate that these four UDP-sugars are full agonists and exhibit relatively similar potencies. It remains to be elucidated which one or more of these molecules is the endogenous agonist(s) for the receptor. Indeed, it is likely that multiple UDP-sugars are physiological agonists for the P2Y₁₄-R, such that the activating ligand may differ according to tissue or cell type.

Our findings that neither UDP-Glc nor fMLP had an effect on stimulated cyclic AMP accumulation in differentiated HL-60 cells indicates that activated Gi does not couple to inhibition of adenylyl cyclase in these cells. Perhaps the isoforms of adenylyl cyclase expressed in these cells are not subject to inhibition by Gi. HL-60 cells gain a neutrophil phenotype upon differentiation, and therefore are likely to reflect receptor-promoted signaling responses that are characteristic of neutrophils. Receptor-promoted inhibition of adenylyl cyclase has not been unequivocally demonstrated in neutrophils, and we are unaware of studies clearly defining the signaling pathways downstream of Gi-coupled

receptors in this tissue. A small inhibition of cyclic AMP accumulation was reported to occur upon incubation of neutrophils with UDP-Glc (Scrivens and Dickenson, 2006). However, since none of the other P2Y₁₄-R agonists inhibited forskolin-promoted cyclic AMP formation in neutrophils, it is unclear whether this effect was in fact dependent on either UDP-Glc or the P2Y₁₄-R.

Gi-coupled GPCR predictably activate MAP kinase signaling, and we illustrate here that UDP-Glc-dependent activation of ERK1/2 occurs in P2Y₁₄-R-HEK293 cells. Although P2Y₁₄-R were not detected in undifferentiated HL-60 cells, message for the P2Y₁₄-R was observed upon differentiation of HL-60 cells, and occurrence of UDP-Glc-promoted MAP kinase signaling indicated the presence of functional P2Y₁₄-R. HL-60 cells have been used as a model of neutrophil-like cells that undergo differentiation-associated morphological and functional changes including up-regulation of chemoattractant receptors and the capacity to chemotax (Hauert *et al.*, 2002). Differentiated HL-60 cells exhibit capacities to generate superoxide, ingest particles, and degranulate with efficiencies similar to that of neutrophils (Newburger *et al.*, 1979). In addition, they have distinct technical advantages over primary cells, such as viability and transfectability. Differentiated HL-60 cells also have been used as a model system for studies of FPR, and consistent with previous observations (Rane *et al.*, 1997; Christophe *et al.*, 2002; Paruch *et al.*, 2006), we observed fMLP-promoted ERK1/2 activation in differentiated HL-60 cells. These findings establish differentiated HL-60 cells as a model system for investigation of biological functions of the P2Y₁₄-R.

The duration of P2Y₁₄-R-promoted ERK1/2 phosphorylation in HEK293 cells and HL-60 cells was prolonged compared with that of other G protein coupled receptors. PAR2, which promoted very transient ERK1/2 activation in HEK293 cells, is known to couple to Gi,

as well as to G12/13 and Gq (Fyfe *et al.*, 2005). The fMLP receptor, FPR, has been reported to couple to Gi, but the mechanism linking FPR to ERK1/2 phosphorylation is not clear (Selvatici *et al.*, 2006; Huet *et al.*, 2007; Kam *et al.*, 2007). Therefore, it is possible that the signaling pathway(s) responsible for P2Y₁₄-R-promoted MAP kinase signaling differs from that engaged by PAR2 or FPR. We speculate that pertussis toxin-sensitive G α -subunits are necessary but not sufficient and additional pathways or regulatory mechanisms are involved in the MAP kinase response downstream of one or more of these receptors. Observation of receptor-specific differences in the time course of stimulation of ERK1/2 phosphorylation has led to the suggestion that short term (e.g. 5 min) versus long-term receptor-dependent activation (e.g. 30-60 min) may promote distinct cellular functions. For example, short-term ERK1/2 activation may be important for cell migration whereas sustained ERK1/2 activation may play a more critical role in cell proliferation (Luttrell, 2005; May and Hill, 2008). Our studies do not rule out the possibility that the P2Y₁₄-R desensitizes at a slower rate than PAR2 in HEK293 cells or FPR in HL-60 cells. Additional studies will be necessary to address questions about the mechanism of P2Y₁₄-R-dependent activation of MAP kinase, but its pertussis toxin sensitivity clearly indicates that Gi is an important signaling component in the pathway.

In summary, this work unequivocally demonstrates that the human P2Y₁₄-R promotes inhibition of adenylyl cyclase and activation of MAP kinase signaling pathways. Our work also provides several model cell lines for study of P2Y₁₄-R signaling as well as its potential role in neutrophil biology.

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Table 4. EC₅₀ values for P2Y₁₄-R agonists in P2Y₁₄-HEK293 and P2Y₁₄-C6 cells. [3H]Adenine-labeled cells were treated with IBMX (200 μM), forskolin (30 μM), and varying concentrations of either UDP-glucose, UDP-galactose, UDP-glucuronic acid, or UDP-N-acetylglucosamine for 15 min. [3H]Cyclic AMP was quantified as described in Methods. EC₅₀ values were determined with GraphPad Prism software and are presented as mean ± SE of results from three experiments.

