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Functional characterization of an endogenous Xenopus oocyte adenosine receptor

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- 1 To investigate the effects of adenosine on endogenous Xenopus oocyte receptors, we analysed defolliculated oocytes injected with mRNAs for the G protein-activated inwardly rectifying K+ (GIRK) channels.
- 2 In occytes injected with mRNAs for either GIRK1/GIRK2 or GIRK1/GIRK4 subunits, application of adenosine or ATP reversibly induced inward K+ currents, although ATP was less potent than adenosine. The responses were attenuated by caffeine, a non-selective adenosine receptor antagonist. Furthermore, in uninjected oocytes from the same donor, adenosine produced no significant current.
- The endogenous receptor was activated by two selective A₁ adenosine receptor agonists, N⁶cyclopentyladenosine (CPA) and No-cyclohexyladenosine (CHA), and antagonized by a selective A1 adenosine receptor antagonist, 1,3-dipropyl-8-cyclopenylxanthine (DPCPX) at moderate nanomolar concentrations, but insensitive to micromolar concentrations of selective A2A and A3 adenosine 2-[p-(2-carbonyl-ethyl)-phenylethylamino]-5'-N-ethylcarboxamidoadenosine (CGS21680) and No-(3-iodobenzyl)-5'-(N-methylcarbamoyl)adenosine (IB-MECA), respectively. However, the pharmacological characteristics of the receptor were different from those of the cloned Xenopus A1 adenosine receptor and previously proposed adenosine receptors.
- The adenosine-induced GIRK currents were abolished by injection of pertussis toxin and CPA inhibited forskolin-stimulated cyclic AMP accumulation.
- We conclude that an adenosine receptor on the Xenopus oocyte membrane can activate GIRK channels and inhibit adenylyl cyclase via $G_{i/o}$ proteins. Moreover, our results suggest the existence of an endogenous adenosine receptor with the unique pharmacological characteristics. As the receptor was activated by nanomolar concentrations of adenosine, which is a normal constituent of extracellular fluid, the receptor may be involved in some effects through the Gi/o protein signalling pathways in ovarian physiology.

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Abbreviations:

Keywords: Adenosine receptor; G_{i/o} protein; G protein-activated inwardly rectifying K* (GIRK) channel; Xenopus oocyte Ado, adenosine; CHA, N⁶-cyclohexyladenosine; CGS21680, 2-[p-(2-carbonyl-ethyl)-phenylethylamino]-5'-N-ethylcarboxamidoadenosine; CPA, N⁶-cyclopentyladenosine; DMSO, dimethyl sulphoxide; DPCPX, 1,3dipropyl-8-cyclopenylxanthine; E_K , K^+ equilibrium potential; $G\beta\gamma$, G protein $\beta\gamma$ -subunits; $G_{i/o}$, G_i and G_o ; GIRK, G protein-activated inwardly rectifying K^+ channel; GPCR, G protein-coupled receptor; hK, high-potassium; IB-MECA, N^6 -(3-iodobenzyl)-5'-(N-methylcarbamoyl)adenosine; ND98, K^+ -free high-sodium;

NECA, 5'-(N-ethylcarboxaminido)adenosine; n_H, Hill coefficient; PCR, polymerase chain reaction; PTX, pertussis toxin; XA₁, Xenopus A₁ adenosine receptor; XIR, endogenous Xenopus oocyte GIRK-related polypeptides

Introduction

Xenopus ovarian follicles consist of an oocyte surrounded by a vitelline envelope, follicle cells and thecal tissues (Fraser & Djamgoz, 1992). Mature follicular oocytes (stage V and VI) are known to possess receptors for adenosine and ATP as well as for acetylcholine, serotonin, dopamine, prostaglandins and progesterone (Dascal, 1987; Fraser & Djamgoz, 1992). The maturation phenomenon of Xenopus oocytes serves as a useful experimental model for studying its complicated mechanism, and is affected by adenosine (Gelerstein et al.,

1988). Oocytes of Xenopus laevis are also used widely in studies of mammalian neurotransmitter/hormone receptors and ion channels, which can be expressed in the oocyte membrane by microinjection of foreign RNAs. Examining receptor systems and channels in naive oocytes is therefore important in terms of ovarian physiology and for interpreting the functions of foreign receptors and channels when expressed in oocytes.

