

Cloning and functional expression of a brain G-protein-coupled ATP receptor

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A cDNA encoding a novel member of the G-protein-coupled receptor (GCR) superfamily, an ATP receptor, has been isolated from an embryonic chick whole brain cDNA library by hybridization screening. The encoded protein has a sequence of 362 amino acids (41 kDa) and shares no more than 27% amino acid identity with any known GCR. When expressed as a complementary RNA (cRNA) in *Xenopus* oocytes a slowly-developing inward current was observed in response to application of ATP. The pharmacology of this expressed protein defines it as a P_{2Y} purinoceptor.

G-protein-coupled receptor; ATP; P₂ purinoceptor; P_{2Y} subtype; Chicken brain

1. INTRODUCTION

Evidence has accrued for many years that ATP can act as a neurotransmitter or modulator in both the peripheral and the central nervous system [1–3]. The effects of extracellular ATP are mediated via specific receptors, the P₂ purinoceptors: which are entirely distinct from those that bind adenosine [2]. At least five subtypes of P₂ purinoceptors have been proposed pharmacologically [2,4], with P_{2X} and P_{2Y} purinoceptors the best described. However, none has as yet been characterised at the molecular level. The P_{2X} purinoceptor has the properties of an ATP-gated cation channel [5], whereas other P₂ purinoceptor subtypes appear to be members of the GCR superfamily [4,6].

At around the time of hatching, the brain of the chick is known to be in a phase of highly active expression of many receptor mRNAs, as confirmed in oocyte expression studies [7,8]. Investigating sources of ATP receptors, we found that this brain is, in fact, exceptionally rich in high-affinity ATP-binding sites of the P_{2Y} subtypes (J.S. and T.E.W., unpublished). We have cloned a brain partial cDNA [9] that encodes the guinea pig equivalent of an unidentified receptor [10] of the G-protein-coupled class, RDC1, which is most related in

sequence to canine adenosine receptors [10]. To isolate related sequences, we used this clone to screen an embryonic chick whole brain cDNA library. In this report we describe the cloning and expression of a cDNA encoding a novel GCR that binds ATP. This receptor displays a P_{2Y} purinoceptor pharmacology distinct from the classical [2,4] type. On the basis of this pharmacological evidence, we designate this novel subtype as a P_{2Y1} purinoceptor. This designation is supported by the restricted expression of the corresponding mRNA transcript.

2. MATERIALS AND METHODS

2.1. Polymerase chain reaction, cDNA library screening and DNA sequencing

Two degenerate oligonucleotide primers, from transmembrane domains II and VI of G-protein-coupled receptors. 5'-TAGGTC GAC(G/C)(G/C)TGT(G/C)(T/C)CTGGC(C/T)GTGGC(C/T)GC-(A/C)T-3' and 5'-AGGACGAATTCTGGG(G/A/C)(G/A)ICCAAGT CAG(A/G)AT(G/A)AAG(G/A)C-3', were used to amplify other members of the GCR superfamily from guinea pig brain first-strand cDNA. The amplification conditions were as follows: 94°C, 1 min, 55°C, 1 min, 72°C, 1 min; 30 cycles [9]. Amplification products were subcloned, making use of the restriction endonuclease sites incorporated into the 5'-ends of each primer, into complementary restricted M13mp18 for sequence analysis (Sanger dideoxy chain termination, Sequenase kit, USB).

A 497-bp cDNA fragment that encoded part of a RDC1-like sequence [9] was labelled (random primer method) to a specific activity of approximately 1 × 10⁹ dpm/μg and used to screen 5 × 10⁵ recombinants of an embryonic chick whole brain cDNA library (λgt10, gift of A. Hicks [11]). Hybridisation was in 6 × SSC at 65°C for 18 h; the final wash conditions were 1 × SSC at 55°C. Three hybridization classes of strong to weak intensity were distinguished DNA from a