Agonist	<u>P2Y₁₄-HEK293</u> EC₅₀ ± SE, nM	<u>P2Y₁₄-C6</u> EC₅₀ ± SE, nM
UDP-glucose	82 ± 11	92 ± 51
UDP-galactose	96 ± 29	240 ± 53
UDP-glucuronic acid	60 ± 7	108 ± 66
UDP-N-acetylglucosamine	919 ± 205	225 ± 68

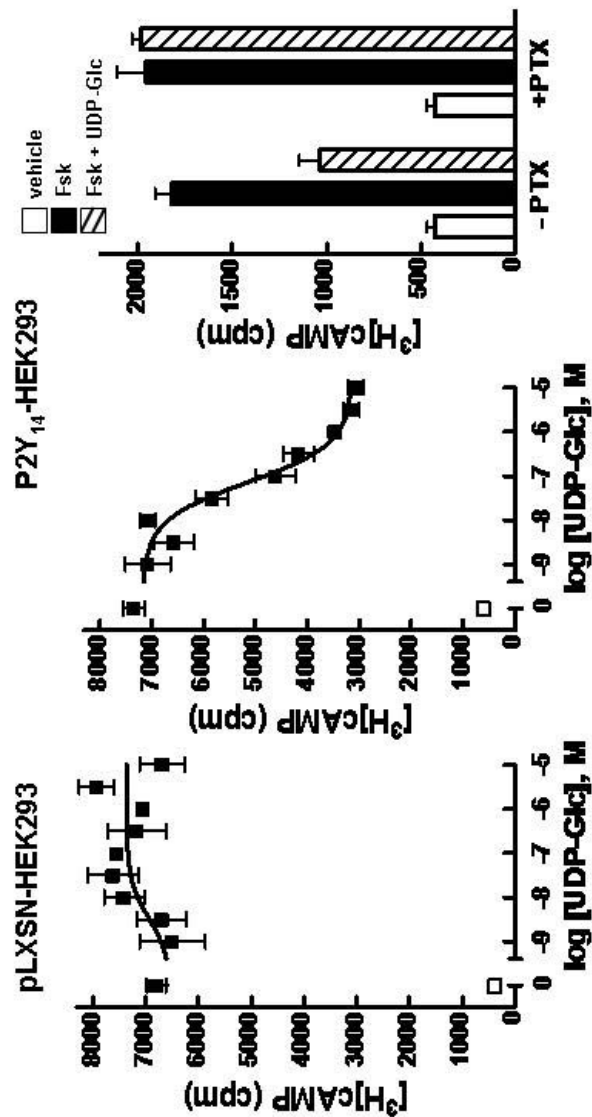


Figure 15. Concentration-dependent and pertussis toxin-sensitive inhibition of cyclic AMP accumulation promoted by UDP-Glc in P2Y₁₄-HEK293 cells. Empty vector-infected (left panel) or P2Y₁₄-R-expressing (middle panel) cells were labeled with [³H]adenine 18 h prior to assay. Cells were incubated with 200 μ M IBMX in the absence (\square) or presence of 30 μ M forskolin and the indicated concentrations of UDP-Glc (\blacksquare) for 12 min prior to quantification of [³H]cyclic AMP accumulation. P2Y₁₄-R-expressing (right panel) cells were preincubated with 100 ng/mL pertussis toxin for 4 h, and [³H]cyclic AMP accumulation was measured in the presence of 200 μ M IBMX alone (open bars), 200 μ M IBMX + 30 μ M forskolin (filled bars), or 200 μ M IBMX + 30 μ M forskolin + 10 μ M UDP-Glc (hatched bars). The data shown are presented as mean \pm SE and are representative of results from three independent experiments.

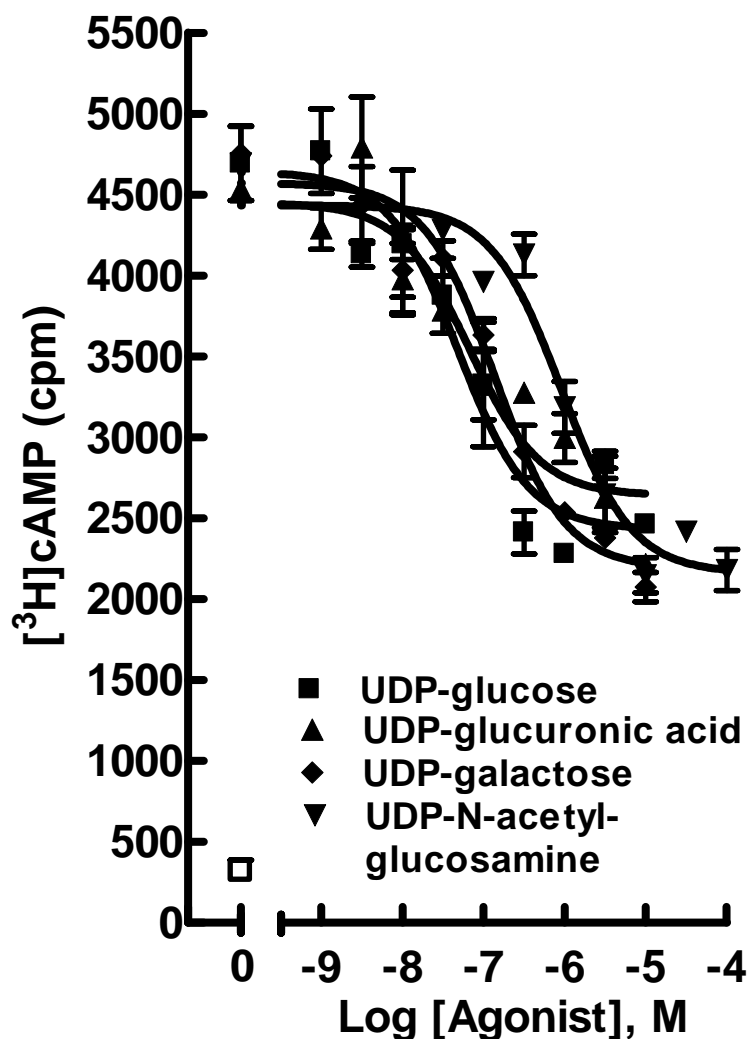


Figure 16. UDP-galactose, UDP-glucuronic acid, and UDP-N-acetylglucosamine inhibit accumulation of cyclic AMP in P2Y₁₄-HEK293 cells. [³H]Adenine-labeled P2Y₁₄-HEK293 cells were incubated with 200 μ M IBMX alone (\square) or IBMX with 30 μ M forskolin and varying concentrations of UDP-glucose (\blacksquare), UDP-galactose (\blacklozenge), UDP-glucuronic acid (\blacktriangle), or UDP-N-acetylglucosamine (\blacktriangledown). Data shown are mean \pm SE and are representative of results of three independent experiments.