Adenosine is a normal constituent of intra- and extracellular fluids (Fredholm, 1995). Adenosine is released from cells that are metabolically active or stressed, and modulates the activity of various cells via the adenosine receptors (Collis & Hourani, 1993; Fredholm, 1995). To date, four adenosine receptor subtypes, A1, A2A, A2B and A3, have been identified

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and pharmacologically characterized (Collis & Hourani, 1993; Poulsen & Quinn, 1998; Ralevic & Burnstock, 1998). All of these subtypes belong to the superfamily of G proteincoupled receptors (GPCRs), with the A1 and A3 adenosine receptors interacting with pertussis toxin (PTX)-sensitive G proteins, including G_i and $G_o\ (G_{i/o})$ proteins, and the A_{2A} and A_{2B} adenosine receptors interacting with G_s protein. Also, the A2B and A3 adenosine receptors are coupled to Gq protein. Furthermore, physiological, pharmacological and biochemical studies have suggested the existence of additional adenosine receptors that have not yet been identified. In follicular oocytes of Xenopus laevis, adenosine activated adenylyl cyclase and elicited cyclic AMP-mediated outward K+ currents (Lotan et al., 1982; 1985) but the effects were either abolished or markedly reduced by defolliculation, indicating that the receptors for adenosine are located in the follicle cells (Miledi & Woodward, 1989; Greenfield et al., 1990a,b; King et al., 1996). However, Gelerstein et al. (1988) showed that adenosine elevated cyclic AMP levels in defolliculated oocytes to the same extent as in follicular oocytes, suggesting that an adenosine receptor is also located on the oocyte membrane. In contrast, adenosine at high micromolar concentrations inhibited adenylyl cyclase activity in the defolliculated oocyte membrane fraction (Finidori et al., 1982). In addition, previous studies using a variety of mammalian tissue preparations have suggested the existence of putatively additional subtypes of adenosine receptors (Shinozuka et al., 1988; Daut et al., 1990; Kirsch et al., 1990; Forsyth et al., 1991; Cornfield et al., 1992; Abebe et al., 1994). These findings suggest the possibility that there are additional endogenous adenosine receptors on the oocyte membrane. Although extensive studies using molecular biological techniques have elucidated the functional roles of the adenosine receptor subtypes (Nyce, 1999), the molecular and cellular mechanisms of action of the adenosine receptors in Xenopus oocytes remain poorly understood.

Various GPCRs, such as M₂ muscarinic, α₂ adrenergic, D₂ dopamine, opioid, nociceptin/orphanin FQ receptors and A1 adenosine receptor, functionally couple to G proteinactivated inwardly rectifying K+ (GIRK) channels via interaction with Gi/o proteins (North, 1989; Brown & Birnbaumer, 1990; Ikeda et al., 1995; 1996; 1997; Pfaff & Karschin, 1997). Taken together with inhibition of adenylyl cyclase by adenosine in the oocyte membrane (Finidori et al., 1982), unknown oocyte receptors for adenosine may also be able to activate GIRK channels as a signalling pathway. Hence, we examined the responses of endogenous Xenopus oocyte receptors to adenosine in defolliculated oocytes expressing GIRK channels. Here we demonstrate that an endogenous adenosine receptor on the Xenopus oocyte membrane can activate GIRK channels via Gi/o proteins and inhibit forskolin-stimulated cyclic AMP accumulation and that the receptor shows unique pharmacological characteristics for adenosine receptor ligands.