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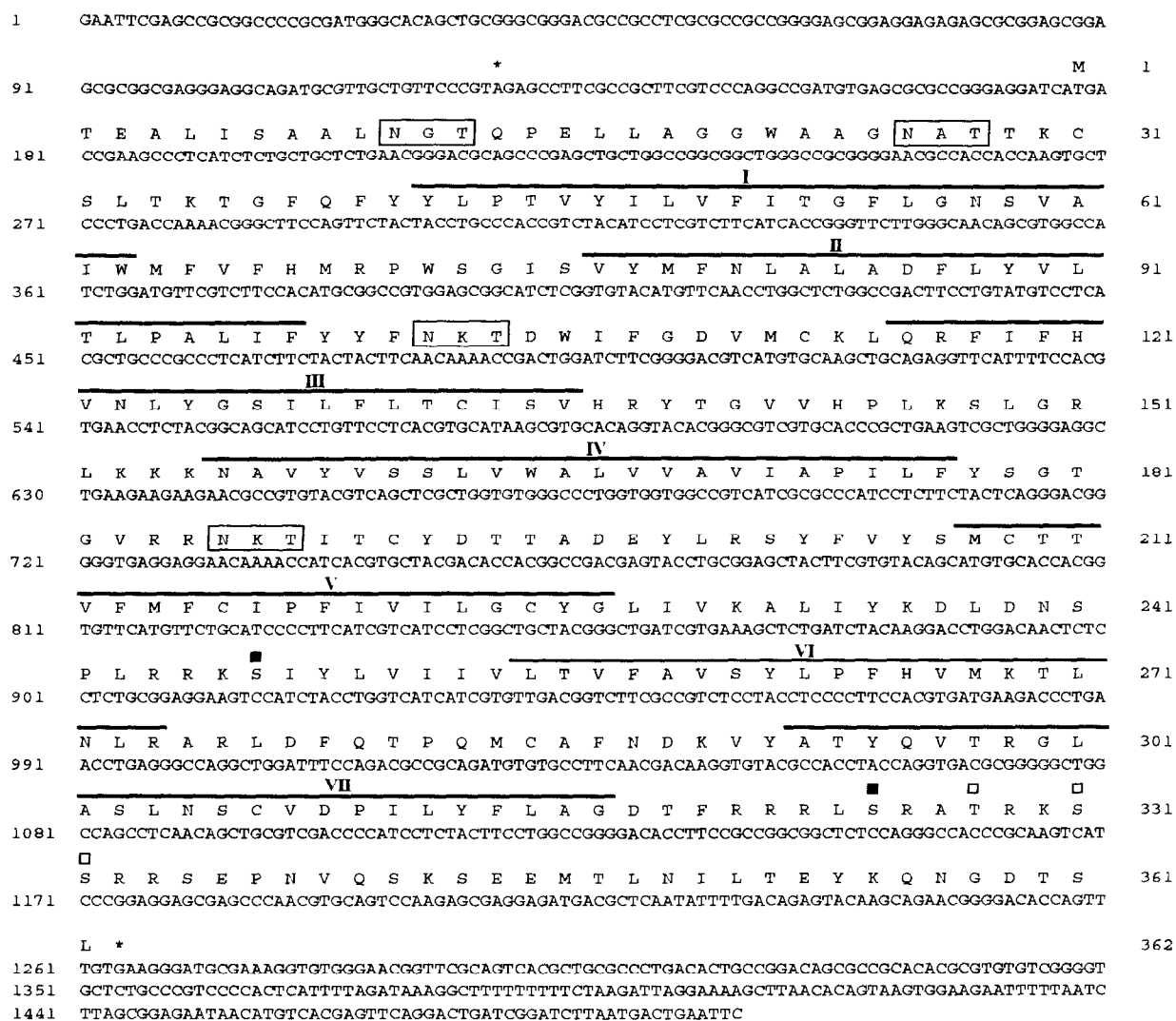


Fig. 1. Nucleotide and predicted amino acid sequence (single letter code) of the 803 protein. Putative transmembrane domains as determined by the Kyte-Doolittle algorithm [15] are overlined and numbered. Potential sites for N-linked glycosylation are boxed. Potential sites for phosphorylation by protein kinase A and protein kinase C are indicated by solid and open squares, respectively.