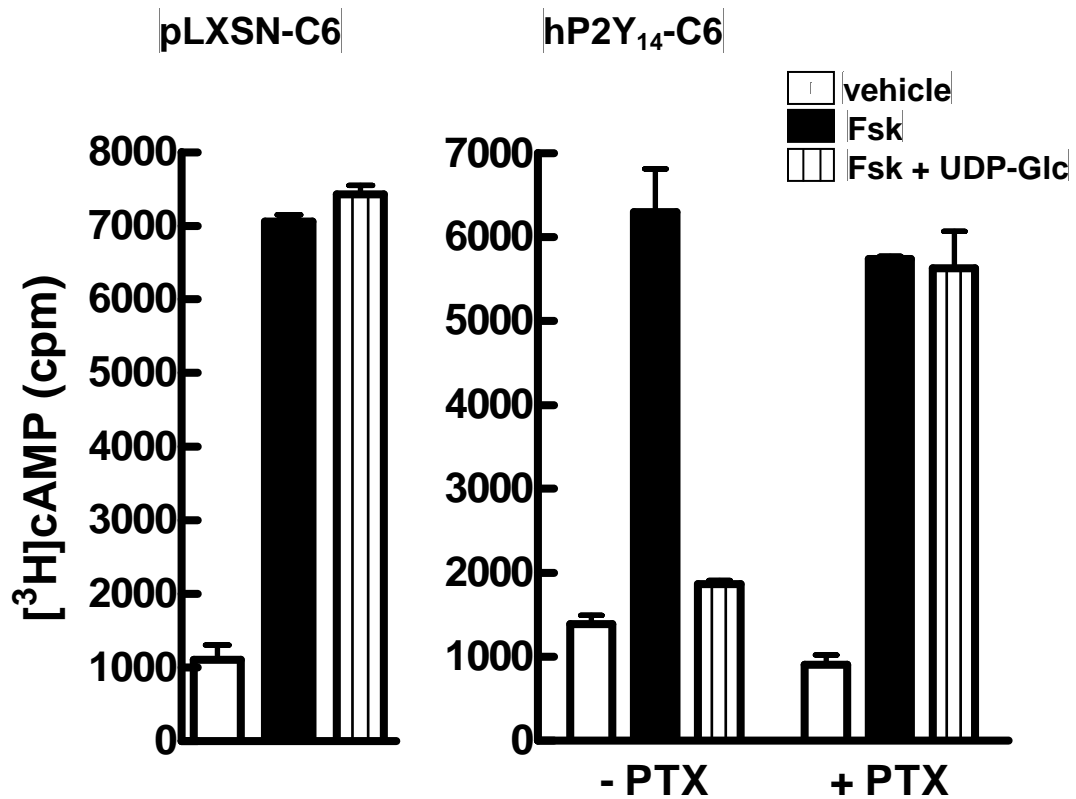


Figure 17. UDP-Glc promotes pertussis toxin-sensitive inhibition of cyclic AMP accumulation in P2Y₁₄-C6 cells. Empty vector-infected (left panel) C6 rat glioma cells were prelabeled with [³H]adenine and then incubated in the presence of 200 μ M IBMX alone (open bar), 200 μ M IBMX + 30 μ M forskolin (filled bar), or 200 μ M IBMX + 30 μ M forskolin + 10 μ M UDP-Glc (striped bar). P2Y₁₄-C6 cells (right panel) were incubated in the absence or presence of 100 ng/mL pertussis toxin prior to quantification of [³H]cyclic AMP accumulation in the presence of 200 μ M IBMX alone (open bars), 200 μ M IBMX + 30 μ M forskolin (filled bars), or 200 μ M IBMX + 30 μ M forskolin + 10 μ M UDP-Glc (striped bars). Data shown are presented as mean \pm SE and are representative of results from three independent experiments.

