Phosphodiesterase 8A, cAMP-specific

Enrico Patrucco¹, Stephen Kraynik¹, Joseph A Beavo¹

Phosphodiesterase 8A (PDE8A) is a 3’,5’-cyclic-nucleotide phosphodiesterase that specifically catalyses the hydrolysis of cAMP to AMP. PDE8A is one of the two isoenzymes of the PDE8 family, the other being PDE8B. These two highly similar proteins have several common features that distinguish them from other cAMP-specific PDEs: they have very high affinity for the substrate cAMP; they are insensitive to the non-specific PDE inhibitor IBMX. They contain a PAS (Per, Arnt and Sim) and a REC (receiver) domain, both of which are observed in many signal transduction proteins. The possible function(s) of the PAS domain in PDE8 is still unknown. PDE8A mRNA is not expressed in all tissues but has been detected in several and is highest in testis, spleen, small intestine, heart, ovary, colon and kidney. Until early 2009, the lack of specific small-molecule inhibitors slowed the study of the physiological relevance of PDE8A; thus to date many aspects of this PDE’s functions (that is, whether it is activated or regulated during certain cellular process) remain in large part unknown. So far, functions for PDE8A have been described in Leydig cells, where lack of PDE8A causes increased testosterone production in response to luteinizing hormone; T cells, where it seems to be induced during T cell activation and may control chemotaxis; and cardiocytes, where it seems to regulate calcium handling.

KEYWORDS
mmPDE8A; Pde8a; PDE8A; Phosphodiesterase 8A, cAMP-specific

IDENTIFIERS
Molecule Page ID:A001760, Species:Mouse, NCBI Gene ID:18584, Protein Accession:AAC40194.1, Gene Symbol:Pde8a

PROTEIN FUNCTION
CAMP and cGMP are intracellular second messengers that mediate the response to a wide variety of hormones and neurotransmitters and modulate many metabolic processes. Their concentration into the cell is finely regulated in time and space by the balance between their synthesis, mediated by adenylate and guanylate cyclases, and their degradation by phosphodiesterases.

Cyclic nucleotide phosphodiesterases (PDEs) are a family of related phospho-hydrolases that selectively catalyse the hydrolysis of the 3′ cyclic phosphate bonds of cAMP and cGMP. To date, 11 families of PDEs have been described, comprising 21 different gene products. Each gene can give rise to several different mRNA products through alternative transcriptional start sites and alternative splicing, which brings the number of estimated functional PDE enzymes to more than 100.

The PDE8 family comprises two distinct but highly similar genes in mammals, PDE8A and PDE8B, and was the first of four families of PDEs to have been identified, initially with the help of bioinformatic analysis of the expressed sequence tag (EST) cDNA databases (Soderling et al. 1998; Fisher et al. 1998; Gamanuma et al. 2003). PDE8A and PDE8B both have the carboxy-terminal catalytic domain that is common to all PDEs, but they differ from other PDE families in the amino-terminal region, which contains two putative regulatory domains. First, there is a REC domain, homologous to the “receiver” domains of bacterial two-component signaling systems (Galperin et al. 2001). This is followed closely by a PAS (Period, Arnt and Sim) domain, which was first described as a regulatory domain present in several proteins involved in the control of circadian rhythms (Dunlap et al. 1999; Gilles-Gonzalez and Gonzalez 2004). PDE8 enzymes are cAMP-specific and have highest affinity for this substrate of all the PDEs (K_M 40-150 nM for cAMP, K_M >100 μM for cGMP) (Fisher et al. 1998; Gamanuma et al. 2003; Soderling et al. 1998). Hence, PDE8 has no appreciable activity towards cGMP.

The first indication of a possible function for PDE8A came from work by Glavas et al. (2001), in which a full-length PDE8A protein was identified in human T cells and its expression showed to be upregulated in CD4+ T cells after stimulation. Another study on mouse splenocytes showed that Pde8 mRNA levels are increased following cell stimulation with concanavalin A, a lymphocyte mitogen (Dong et al. 2006). Moreover, T cell migration in response to chemokine attractants was diminished when Pde8 activity was inhibited with the non-selective PDE inhibitor, dipyridamole. Dipyridamole was shown to inhibit PDE8A with a reported IC50 of 4-9 μM (Soderling et al. 1998; Fisher et al. 1998).