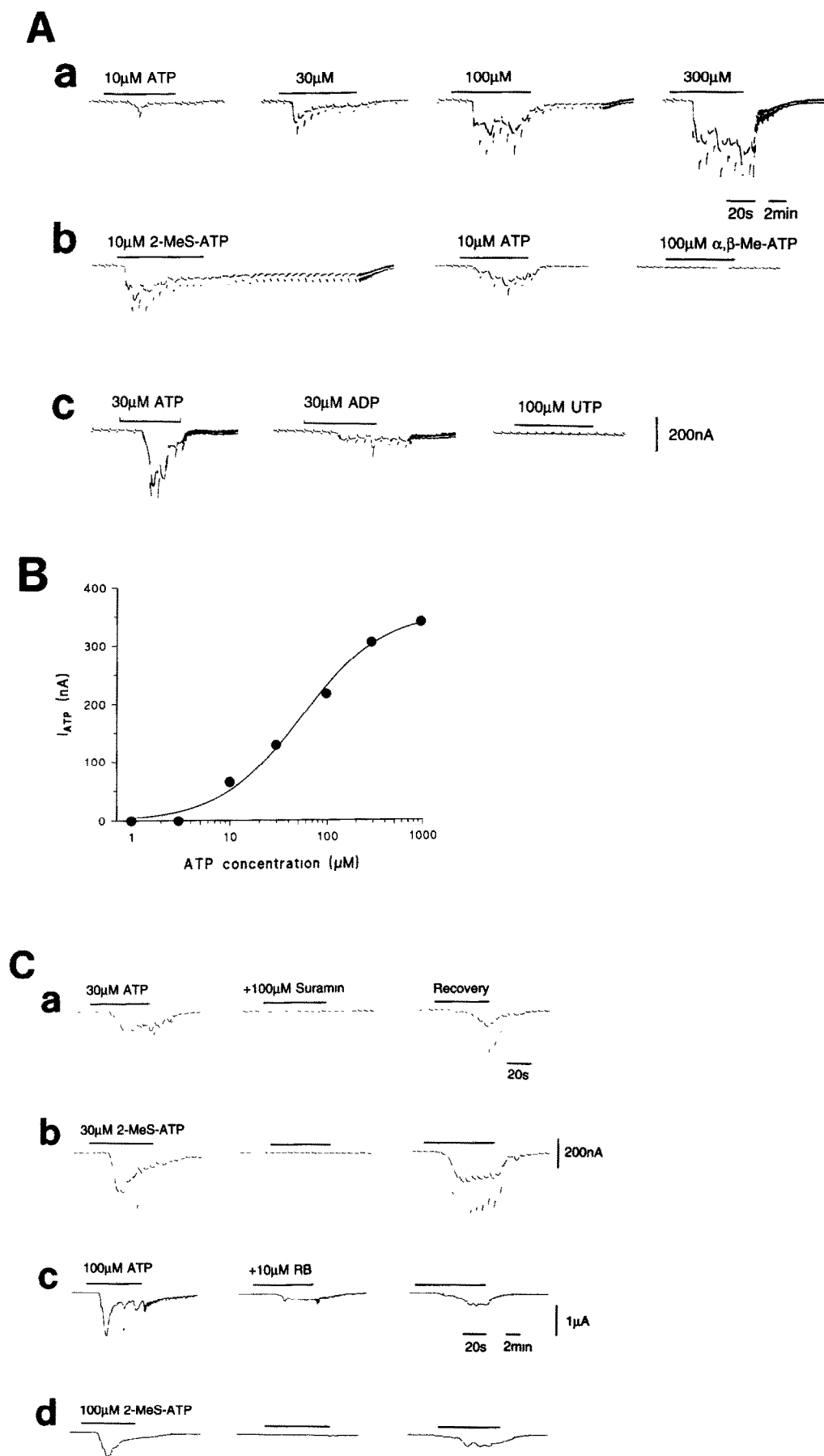
phage of middle intensity, clone 803, was isolated by standard procedures and the whole *EcoRI* insert was subcloned to the same site in M13mp18 and subjected to sequence analysis.