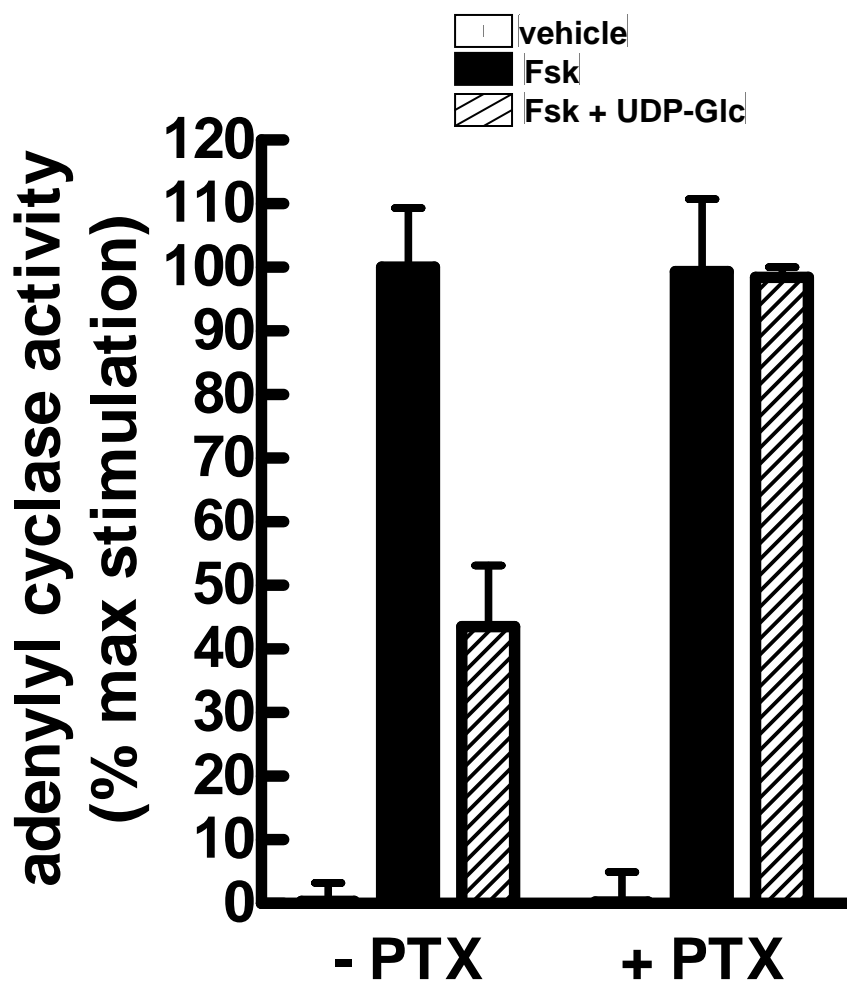


Figure 18. UDP-Glc-dependent inhibition of adenylyl cyclase by UDP-Glc in membranes from P2Y₁₄-C6 cells. Membranes were isolated from P2Y₁₄-C6 cells or from cells pretreated with 100 ng/mL pertussis toxin overnight. Membranes were incubated with 200 μ M IBMX in the absence (open bars) or presence (filled bars) of 30 μ M forskolin, or with 200 μ M IBMX + 30 μ M forskolin + 10 μ M UDP-Glc as described in Methods. [³²P]Cyclic AMP was isolated by sequential Dowex-alumina chromatography. Data shown are the mean \pm SE of three independent experiments, plotted as a percentage of maximal forskolin-stimulated enzyme activity.

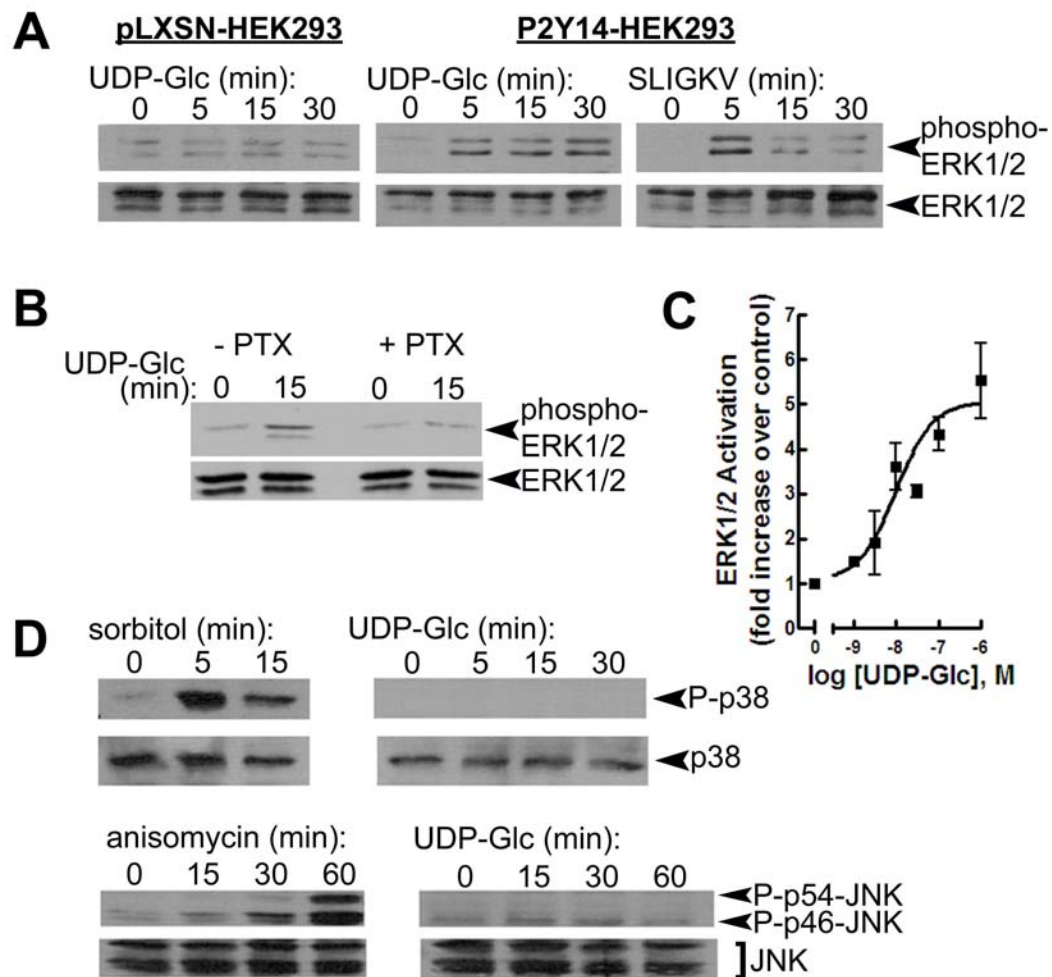


Figure 19. UDP-Glc-promoted activation of MAP kinase signaling in P2Y₁₄-HEK293 cells. A) Empty vector or P2Y₁₄-R-expressing HEK293 cells were serum-starved for 18 h and then incubated with 100 μ M UDP-Glc or 100 μ M SLIGKV for the times indicated. Samples were probed for phospho-ERK1/2 and ERK1/2 as described in Methods. B) Cells were pretreated in the absence (-PTX) or presence (+PTX) of 100 ng/mL pertussis toxin overnight, then treated with UDP-Glc for 15 min. C) Cells were incubated with varying concentrations of UDP-Glc for 15 min. Phospho-ERK1/2 and ERK1/2 were quantified using Scion Image software (Frederick, MD) and graphed using GraphPad Prism software (San Diego, CA). Each phospho-ERK1/2 lane was normalized to the corresponding ERK1/2 control and plotted as fold stimulation over control. Data shown are the average \pm SE of four independent experiments. D) P2Y₁₄-HEK293 cells were treated with either 0.2 M sorbitol, 0.01 mg/mL anisomycin, or 100 μ M UDP-Glc for the indicated times. Phospho-p38, phospho-JNK, total p38, and total JNK were determined as described in Methods.