From northern blot analysis, PDE8A is particularly abundant in testis, and protein expression was confirmed in spermatozoa (Baxendale and Fraser 2005; Vasta et al. 2006). In addition, using a Pde8a knockout mouse as model, Vasta and colleagues showed that PDE8A is also present in Leydig cells in testes, where it contributes to controlling the steroidogenic response to luteinizing hormone.

PDE8 inhibition using dipyridamole in a dose-dependent manner increased cAMP levels in bovine cumulus-oocyte complexes and subsequently delayed oocyte nuclear maturation (Sasseville et al. 2009). Also, PDE8A modulates excitation-contraction coupling in ventricular myocytes, where its ablation is marked with an increase in calcium transients and calcium spark frequency (Patrucco et al. 2010).

It was recently shown that increasing cAMP in effector T cells by inhibiting PDE8 with a new selective small molecule inhibitor (PF-04957325) suppressed the expression of integrins...
required for adhesion to endothelial cells (Vang et al. 2010). In addition, using Pde8-ablated mice and using the inhibitor PF-04957325 Tsai et al. showed that Pde8a and Pde8b both regulate corticosterone production in the mouse adrenal gland.

REGULATION OF ACTIVITY
As with other PDEs, PDE8A activity depends on the presence of divalent cations, and sequence analysis has revealed the presence of conserved metal binding sites in the catalytic domain. In vitro experiments showed that maximal PDE8A activity is obtained in the presence of either Mg$^{2+}$ or Mn$^{2+}$ at concentration above 1 mM (Fisher et al. 1998). Kinetic studies on recombinant human PDE8A catalytic domain showed that manganese is slightly more efficient than magnesium, and thus might serve as the catalytic metal ion in a physiological setting. However, a biological preference remains to be shown (Wang et al. 2008).

Computational analysis of the coding sequence of PDE8A indicated several potential phosphorylation sites (at least three protein kinase A/protein kinase G and tyrosine kinase consensus sequences, plus a site for protein kinase C phosphorylation). Whether PDE8A is phosphorylated or whether this modification regulates the catalytic activity has not been shown (Wang et al. 2001).

IBMX, a non-selective inhibitor for most PDE families with IC50 of 2–50 μM, does not effectively inhibit PDE8 activity, unless the concentration of drug is increased to beyond 200 μM (Fisher et al. 1998; Soderling et al. 1998; Gamanuma et al. 2003). The crystal structure of PDE8A’s catalytic domain bound to IBMX has been resolved, and data interpretation indicates an important role for Tyr 748 in the unfavorable interaction between IBMX (and presumably other common PDE inhibitors) and the catalytic pocket (Wang et al. 2008). Mutation of Tyr 748 to phenylalanine increased the sensitivity of PDE8A to IBMX about tenfold, confirming a pivotal role of this residue in determining PDE8A’s selectivity to inhibitors.

The PDE8-selective inhibitor (PF-04957325) has a reported in vitro IC50 of 0.7 nM for PDE8A and < 0.3 nM for PDE8B, and is ≥ 2,000-fold more selective over other PDE isoforms (IC50 > 1.5 μM). This inhibitor also shows no activity in an in vitro system (Wu and Wang 2004; see also next section). Thus, the PAS domain seems to enhance the catalytic activity of PDE8A.

A similar conclusion was achieved by comparing the kinetic and structural properties of recombinant human PDE8A forms that contained or lacked the PAS domain (Wang et al. 2008). The authors suggest that deleting the PAS domain results in a misfolding of the catalytic domain, which negatively affects its catalytic properties.

INTERACTIONS
Some, but not all, PAS domains bind cofactors such as metabolites, ions, and flavin nucleotides (Möglich et al. 2009). It is likely that many PAS domains exert their physiological role in the absence of any cofactor. So far, no cofactor has been found to bind the PDE8A PAS domain.