Methods

Molecular biology

Plasmids containing the entire coding sequences for mouse GIRK1, GIRK2 and GIRK4 channel subunits were obtained

using the polymerase chain reaction (PCR) method as described previously (Kobayashi et al., 1995; 2000). Based on the cDNA sequence for the Xenopus A1 adenosine (XA1) receptor (GenBank/EMBL/DDBJ databases: accession number AJ249842), a pair of oligonucleotide primers corresponding to the regions containing either a translational initiation codon or a stop codon were synthesized. Primers for the XA₁ receptor 5'-GCCCATGGGAATCCCAGCCTCGCTTGCT-3' 5'-GCTCTAGAGGACATTTTTAGAACTCTCAC-3'. The template cDNA was synthesized using mRNA prepared from Xenopus laevis oocytes and surrounding tissues and the 1st-Strand cDNA Synthesis Kit (Clontech) as described previously (Ikeda et al., 2001). PCR was carried out using Pfu DNA polymerase (Stratagene) as described previously (Ikeda et al., 1995). The PCR product was inserted into the plasmid pSP35T to yield the plasmid pSPXA1 and the cDNA insert was sequenced using an automated DNA sequencer model 373S (Applied Biosystems Inc.). The specific mRNAs were synthesized in vitro from the linearized plasmids using the mMESSAGE mMACHINETM In Vitro Transcription Kit (Ambion).

Electrophysiological analyses

Adult female Xenopus laevis frogs were purchased from Copacetic (Soma, Aomori, Japan) and maintained in the laboratory until use. Frogs were anaesthetized by immersion in water including 0.15% tricaine (Sigma Chemical Co.), A small incision was made on the abdomen to remove several ovarian lobes from the frogs that were humanely killed after the final collection. Oocytes (Stage V and VI) were isolated manually from the ovary and maintained in Barth's solution (composition in mm: NaCl 88, KCl 1, Ca(NO₃)₂ 0.33, CaCl₂ 0.41, MgSO₄ 0.82, NaHCO₃ 2.4, Tris-HCl 7.5 (pH 7.4), and 0.1 mg ml⁻¹ gentamicin sulphate; Wako Pure Chemical Industries). Oocytes were injected with either GIRK1 and GIRK2 mRNAs or GIRK1 and GIRK4 mRNAs (~0.6 ng of each mRNA per oocyte) and/or XA1 receptor mRNA (~10 ng per oocyte). The oocytes were incubated at 19°C in Barth's solution, and defolliculated by manual dissection after treatment with 0.8 mg ml-1 collagenase (Wako Pure Chemical Industries) for 1 h (Kobayashi et al., 1998). Wholecell currents of the oocytes were recorded at 18-19°C from 2 to 7 days after injection with a conventional two-electrode voltage clamp (Kobayashi et al., 2000). The membrane potential was held at -70 mV, unless otherwise specified. Microelectrodes were filled with 3M KCl. The oocytes were placed in a 0.05 ml narrow chamber and superfused continuously with a high-potassium (hK) solution (composition in mm: KCl 96, NaCl 2, MgCl₂ 1 and CaCl₂ 1.5) or a K+-free high-sodium (ND98) solution (composition in mm: NaCl 98, MgCl₂ 1 and CaCl₂ 1.5) at a flow rate of 2.5 ml min⁻¹. In the hK solution, the K⁺ equilibrium potential (EK) is close to 0 mV and enables K+ inward current flow through inward-rectifier K+ channels at negative holding potentials. Agonist effect was expressed as a ratio of maximal effect induced by adenosine. Antagonist effect was quantified by dividing amplitude of adenosine-induced current in the presence of an antagonist by amplitude of adenosine-induced current without the antagonist. Data were fitted to a standard logistic equation using SigmaPlot (Jandel Scientific) to compute the EC50, the IC50 and the Hill

coefficient (n_H) in analysis of concentration-response relationships.