2.2. In vitro transcription, oocyte preparation, microinjection and electrophysiological measurements

The 1.5-kb cDNA insert from 803, was subcloned into the *EcoRI* site of the expression vector pSG5 (Stratagene). Capped and polyadenylated cRNA was transcribed in vitro from this construct, linearised

with *Bam*HI, using a riboprobe kit (Promega). cRNA (~50 ng in 50 nl per oocyte) was injected into oocytes retaining their follicular envelope, as previously described [8]. After 2–3 days at 18°C in modified Barth's medium, they were maintained at 4°C for at least 11 days [8]. Two-electrode voltage clamping (Axoclamp 2A amplifier) was used at room temperature. The voltage-recording and current-injecting electrodes were filled with 0.6 M K_2SO_4 and 3 M KCl, respectively. Oocytes were superfused at a rate of 10 ml/min (bath volume 0.2 ml) with an amphibian Ringer (mM), 110 NaCl, 2 KCl, 5 HEPES, 2

Fig. 2. Responses in cRNA-injected *Xenopus* oocytes (at -40 mV). (Aa) Dose-dependence of membrane currents evoked by ATP (10–300 μ M). The transient downward deflections monitor the input conductance following hyperpolarizing voltage steps (-10 mV, applied every 5 s for 1 s). Similar results were observed in two other oocytes. (Ab,c) In two oocytes, the agonist selectivity was assessed using 2-MeSATP, ATP, ADP, α,β -MeATP and UTP. Holding potentials, -40 mV. (B) ATP concentration-response relationship. The membrane current amplitude (I_{ATP}) was measured using the initial peak inward current induced by each ATP concentration. (C) Suramin antagonized the responses to (Ca) ATP and (Cb) 2-MeSATP. RB also inhibited the responses to (Cc) ATP and (Cd) 2-MeSATP. Note, in (A) and (C), the slower chart speed in some records during drug washout and the incomplete recoveries following treatment with RB. Bar indicates ligand application.