A study by Ping Wu and Peng Wang found that overexpressed recombinant human PDE8A1 (a splice form; see the "Splice Variants" section) can associate with endogenous IκB proteins in human embryonic kidney HEK cells via its PAS domain (Wu and Wang 2004). Functionally, the IκB binding seems to increase PDE8A activity significantly, at least in an in vitro system. Whether this interaction occurs under physiological conditions in any tissue or cell that expresses PDE8A remains to be investigated.

PHENOTYPES
In 2006, Vasta et al. were the first to describe the generation and characterization of the Pde8a knockout mouse. Leydig cells from Pde8a ablated mice show elevated testosterone production compared with wild-type control cells in response to increasing doses of luteinizing hormone (Vasta et al. 2006). Cardiomyocytes from these mice also exhibit increased calcium transients and spark frequency than wild-type cells (Patrucco et al. 2010). The mechanism by which Pde8a’s absence causes either of these phenomena remains unclear. It was also shown that the Pde8 inhibitor PF-04957325 still potentiated pregnenolone production in primary adrenal cells from Pde8b knockout animals, while having no effect on Pde8a/Pde8b double knockout cells. This indicates that Pde8a has some role in adrenal steroid production, although the extent of this is unknown (Tsai et al. 2010).

Phenotypes associated with overexpression of PDE8A are unknown.

MAJOR SITES OF EXPRESSION
Northern blot analysis with a PDE8A probe on human mRNA samples from different tissues showed that the messenger transcript is widespread, with higher abundance in testis, ovary, colon and small intestine (Fisher et al. 1998). The same analysis conducted on mouse tissues showed high level of mRNA in testis and, progressively decreasing, in liver, kidney, skeletal muscle, heart, eye, ovary, lung and brain (Soderling et al. 1998), thus indicating a similar but not totally overlapping expression pattern to human. In rat major expression is found in testis, followed by liver, kidney, heart, thyroid and brain (Kobayashi et al. 2003).

Quantitative real-time PCR analysis conducted to detect the tissue distribution of the two major splice variants of human PDE8A (PDE8A1 and PDE8A2) gave the following results (in decreasing order):

**PDE8A1**: testis, spleen, colon, small intestines, ovary, placenta, lymph nodes, prostate, pancreas, kidney, T helper 1 (Th1) cells, Th2 cells, total leukocytes, lung, brain, liver, thymus, heart, bone marrow and skeletal muscle.

**PDE8A2**: spleen, testis, ovary, placenta, prostate, colon, pancreas, leukocytes, kidney, brain, Th1 cells, lymph nodes, heart, lung, small intestines, Th2 cells, liver, thymus, bone marrow, skeletal muscle (Wang et al. 2001).

Protein expression of PDE8A was reported in the following organisms, tissues and cell lines:
- T cells (human) (Glavas et al. 2001)
- Spermatozoa (mouse) (Baxendale et al. 2005; Vasta et al. 2006)
- Leydig cells (mouse) (Vasta et al. 2006)
- Ovary (mouse and bovine) (Sasseville et al. 2009)
- Brown adipose tissue (Zapala et al. 2005; Kraynik et al. 2009)
- Ovary theca cells (human) (Chen et al. 2009)
- CCRF-CEM T leukemic cells and Jurkat cells (human origin) (Dong et al. 2010)
- Adrenal gland (mouse) (Tsai et al. 2010)

Please view the EST and GEO Expression profiles for more information.

**Additional reference**

**SPLICE VARIANTS**
The human PDE8A gene has several transcript variants that seem to be produced by alternative splicing and alternative start sites (Wang et al. 2001). PDE8A2 is a spliced variant of PDE8A1 that lacks the PAS domain, and PDE8A3 is a truncated protein lacking both the PAS and REC domains. PDE8A4 and PDE8A5 are identical truncated proteins, with different untranslated sequences, that are longer than PDE8A3 but are still missing both the PAS and REC domains. Experimental evidence that each transcript variant corresponds to a different protein isoform is still missing.
REFERENCES


Proc Natl Acad Sci U S A, 103, 52.