Pertussis toxin treatment

For PTX (Sigma Chemical Co.) experiments (Kobayashi et al., 1999), ~ 1.38 ng of PTX (0.1 $\mu g \mu l^{-1}$ in distilled water) per oocyte was injected 7 h before recording using a Nanoliter injector (World Precision Instruments). Oocytes of the control group were prepared from the same donor and sham injected with the same volume of distilled water.

Cyclic AMP assay

Cyclic AMP levels in *Xenopus* oocytes were determined using the BiotrakTM cAMP enzymeimmunoassay system (Amersham Pharmacia Biotech). Groups of 25 defolliculated oocytes carefully selected from the same donor on the basis of morphological similarity were incubated at room temperature for 30 min in Barth's solution containing N⁶-cyclopenty-ladenosine (CPA) or forskolin (Wako Pure Chemical Industries). The incubation solution was replaced with a lysis reagent buffer containing 0.25% dodecyltrimethylammonium bromide in the kit, homogenized and centrifuged at $10,000 \times g$ for 10 min at 4°C. The measurements of cyclic AMP contents in the diluted supernatants were conducted according to the manufacture's procedure.

Statistical analysis of results

The values obtained are expressed as mean \pm s.e.mean, and n is the number of oocytes tested. Statistical analysis of differences between groups was carried out using Student's t-test. A probability of 0.05 was taken as the level of statistical significance.

Compounds

All the compounds used were purchased from Research Biochemicals International. N⁶-(3-iodobenzyl)-5'-(N-methyl-carbamoyl)adenosine (IB-MECA) and 1,3-dipropyl-8-cyclopenylxanthine (DPCPX) were dissolved in dimethyl sulphoxide (DMSO). Other compounds were dissolved in distilled water. The stock solutions of all compounds were stored at -20°C until use. Each compound was added to the perfusion solution in appropriate amounts immediately before the experiments.

Results

Activation of GIRK channels by an endogenous adenosine receptor in Xenopus oocytes

Using the *Xenopus* oocyte system expressing GIRK channels (Kobayashi *et al.*, 1999), we investigated whether endogenous adenosine receptors in defolliculated oocytes activate GIRK channels. In oocytes injected with mRNAs for GIRK 1 and GIRK2 subunits, application of adenosine reversibly induced inward currents in a concentration-dependent manner in hK perfusion solution containing 96 mM K^+ and 2 mM Na^+ (Figure 1a, b). The EC₅₀ and n_H values obtained from the

concentration-response relationships were 917.3 ± 69.4 nM and 0.88 ± 0.02 (n = 10), respectively (Figure 1b and Table 1). The current responses to 3 µM adenosine were attenuated by caffeine, a non-selective adenosine receptor antagonist of methylxanthines, with the IC₅₀ value of 245.5 \pm 18.5 μ M and n_H value of 0.72 \pm 0.04 (n=8) (Figures 1a and 2d). Although micromolar concentrations of ATP also induced inward currents, which were sensitive to caffeine, ATP was much less potent than adenosine (Figure 1b). These results suggest the existence of an endogenous receptor for adenosine in defolliculated oocytes. Moreover, the current responses to adenosine were completely abolished in the presence of 3 mm Ba²⁺, a GIRK channel blocker (Dascal et al., 1993), (n=8,Figure 1a) which also blocked basally active GIRK currents (IC₅₀ value of 170.7 \pm 12.2 μ M, n = 6; Kobayashi et al., 2000). In contrast, in uninjected oocytes from the same donor, no significant current response was observed by application of 10 μ M adenosine, 10 μ M ATP or 3 mM Ba²⁺ (1.9+0.7 nA, n=6; 0.9 ± 0.6 nA, n=6; 5.0 ± 1.3 nA, n=10, respectively; Figure 1a). These results suggest that the adenosine-induced currents are mediated by GIRK channels. In addition, responses to adenosine were not observed in ND98 solution containing 98 mm Na+ and no K+ instead of the hK solution (n=8); data not shown), suggesting that the currents show K^+ selectivity. The current-voltage relationship of the response to 3 μ M adenosine showed strong inward rectification (Figure Ic), typical of a current response mediated by GIRK channels. In addition, similar results were obtained in oocytes injected with mRNAs for GIRK 1 and GIRK4 subunits (data not shown). These results suggest that an endogenous adenosine receptor can functionally couple to GIRK channels.