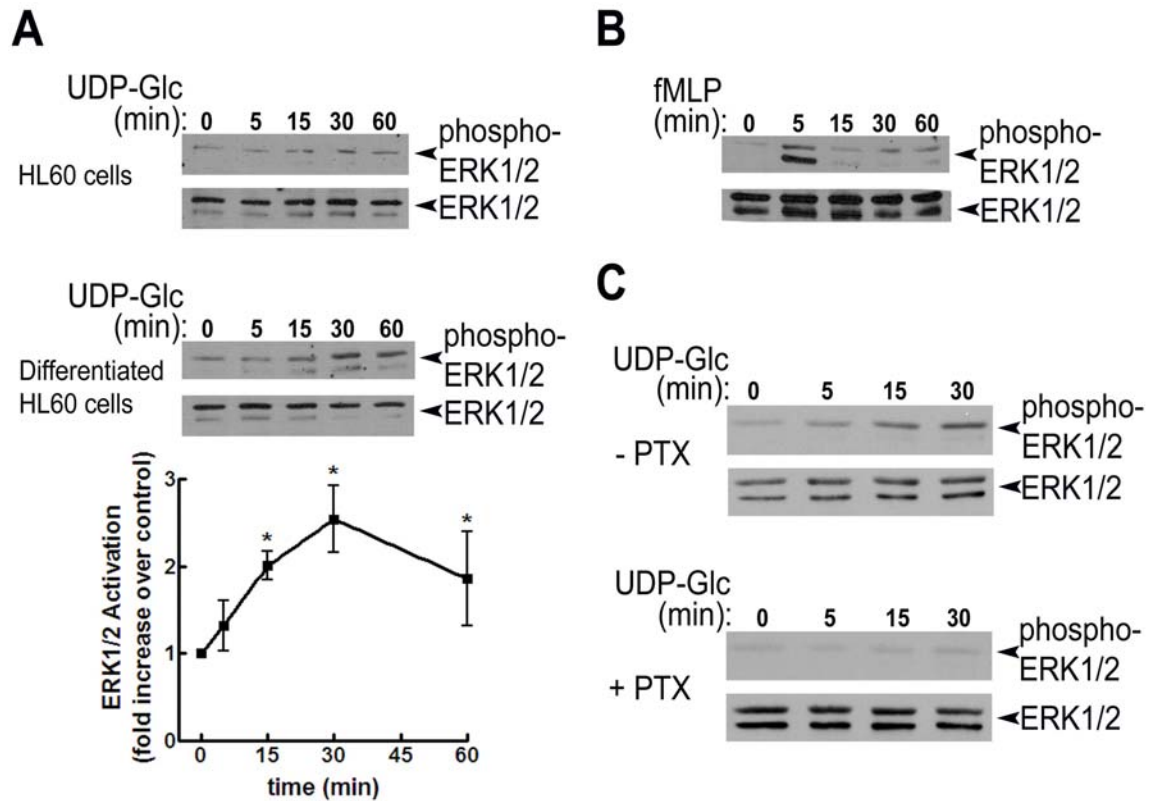


Figure 20. UDP-Glc-promoted activation of MAP kinase activation in differentiated HL-60 cells. A) Wild-type or differentiated (see Methods) HL-60 cells were serum-starved for 18 h prior to addition of 100 μ M UDP-Glc and incubation continued for the indicated times. Western blots for phospho-ERK1/2 and ERK1/2 were generated as described in Methods. Phospho-ERK1/2 was quantified using Scion Image software (Frederick, MD) and graphed using GraphPad Prism software (San Diego, CA). Each phospho-ERK1/2 lane was normalized to the corresponding ERK1/2 control and plotted as fold stimulation over control. Data shown are the mean \pm SE of six independent experiments (* $p < 0.02$). B) Serum-starved, differentiated HL-60 cells were incubated with 1 μ M formyl-Met-Leu-Phe for the indicated times, and lysates were analyzed as described in Methods. C) Differentiated HL-60 cells were treated in the absence (-PTX) or presence (+PTX) of 200 ng/mL pertussis toxin for 4 h prior to assay. Cells were incubated for the indicated times with 100 μ M UDP-Glc and phospho-ERK1/2 and total ERK1/2 was quantified as described in Methods.

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Chapter V. Conclusions

Ligand development studies have met with considerable success for the P2Y₁-R and P2Y₁₂-R, and we have applied a structure-activity relationship approach to develop ligands for the P2Y₁₄-R. Additionally, molecular modeling studies have been useful in guiding these studies. Our studies on the P2Y₁₄-R are focused on developing high affinity, selective, and non-hydrolyzable agonists and antagonists. These studies, reviewed in Chapter 2, have yielded several novel agonists at the P2Y₁₄-R, including 2-thio-UDP-Glc, an agonist that exhibits six-fold greater potency than UDP-Glc (Ko et al., 2007). Molecular modeling studies have aided our conceptualization of the P2Y₁₄-R tertiary structure (Ivanov et al., 2007), and guided a methodical analysis of the parameters of the ligand pharmacophore. Identification of the hexose moiety of UDP-Glc as a fertile region for modification leads to a newly focused approach for future development of ligands. Ongoing studies are aimed toward producing pharmacological tools that will be useful in further characterization of the P2Y₁₄-R. A high affinity, selective radioligand would be useful for binding assays, while a fluorophore-conjugated ligand could be useful for monitoring receptor expression and localization with microscopy.