P _{2y1}	MTEALISAALNGTQPELLAGGWAAGNAT TKCS -LTKTGFQ FY ---- YLPTV	46
RDC1	MDLHLFDYAEPGNFSDISWPCNSSDCIVVD TVLCPNMPNKS VLLY----- TL SFI	50
ANG II	MILNSSTEDGIKRIQDD CPKAGR HNYI FV ----- MIPTL	34
Thrombin	MGPRRLLLVAACFSLCGPL-(54)-INKSSPLQKQLPAFISEDASGYLTSSWLTFLV PSV	108
PAF	MELNSSSRVDSEFRY--- TLF-P IV	21
A1	MPPAISAFQAAYIG-I	15
A2	MS-TMGSW-- VYIT-V	12
P _{2y1}	YILVF ITG FLGNS VAI WMF -- VFHM RPWSGIS VYMFNL ALADFLY- VLTL PALIF YFF NK	103
RDC1	YIFI FVIGMIANSVV VWN --IQAKTTGYDTHCYIL NLAI ADLWV- VVTIP VWVVS L VQH	107
ANG II	YSII FVVGIFGNSLVVVI-- YFY MKLKT VASV FL NLAL ADLCF- LLTL PLWAV Y TAME	91
Thrombin	YTG VFVVS LPLN IMAI VVF --IL KMK VKKPA VYML HLATAD VLF - VSVLP FKIS Y YFSG	165
PAF	YSII FVL GII ANGYVL WVF ARLYPSKKLNEIKI FMV NLT VAD LLF- LI TLPLWIV Y YSNQ	80
A1	EV LIAL VSVP GNVL VIWAV--KVNQALRDATFCFIV SLAV ADVAVGALV IP LAILINIGP	73
A2	ELAI AVL AIL LGN VLVCWAV--WLNSNLQNV TNYFV VS LAA ADIAVG VLAI PF AIT ISTGF	70
P _{2y1}	TDWI FGDVMCKLQRFIF HVN LYGS SIL FL TCIS VHRYTG VVH PLK SLGR LKKKN AVY VSSL	163
RDC1	NQW PMGELT CKI TH LIFS IN LFGS IF FLTC MSVDRYLSITYFASTSS RRK VVRRAVC VL	167
ANG II	YRW PF GN YL CKI ASASVS FN LYAS VFL TL CL SIDRYLAI VHP MKSRLR RTM LVA KV TCII	151
Thrombin	SDW QFGSEL CRF VTAA FYCN MYAS ILL MT VIS IDRFLAV VYPM Q SL SWRTLGRAS FT CLA	225
PAF	GNW FLPKFLCNLAGCL FFIN TYCS VAF LGVITYNR FQAV KY PIK TAQAT TR KRGIAL SLV	140
A1	RTYFHT--- CLM VACPV LILT QSS SIL ALLAI AVD RYLR VKI PLRYKT VVT PRRA AV AIAG	130
A2	CAACHN--- CLF FACFVL VLT QSS SIFS LLAI AI D RYIA IR PL RYNG LVT G TRAK GIIAV	127
P _{2y1}	VWAL VVA VI AP ILF ---- YSCT GV RRNK ---- TIT -CYDTT AD EY LR S YF VY-SMCT TVF	213
RDC1	VWLL AFCV SL PD TY ---- Y LKT VT SA SN ---- NET YCRSFY PEH SVKE WL ISMELV SV VL	219
ANG II	IWLL AGLAS LP AI II ---- HRN VFF IENT ---- NIT VCAF HYE SQ N -ST LP IGLGL T KNIL	202
Thrombin	IWAL AIAGV VPL VL---- KEQ TIQ VP GL---- NIT TC HD VLNET L LEG Y AY Y FS AF SAV	277
PAF	IWVA IVAA ASY FLV---- MD ST NV VS NK AGSG NIT RC FE HYEKGS KP VL II --- HIC IVL	193
A1	VWIL SFVVGL TP LF GW NRLGE AQ RAWAANGSGGEP VIK CE FE KVIS MEY M VY FN FF VWVL	190
A2	CWV LS FA IGL TP ML GW NNCS Q PK EG R NY S Q CGEG Q VAC L FEDV VP M NY M VY FN FF AFVL	187
P _{2y1}	M-FC IP FF IVIL GCY GLI VK ALI YK ----- DL DNS PL -- RRK SI YLV II VL TV- FAV SYL	263
RDC1	G-FA IP FC VI AV FY CL LAR IAS ----- SD QEK SS -- R ----- KI IFS YVV VL VC WL	266
ANG II	G-FL FP FL I IL TSY PL I WK AL KKA ----- YEI Q KN K P -- R ND DI FKI IM AI VL FF FS WI	254
Thrombin	F-FF V PL I IST VCY VS I IR CL S -S----- SAV AN RSK -- K S R AL FL SA AV FCI- F II CF G	327
PAF	G-FF IV FL L IL FC N LVII HT LR Q ----- PV K Q R NA EV RR RAL WM V CT VL AV - F VI CF V	246
A1	P LLL ML VLI Y LEV FY L IR R Q L GK K V SAS-SG DP Q KY - Y G K EL KI AK SL AL IL FL FAL SWL	248
A2	V LLL ML G VY LR IF LAARR Q L Q MES Q PL P GERAR ST L Q KE V HA AK SLAI IV GL FAL CWL	247
P _{2y1}	PFH VMK TLN L R AR LD F Q TP Q MC AF ND KV YAT YQ VR GL AS LN SC VD PI LY FL AG DT FR RR	323
RDC1	PYH VV LLD I F SIL HY - I P FT C Q LEN FL FTAL HVT Q CL SL VH CC VN P V LY S FIN RY - RY	324
ANG II	PHQ IF TF LD VLI Q LGI - IR - D C R IA D IV DT AMP IT IC I AY FN NC LN P LF Y G FL GK K FK RY	312
Thrombin	PTN VL--- LI A HY S FL S HT -- ST TEA AY FAY LL C V CV SS IS SC ID PL I Y Y AS SEC Q RY	381
PAF	PHH MQ LP W TLA EL GM W PS --- SN HQ A INDA HQ VT LC LL ST NC VL D P VI Y CF LT KK FR KH	303
A1	PLH ILNCIT LF CP----- SCR K P SI-L- MY IA IF L TH GN S AM NP I V Y AF RI Q FR VT	298
A2	PLH IINC FT FFCP----- EC SHAP LWL - MY LT IV LS HT NS V V NP FI Y AY R IRE FR QT	298
P _{2y1}	LSR AT RK SS RR SEPN VQ SK SE MT LN IL TEY K Q NGD TS L	362
RDC1	ELM KAF IF KY SA KT GL TK LID AS RV SE- TEY SA LE Q NA K	362
ANG II	FLQ --- LL KY IP PKAK SH SN LST K MST LSY RP SD NV SS ST KK PAP CFEVE	359
Thrombin	V SIL CK ESS DP SS YN SS GQ L MA SK MD TC SS N LN NSI YK KL LT	425
PAF	L SE KL NIM R SS GK CS RV TT DT G TE MA IP IN HT PV N PI KN	342
A1	FLK I W ND H FR CQ PT P VD ED P PE APHD	326
A2	PRK II R SHV LR RR EP FKAG GT SAR ALA A HG SD GE QIS LR LN GH PP GV WANG SAP H-(58)	411