In the present study, although basally active GIRK currents sensitive to Ba2+ were observed in all oocyte batches injected with GIRK mRNAs, the successful responses to adenosine were observed in oocyte batches prepared from 14 of 56 donors (25.0%). The GIRK currents induced by 3 μ M adenosine were variable among oocytes prepared from the same donor, and amplitudes of responses to adenosine were not significantly correlated with amplitudes of the 3 mm Ba²⁺-sensitive current components (Figure 1d). Also, similar results were obtained in other oocyte batches from different donors (data not shown). In contrast, the unsuccessful responses to adenosine in oocytes prepared from most donors showed little or no inward current $(11.9 \pm 1.3 \text{ nA})$ at 3 μ M, n=304), although amplitudes of the Ba²⁺-sensitive current components, which are related to expression levels of GIRK channels (Kobayashi et al., 2000), were large enough in the same oocytes (821.5 \pm 58.7 nA, n=304). Taken together, these results indicate that the expression level of an endogenous receptor for adenosine in defolliculated oocytes may be dependent on the oocyte batch from donors and may be variable from cell to cell among oocyte batches.

Pharmacological characteristics of a Xenopus oocyte adenosine receptor

To investigate the pharmacological characteristics of the *Xenopus* oocyte adenosine receptor found in the present study, we examined the effects of various adenosine receptor ligands in oocytes expressing GIRK channels. Two selective A₁ adenosine receptor agonists, CPA and N⁶-cyclohexyladenosine (CHA), and a non-selective adenosine receptor agonist, 5'-(N-ethylcar-

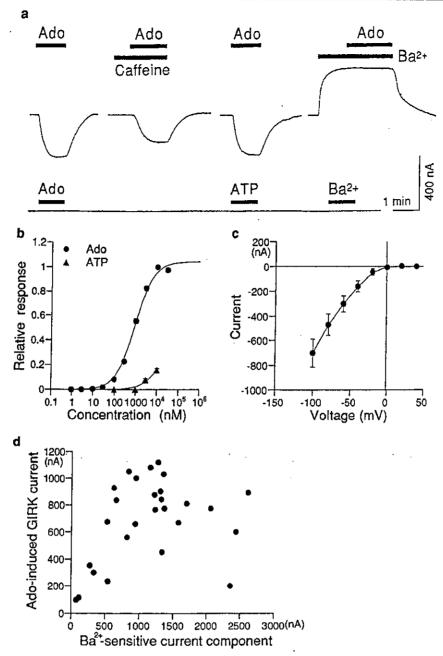


Figure 1 Effects of adenosine in *Xenopus* oocytes expressing GIRK channels. (a) Upper row, in a defolliculated oocyte injected with GIRK1 mRNA and GIRK2 mRNA, current responses to adenosine (Ado), Ado in the presence of $100 \, \mu\text{M}$ caffeine, Ado and Ado in the presence of $3 \, \text{mm}$ Ba²⁺ are shown. The concentration of Ado used was $3 \, \mu\text{M}$. Lower row, in an uninjected oocyte, current responses to $10 \, \mu\text{M}$ Ado, $10 \, \mu\text{M}$ ATP and $3 \, \text{mm}$ Ba²⁺ are shown. Current responses were measured at a membrane potential of $-70 \, \text{mV}$ in a high-potassium solution containing $96 \, \text{mm}$ K⁺. Bars show the duration of application. (b) Concentration-response relationships for GIRK channel activation induced by Ado or ATP. Effects of these drugs were normalized to the magnitudes of $10 \, \mu\text{M}$ Ado-induced GIRK currents, which were $556.4 \pm 64.0 \, \text{nA}$ (n = 20). Each point and error bar represents the mean and s.e.mean of the relative responses obtained from $10 \, \text{oocytes}$. Data points were fitted using a logistic equation. (c) Current-voltage relationship of $3 \, \mu\text{M}$ Ado-induced GIRK currents in oocytes expressing GIRK1/2 channels (n = 8). (d) Correlation between the amplitudes of current response to $3 \, \mu\text{M}$ Ado and of the $3 \, \text{mm}$ Ba²⁺-sensitive current component in oocytes prepared from the same donor. The correlation coefficient was $0.317 \, (P > 0.1, n = 27;$ correlation analysis).