As a result of our ligand development studies, it is clear that most UDP-sugars activate the P2Y₁₄-R (Ko et al., 2009). Release of UDP-Glc from cells has been established (Lazarowski et al., 2003; Kreda et al., 2007; Kreda et al., 2008) and it is likely that other UDP-sugars are released from cells as well. Our finding that other UDP-sugars, in addition to the originally identified four, are agonists at the P2Y₁₄-R

necessitates our re-thinking the profile of cognate agonists for the P2Y₁₄-R and specifically, we must consider the possibility that the P2Y₁₄-R has many cognate agonists. Most UDP-sugars are equipotent at the P2Y₁₄-R and so could theoretically activate the receptor in place of UDP-Glc. Depending on the extracellular environment at the site of P2Y₁₄-R expression, one or more UDP-sugars may activate the P2Y₁₄-R endogenously.

The P2Y₁₄-R was classified as a P2Y₁₂-like receptor based on sequence homology, and has been suspected to couple to the Gi family of G proteins, as does the P2Y₁₂-R. With the work presented in Chapter 4, we unambiguously established that the P2Y₁₄-R couples to inhibition of adenylyl cyclase stimulation, and to ERK1/2 phosphorylation, in an agonist-dependent and pertussis toxin-sensitive manner (Fricks et al., submitted). While the inhibition of adenylyl cyclase activity is likely to occur through Gi activation, the signaling from Gi-coupled receptors to activate MAPK is not well delineated, although previous evidence suggests that it may be dependent on Gβγ. Both Gα_i subunits and Gβγ dimers released from activated Gi have been reported to activate ERK1/2 through several distinct mechanisms, however the mechanism by which P2Y₁₄-R couples to ERK1/2 phosphorylation is unknown.

Two mechanisms for Gi-dependent activation of ERK1/2 have been proposed. Gα_{i2} was reported to interact directly with Rap-1-GAP, suggesting that activated Gα_{i2} would lead to inactive Rap-1 (Pace et al., 1995; Mochizuki et al., 1999). Because active Rap-1 sequesters C-Raf away from Ras, alleviation of the Rap/Raf interaction would allow Raf to interact with Ras and consequently activate MAPK signaling downstream. Another model of Gi stimulation of ERK1/2 implicates signaling downstream of adenylyl cyclase.

Upon inhibition of adenylyl cyclase, PKA activation concomitantly decreases, resulting in alleviation of PKA inhibition of C-Raf (Tang and Gilman, 1992; Radhika and Dhanasekaran, 2001). Raf is then free to interact with Ras and activate the MAPK cascade.

Evidence for G $\beta\gamma$ -dependent activation of MAPK has been reported for multiple Gi-coupled GPCRs, including the M2 muscarinic receptor (Lopez-Illasaca et al., 1997). The β 1-adrenergic receptor also is reported to activate MAPK through a G $\beta\gamma$ -dependent mechanism that is partially sensitive to pertussis toxin (Galandrin et al., 2008). Each of the proposed signaling pathways converges on Ras, although the intermediates appear to be different depending on the receptor. Recombinant α 2A-adrenergic receptors in HEK293 cells and COS-7 cells have been suggested to use a pathway involving PLC β and the intracellular calcium-activated Pyk2 kinase, which would activate Src, bringing together the Ras-activating complex Shc and SOS (Della Rocca et al., 1997). A second, distinct pathway involving phosphatidyl-inositol-3-kinase (PI3K) is implicated in activation of ERK1/2 by LPA and thrombin receptors. This model predicts that PI3K activates a not yet identified tyrosine kinase, which would, in turn, promote formation of the Ras-activating complex dynamin II/ Grb2/ SOS (Kranenburg et al., 1997; Kranenburg et al., 1999; Wunderlich et al., 1999). The potential for the P2Y₁₄-R to use one or more of these signaling pathways to activate ERK1/2 could be explored with the use of the G $\beta\gamma$ -sequestering carboxyl tail of β -adrenergic receptor kinase (β -ARK) (Inglese et al., 1994) to determine whether the $\beta\gamma$ dimer is necessary for MAPK signaling. Further studies could utilize pharmacological inhibitors of protein intermediates to identify which proteins are involved in the P2Y₁₄-R-dependent activation of MAPK.

Alternatively to signals downstream of the G protein, the involvement of β -arrestins in agonist-dependent transduction to MAPK cascades has been reported for some GPCRs. In addition to their role in mediating endocytosis of ligand-bound receptor, β -arrestins also act as scaffolding proteins that link some GPCRs, such as the β_2 -adrenergic receptor, to MAPK cascades (Luttrell et al., 1999). In the proposed model, β -arrestin scaffolds the ligand-bound receptor in a complex with the tyrosine kinase Src, subsequently activating Ras-mediated MAPK cascades. The β -arrestins have also been proposed to act as a scaffold protein for the complex associating Raf, MEK1, and ERK (DeFea et al., 2000; Luttrell et al., 2001). While the β -arrestin mechanism of GPCR-induced MAPK signaling has been described for few GPCRs, the array of possible pathways to determine the mechanism of P2Y₁₄-R-dependent MAPK activation will require extensive investigation.