←

Fig. 3. Comparison of the chick P_{2Y1} purinoceptor with the canine orphan RDC1, human angiotensin II type 1 (ANG II), human thrombin, guinea pig platelet activating factor (PAF) and canine adenosine, A1 and A2 receptors. Numbers in parentheses indicate the amino acids removed, and dashes the gaps inserted, to optimise the alignment using the Clustal program [29] (v1.0). Identical results are indicated in bold type.

$CaCl_2$, pH 7.4. Resting potentials varied from -23 to -65 mV and input resistances from 0.5 to 2 M Ω . $I_{Cl(Ca)}$ was activated under voltage clamp, using a step-pulse protocol to establish whether antagonists interfered with the endogenous calcium-activated chloride channel [13] in the oocyte. A command step to -100 mV for 1 s was followed by a depolarising command for 4 s to $+50$ mV to activate $I_{Cl(Ca)}$, before returning to the holding potential of -40 mV. This protocol was repeated every 20 s in the absence and presence of the antagonists. The measured current relaxation was indeed $I_{Cl(Ca)}$ since when external Ca was removed and equimolar $BaCl_2$ was applied the current was substantially reduced.

2.3. Hybridization analysis of chicken RNA

Total cellular RNA from a variety of one-day-post-hatch chick and chicken tissues was prepared by CsCl centrifugation [12]. Poly(A)⁺-selected RNA was prepared by oligo(dT) cellulose chromatography. RNA was electrophoresed through a 1% formaldehyde 0.8% agarose gel. Following electrophoresis, RNA was blotted to Hybond-N nylon membrane (Amersham) and hybridisation was performed at 42°C in 50% formamide [12]. The hybridisation probe was an antisense 45 -base oligonucleotide corresponding to the DNA sequence encoding amino acids 1 – 15 of 803 and was labelled by terminal deoxynucleotidyl transferase to a specific activity of approximately 1×10^9 dpm/ μg . The filter was washed at 65°C in $1 \times \text{SSC}$, 0.1% SDS for 15 min before being exposed to an X-ray film at -70°C with an intensifying screen. Exposure: 10 days (1 day for chick brain).

3. RESULTS AND DISCUSSION

A guinea pig partial cDNA [9] was used to screen 5×10^5 recombinants of an embryonic chick whole brain cDNA library. Sequence analysis of one of the isolated clones, 803 , revealed the presence of an open reading frame of $1,068$ bp. The predicted amino acid sequence and the nucleotide sequence are presented in Fig. 1. The putative initiator methionine is in agreement with the optimal sequence for translation [14] and the presence of an in-frame stop codon upstream of this methionine codon indicates that 803 encodes the entire coding region of a polypeptide of 362 amino acids with a calculated molecular weight of 41 kDa. The hydrophobicity profile [15] (not shown) of the predicted amino acid sequence revealed the typical pattern of a GCR and exhibited seven hydrophobic domains. The sequence possesses other common features [16] of the GCR superfamily, including: (a) consensus sequences for N-linked glycosylation near the amino terminus and in the first two extracellular loops; (b) two conserved cysteine residues, one in each of the first two extracellular loops, that are believed to form a disulphide bond which stabilises the functional protein structure; (c) serine and threonine residues in the third cytoplasmic loop and COOH-terminal domain, which represent potential phosphorylation sites and may play a role in receptor desensitization (Fig. 1).