boxaminido)adenosine (NECA), concentration-dependently induced inward current responses at nanomolar concentrations (Figure 2a,c and Table 1), whereas at the highest concentration used they induced no current response in uninjected oocytes (n=5); data not shown). The rank order of potency for these adenosine receptor agonists was CHA \geq CPA>NECA>ade-

nosine, whereas the rank order of efficacy for these agonists was NECA > adenosine > CPA > CHA (Figure 2c and Table 1). The n_H values for the these adenosine receptor agonists were not significantly different from 1 (Student's *t*-test, P > 0.05), suggesting a single site of action for each of the agonists. Furthermore, the current responses to 3 μ M adenosine were

Table 1 Comparison of pharmacological characteristics of an endogenous Xenopus oocyte adenosine receptor and the cloned XA₁ receptor

	Xenopus oocyte adenosine receptor				XA ₁ receptor			
Compound	EC_{50}	Max. efficacy	n_H	(n)	EC_{50}	Max. efficacy	n_H	(n)
Adenosine CPA CHA NECA CGS21680 IB-MECA	917.3±69.4 96.7±10.1 86.7±28.3 398.6±117.9 N.D. N.D.	1 0.81±0.03 0.65±0.02 1.70±0.20* N.D. N.D.	0.88 ± 0.02 0.91 ± 0.03 0.89 ± 0.04 0.95 ± 0.05 N.D. N.D.	(10) (6) (9) (5) (5) (4)	2.91 ± 0.54 5.72 ± 0.87 3.60 ± 0.89 0.56 ± 0.05 205.6 ± 20.3 135.2 ± 12.8	$ \begin{array}{c} 1\\ 1.03 \pm 0.01\\ 1.11 \pm 0.04\\ 0.96 \pm 0.02\\ 0.87 \pm 0.03\\ 0.96 + 0.04 \end{array} $	0.83 ± 0.11 0.99 ± 0.03 0.96 ± 0.07 0.92 ± 0.04 0.90 ± 0.04 $0.97 + 0.02$	(5) (6) (5) (5) (5)

The EC₅₀ values are shown as mean \pm s.e.mean in nm. The values of maximal efficacy (Max. efficacy) were normalized to magnitude of GIRK currents induced by adenosine at 10 μ m in an endogenous *Xenopus* oocyte adenosine receptor and at 1 μ m in the XA₁ receptor. The n_H values indicate the mean \pm s.e.mean of the Hill coefficients. The numbers of oocytes tested are indicated in parentheses. N.D. means that these values were not determined because these compounds induced only small GIRK responses at micromolar concentrations. *The high efficacy raises the possibilities that NECA, a non-selective adenosine receptor agonist, may cause a distinct conformational change of the endogenous adenosine receptor and that there may be additional types of oocyte adenosine receptors which are activated not by A₁ adenosine receptor agonists but by NECA.