In addition to the tissue specific $G\alpha_t$, $G\alpha_z$, and $G\alpha_{\text{gust}}$, the Gi family of proteins includes $G\alpha_{i1}$, $G\alpha_{i2}$, $G\alpha_{i3}$, and $G\alpha_o$. Which Gi proteins may be preferred by the P2Y₁₄-R will be a topic of future study. Indeed which Gi isoform couples to P2Y₁₄-R may be dependent on the cell or tissue type, and relative expression of each of the Gi proteins. Functional studies in cells lacking each of the $G\alpha$ subunits, such as with siRNA or from knockout mouse-derived cells, may provide some insight as to which of the Gi proteins the P2Y₁₄-R may couple.

The possibility that the P2Y₁₄-R couples to other Gi or G $\beta\gamma$ signaling pathways such as ion channels, phospholipases, protein kinases, and receptor tyrosine kinases is a viable hypothesis, and awaits further investigation. There are many proteins reported to interact

with G $\beta\gamma$, and the potential for P2Y₁₄-R to activate signaling pathways through G $\beta\gamma$ has not been explored.

Another observation reported in Chapter 4 was that the natively expressed P2Y₁₄-R does not couple to inhibition of adenylyl cyclase in differentiated HL-60 cells. Differentiated HL-60 cells are a cell model system frequently used to study neutrophil biology, and inhibition of adenylyl cyclase by GPCRs has not been unequivocally demonstrated in neutrophils nor in HL-60 cells, despite the abundant expression of Gi in both cell types. Moreover, the Gi-coupled chemoattractant receptor FPR coupled to activation of adenylyl cyclase in neutrophils (Mahadeo et al., 2007). Adenylyl cyclases I, V, and VI are the primary isoforms capable of inhibition by Gi (Watts and Neve, 2005). Neutrophils have been reported to express only adenylyl cyclases III, IV, VII and IX (Mahadeo et al., 2007), and therefore one would not expect to observe inhibition of adenylyl cyclase in neutrophils. It is likely that Gi-coupled receptors such as the P2Y₁₄-R have a unique signaling profile in this specialized cell type, and while we have established that the P2Y₁₄-R couples to ERK1/2 phosphorylation in differentiated HL-60 cells, it is possible that other signaling processes also are activated by the P2Y₁₄-R. More detailed signal transduction studies using differentiated HL-60 cells will delineate the signaling pathways activated by the P2Y₁₄-R, and may reflect a potential function for the P2Y₁₄-R in neutrophils.

In addition to studies of signal transduction, the HL-60 cell model also will be a useful means for studies of P2Y₁₄-R-regulated biology. Expression of P2Y₁₄-R mRNA has been demonstrated in neutrophils, but HL-60 cells have technical advantages over neutrophils. Many of the GPCRs that are expressed on neutrophils are Gi-coupled

chemokine receptors that regulate immune responses such as chemotaxis. Studies of UDP-Glc-dependent cellular processes in differentiated HL-60 cells may lead to elucidation of a P2Y₁₄-R function in immune cells.

The cell models developed for studies of the P2Y₁₄-R will circumvent problems with the previously used cell system in which the P2Y₁₄-R was coupled to the chimeric Gq/i. In previous studies, receptor-dependent signaling was observed in the absence of agonist. This phenomenon appeared to be somewhat dependent on agonist in the medium on the cultured cells because treatment of the cells with UDP-sugar hydrolyzing enzymes, such as E-NPP or UDP-Glc pyrophosphorylase reduced such activity. However, a residual component of the activation in the absence of agonist could not be explained by the presence of agonist in the medium. In the cell lines stably expressing the P2Y₁₄-R, there is no evidence of receptor activity in the absence of added agonist. Upon measuring accumulation of cAMP, treatment of the cells with pertussis toxin would be expected to significantly increase the forskolin-stimulated level of cAMP if the receptor were constitutively active, because pertussis toxin would prevent Gi activation. Results from such experiments indicate that the level of forskolin stimulation is similar in cells treated with pertussis toxin to those without.

Another fallacy of the system using Gq/i became clear with recent studies of UDP. In Chapter 3, I described the identification of UDP as a competitive antagonist at the P2Y₁₄-R (Fricks et al., 2008), and additional investigations in which the basal activity of the P2Y₁₄-R was reduced with co-expression of E-NPP1 revealed that UDP is in fact, a partial agonist in this experimental system. With the development of a robust cellular assay for assessing P2Y₁₄-R signaling through its cognate G protein, Gi, as described in

Chapter 4, we have begun to characterize P2Y₁₄-R function via its native signaling processes. In contrast to the results in COS-7 cells in which the P2Y₁₄-R and Gq/i were co-expressed, when UDP was studied in a cellular system in which the P2Y₁₄-R coupled to its native G protein, UDP exhibited the efficacy of a full agonist, indicating that the Gq/i chimera may not be the ideal system for characterizing native P2Y₁₄-R function.

In multiple types of mammalian cells stably expressing the P2Y₁₄-R, UDP exhibited agonist activity in assays measuring inhibition of forskolin-stimulated adenylyl cyclase. This was a surprising finding given that no other lab has reported agonist action of UDP at the P2Y₁₄-R despite screens of nucleotides for agonism in many different experimental systems. Results showing that the effect of UDP is P2Y₁₄-R-dependent and pertussis toxin-sensitive will be detailed in a paper soon to be submitted for publication (Carter, Fricks, et al.).

The reason for the seemingly differential action of UDP at the P2Y₁₄-R in the two experimental systems is not immediately clear. The simplest explanation is that the activation state of the receptor is slightly perturbed when coupled to Gq/i, such that it is capable of binding UDP. However, activation of the G protein is not maximal. Indeed UDP appears to have some partial agonist activity in the transfected system, but it also acts to block binding of UDP-Glc, and so appears to be a competitive antagonist.

Interestingly, in parallel studies of the rat P2Y₁₄-R coexpressed with G_{q/i} in COS-7 cells, UDP was a full agonist. The rat and human P2Y₁₄-R share 80% amino acid sequence homology, and by extrapolation, also would be expected to have similar structural features. Despite their similarities, the prospect of the rat P2Y₁₄-R coupling to

Gq/i with a different orientation than the human P2Y₁₄-R, and thus, permitting activation by UDP, is a distinct possibility.