To establish the identity of the 803 protein, *Xenopus laevis* oocytes were injected with in vitro transcribed cRNA prepared from clone 803 [7,8]. ATP ($1 \mu\text{M}$ – 1 mM) caused a slowly-developing inward current associated with a conductance increase, in cRNA-injected oocytes (Fig. 2Aa). The slow but large, concentration-dependent outward currents and conductance increases, which can be seen in non-injected control oocytes, representing activation of native adenosine receptors, were completely inhibited by bath application of $100 \mu\text{M}$ theophylline [17]. Therefore, all experiments were performed in the presence of theophylline, which does not interfere with responses to P_2 receptor activation [17]. After inhibition with theophylline, reapplication of $100 \mu\text{M}$ ATP did not reveal any previously occluded oscillatory inward current in control oocytes. Membrane current and conductance oscillated during and for some time after agonist application. The observed responses, together with a reversal potential of -24 mV, indicated the involvement of a Ca-activated Cl^- current ($I_{Cl(Ca)}$) [13] which is normally evoked in the oocyte by expressed GCRs [18]. Responses to ATP were dose-dependent, with a threshold concentration of approximately $10 \mu\text{M}$ and an EC_{50} (half-maximal concentration) of $49.5 \pm 6 \mu\text{M}$ (Fig. 2Aa,2B). Repeated applications of the same concentration of ATP produced consistent responses, with a negligible decline in response amplitude over time. Inward currents were also induced by 2-methylthio-ATP (2-MeSATP) and ADP. In contrast, UTP and the P_{2X} -selective agonists $[\alpha,\beta\text{-methyl-} \gamma\text{-methylene-ATP}]$ ($\alpha,\beta\text{-MeATP}$), and $\beta,\gamma\text{-methylene-ATP}$ ($\beta,\gamma\text{-MeATP}$) were inactive at concentrations up to 30 – $100 \mu\text{M}$ (Fig. 2A). The relative order of agonist potency (as judged by matched-response amplitudes) was: $2\text{-MeSATP} \geq \text{ATP} > \text{ADP} \gg \alpha,\beta\text{-MeATP}$, $\beta,\gamma\text{-MeATP}$, UTP. This specificity was found likewise in radioligand binding studies performed on chick brain membranes, or on 803 transfected cos-7 cells, with a high-affinity binding site for ATP being present (to be reported elsewhere). In injected oocytes both suramin ($100 \mu\text{M}$) and the P_{2Y} -selective antagonist [19] Reactive Blue 2 (RB) ($10 \mu\text{M}$) antagonised the responses to ATP and to 2-MeSATP (Fig. 2Ca,Cb) without appreciably affecting native $I_{Cl(Ca)}$. The high potency of ATP and the inactivity of the methylene ATPs and of UTP identified this receptor as a P_{2Y} subtype rather than a P_{2X} or P_{2U} subtype. The near equipotency of 2-MeSATP and ATP, and greater potency of ATP over ADP, suggested that this expressed receptor is a novel subtype of the P_{2Y} purinoceptor family. We have therefore designated this receptor as P_{2Y1} .

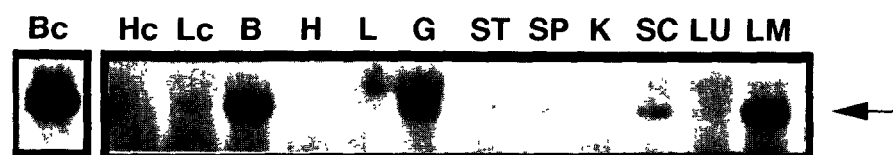


Fig. 4. Tissue distribution of the transcript corresponding to the P_{2Y1} receptor. A Northern blot of chick (one-day-post-hatch) whole brain poly(A)⁺ (10 μ g) and total RNA (30 μ g) from various chick and adult tissues was subjected to Northern analysis as described in Section 2. Tissues were: Bc, chick brain; Hc, chick heart; Lc, chick liver; and from adult chicken. B, brain; H, heart; L, liver; G, gastrointestinal tract; ST, stomach; SP, spleen; K, kidney; SC, spinal cord; LU, lung; LM, leg muscle. Band size (arrow) was determined using RNA standards (BRL). Bands were absent from the regions of the blot not shown

Comparison of the P_{2Y1} purinoceptor with other cloned GCR sequences places it in the major family of these receptors [20]; negligible sequence identity was seen with either the secretin/calcitonin or the glutamate receptor gene families. P_{2Y1} shares no more than 27% identity with known GCR sequences (Table I), suggesting that this receptor protein is in a previously unknown subdivision of this major receptor family. It is of interest that the P_{2Y1} receptor has only a low sequence identity with the adenosine [10] (21%) and cAMP [21] (17%) receptors (Table I, Fig. 3). The P_{2Y1} receptor sequence does not contain ATP binding motifs [22] of the type $G[X]_4GK$. The absence of a linear ATP binding motif is not surprising, since it is likely that the ligand-binding pocket for a molecule the size of ATP will be formed by residues in several transmembrane domains as in the case of the catecholamine receptors [23].

The tissue distribution of the P_{2Y1} transcript was determined by Northern hybridisation. The mRNA (3.1-kb) had a discrete pattern of expression in the adult

chicken: it was present in brain, spinal cord, gastrointestinal tract, spleen and leg muscle (Fig. 4) but was not detected in heart, liver, stomach, lung or kidney. The transcript was also found in the brain of newly-hatched chick (Fig. 4). P_{2Y} purinoceptors are abundant in the mammalian gastrointestinal tract and spinal cord [2] but their distribution in chicken tissues is unknown. However, in developing chick skeletal muscle P_2 purinoceptors have been found in physiological studies, but not of the defined P_{2Y} type [24]. The existence of P_{2Y} purinoceptors in mammalian liver, kidney, pancreas, blood vessels and heart has also been reported [2,25–27], but the observed pharmacology of these receptors differ [5] from the purinoceptor described here. Our data support the hypothesis that the chick P_{2Y1} purinoceptor is distinct from the P_{2Y} purinoceptors described previously in visceral tissues.

ATP is known to act as a fast neurotransmitter in peripheral and central neurones, via P_{2X} purinoceptor cation channels [5,28]. The presence of P_{2Y1} purinoceptors in the brain indicates the involvement of ATP in metabotropic, slow synaptic transmission. Indeed, the high concentration of the P_{2Y1} mRNA and the exceedingly high and specific binding capacity for ATP in the developing chick brain (J.S. and T.E.W., unpublished) is indicative of a more significant role for a P_{2Y} purinoceptor in the brain than has hitherto been suspected.

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Table I

Percentage identity of chick P_{2Y1} purinoceptor with known G-protein-coupled receptors

Receptor	Species	% Identity with P_{2Y1}
RDC1	canine	27
Angiotensin II type 1	human	27
Thrombin	human	25
Platelet activating factor	guinea pig	25
CSa anaphylatoxin	human	23
Neuromedin K	rat	23
Interleukin 8	human	22
Bradykinin B2	rat	22
Neurotensin	rat	21
Endothelin B	human	21
Gastrin-releasing peptide	mouse	21
Adenosine A1	canine	21
Substance P	human	20
Neurokinin 2	human	20
Adenosine A2	canine	18
cAMP	slime mold	17

The most related sequences are shown, along with adenosine and cAMP receptors. Amino acid sequences were obtained from the Protein Identification Resource (PIR) and were aligned using the Clustal program [29] (v1.0).

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