Studies of the β 1 Adrenergic receptor suggest that different ligands can promote different conformation states of the receptor and in so doing, engage distinct signaling pathways (Galandrin et al., 2008). In effect, it is likely that for some GPCRs, the receptor conformation attained with a particular ligand dictates the receptor's G protein selectivity, or possibly alters the efficiencies of receptor coupling to various G proteins. Juxtaposed with the idea of ligand-induced receptor conformations, the availability of particular G proteins as the determining factor for relative agonist selectivity of a receptor is an alternative explanation for the differential action of UDP on the P2Y₁₄-R in separate cellular systems.

While the Gq/i chimera has been used in studies of many Gi-coupled GPCR, the structure of the P2Y₁₄-R may not be amenable to signaling through this engineered protein. It is possible that the P2Y₁₄-R is in a partially activated state when co-expressed with Gq/i, and the activation not attributable to agonist in the medium is due to receptor that is in a partially active conformation. An inverse agonist for the P2Y₁₄-R would allow us to examine this possibility experimentally, but currently none is available.

An altered receptor conformation would also explain the differences observed in UDP activity between the Gq/i system and the stable cell lines. If the agonist binding pocket were oriented in such a way in the Gq/i system that UDP-Glc was accommodated but UDP was not, then it is easy to understand how UDP may appear as a partial agonist/antagonist. When the P2Y₁₄-R coupled to its native G protein, the receptor

binding pocket was potentially in a conformation that would permit UDP binding as an agonist and subsequently, UDP activation at the P2Y₁₄-R.

An alternative explanation implicates receptor expression as responsible for the dichotomous action of UDP in different cellular systems. When increasing amounts of expression plasmid encoding the P2Y₁₄-R are co-transfected with Gq/i, the apparent efficacy of UDP also increases to a level indicative of a partial agonist. While we would expect that retroviral infection of cells would express receptor at levels close to that of an endogenous receptor, overexpression that introduced receptor reserve into the stable cell system would explain UDP's action as an apparent full agonist. Without a radioligand binding assay, however, we do not have the ability to quantify receptor in order to investigate such possibilities.

With the finding that UDP is a P2Y₁₄-R agonist, the relationship of P2Y₁₄-R to the P2Y₆-R must be addressed. Just as the P2Y₁-R and the P2Y₁₂-R are co-expressed on platelets and have a cooperative function when activated by their shared agonist, ADP, to activate two distinct cellular signaling pathways, it is possible that the P2Y₆-R and the P2Y₁₄-R have a similarly important physiological role when co-expressed. Selectively acting antagonists for each of these receptors may provide clues as to whether the P2Y₆-R and P2Y₁₄-R are functionally linked to any pathophysiological processes. In cellular systems, the two receptors are commonly found expressed together. Assays of UDP-dependent activity in cells in which one of the receptors was knocked down by siRNA would aid our understanding of P2Y₁₄-R versus P2Y₆-R signaling. Although the Gq and Gi pathways appear to be distinct, it is becoming more apparent that signaling networks cooperate to regulate some biological functions, and therapeutic development will be

forced to acknowledge the multiple regulatory mechanisms involved with treating any one disorder. Just as with the P2Y₁-R and P2Y₁₂-R, we may find that the P2Y₆-R and P2Y₁₄-R signaling pathways converge to modulate some critical aspect of physiology.

Although much focus has been on the P2Y₁₄-R as a potential immune cell modulator, the P2Y₁₄-R likely has multiple specialized functions depending on the tissue type. Just as the P2Y₁₂-R is both a modulator of platelet aggregation and is involved in microglial migration (Haynes et al., 2006), so too may the P2Y₁₄-R have distinct roles in the various tissues in which it is expressed. In addition to immune cells, high expression levels for P2Y₁₄-R mRNA have been reported in adipose tissue, placenta, brain and stomach.

Recently, an effect of UDP-Glc on smooth muscle contractility was observed in the forestomach of mouse (Bassil et al., 2009). In the same study, a knockout mouse in which the P2Y₁₄-R gene was deleted was generated. Adult P2Y₁₄-R^{-/-} mice were compared to wild type mice and UDP-Glc did not induce contractions in the stomachs of P2Y₁₄-R KO mice, suggesting that the effect of UDP-Glc was P2Y₁₄-R-dependent. Thus, P2Y₁₄-R expressed in stomach may have a role in gastric motility.

While a normal phenotype was reported for the knockout mouse, no investigation of immune system physiology was described. It would seem from this report of the knockout mouse that the P2Y₁₄-R does not have a critical role in development or viability of mice, and may either have a redundant function in mouse, or function as part of a response mechanism, which will only be revealed after some primary insult such as bacterial infection or tissue damage. Demonstration of P2Y₁₄-R mRNA upregulation in rat brain after immunologic challenge (Moore et al., 2003) supports the notion that the P2Y₁₄-R may be important in an organism's response to injury or disease state.

The physiological relevance of the P2Y₁₄-R remains elusive, but the work presented here advances us toward the common goal of understanding the function of the P2Y₁₄-R. The coupling of the P2Y₁₄-R to two signal transduction pathways, inhibition of adenylyl cyclase and activation of ERK1/2, was established. Progress was made toward developing pharmacological tools that will advance our understanding of P2Y₁₄-R function. The cell models that were developed will be crucial for investigations of signal transduction and cell biological functions attributable to the P2Y₁₄-R. As we have no hint of a physiological function for the P2Y₁₄-R from the knockout mouse, we will continue our progress toward characterization of the P2Y₁₄-R even as we continue to develop better tools to make such efforts more accurate, efficient, and relevant.

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