almost completely abolished by 1 μ M DPCPX, a selective A₁ adenosine receptor antagonist, with an IC₅₀ value of 18.0 ± 2.6 nM and a n_H value of 0.96 ± 0.07 (n = 4, Figure 2a,d). However, a selective A_{2A} adenosine receptor agonist, 2-[p-(2-carbonyl-ethyl)-phenylethylamino]-5'-N-ethylcarboxamidoadenosine (CGS21680), and a selective A₃ adenosine receptor agonist, IB-MECA, produced only small current responses as compared with the responses to 10 μ M adenosine (0% at 100 nM, 7.9 ± 0.8% at 1 μ M and 9.9 ± 5.3% at 30 μ M for CGS21680, n = 5; 0% at 100 nM, 1.7 ± 1.7% at 300 nM and 5.7 ± 2.9% at 1 μ M for IB-MECA, n = 4, respectively). In addition, DMSO, the solvent vehicle, at the highest concentration (0.1%) used had no effect in this study.

As the present results indicated that characteristics of the adenosine receptor found here resembled those of the A1 adenosine receptor, we next compared the receptor found with the XA1 receptor identified in Xenopus laevis by Nebreda (GenBank/EMBL/DDBJ databases: accession AJ249842). For functional characterization of the cloned XA_I receptor, we first carried out molecular cloning of the cDNA from oocytes of Xenopus laevis and surrounding tissues by reverse transcription-PCR. The specific PCR product was detected by agarose gel electrophoresis and cloned as described previously (Ikeda et al., 1995). The deduced amino acid sequence of the cDNA for the XA1 receptor was identical with the reported sequence. The XA, receptor shares 72% and 72.5% amino acid sequence identity with the rat and human A1 adenosine receptors, respectively, whereas the overall amino acid sequence identity for the A1 adenosine receptor between the mammalian species is approximately 95%. To investigate functional coupling of the XA1 receptor to GIRK channels and pharmacological characteristics of the receptor, we used oocytes co-injected with mRNAs for the XA, receptor and GIRK channels, when $3 \mu M$ adenosine induced no significant current response in oocytes from the same donor injected with GIRK mRNAs (75.0% of donors). Application of adenosine, CPA or CHA, at low nanomolar concentrations, induced significant inward currents with similarly high potency and similar efficacy (Figure 2b,c and Table 1). However, CGS21680 and IB-MECA induced current responses at relatively high nanomolar concentrations (Table 1). The responses to adenosine were attenuated in the presence of caffeine (IC₅₀ value of 327.1 \pm 34.4 μ M and n_H value of 0.89 ± 0.10 , n=4) and DPCPX (IC₅₀ value of 56.4 ± 5.2 nM

and n_H value of 0.85 ± 0.08 , n=4) (Figure 2d). In oocytes injected with XA1 receptor mRNA alone, 3 µM adenosine induced no significant current response (3.4 \pm 0.7 nA, n=8). These results indicate that the XA1 receptor also couples to GIRK channels and the pharmacological properties of the XA₁ receptor are typical of the A₁ adenosine receptor, although the amino acid sequences for the XA1 receptor and the mammalian A₁ adenosine receptors exhibit relatively low identity. In addition, the XA1 receptor was fully activated by low nanomolar concentrations of adenosine, whereas such low concentrations of adenosine induced little or no response in all the oocyte batches injected with GIRK mRNAs (Figure 2c), suggesting that the XA, receptor may be located exclusively in follicle cells and outer surrounding tissues or only sparsely in the oocyte membrane. Further studies by in situ hybridization analysis and immunohistochemical analysis may identify the location of the XA1 receptor. As shown in Figure 2c and Table 1, the potency and efficacy of adenosine, NECA and A1 adenosine receptor agonists for the adenosine receptor found here are distinct from those of the XA1 receptor. Moreover, the adenosine receptor found here was insensitive to micromolar concentrations of CGS21680 and IB-MECA, whereas the XA₁ receptor was sensitive to moderate nanomolar concentrations of these agonists. While the antagonist effects of caffeine and DPCPX, adenosine receptor antagonists tested, on the adenosine receptor found here and the XA1 receptor were similar (Figure 2d). In addition, the characteristics of the XA₁ receptor were observed similarly even in the oocytes which showed similar magnitudes of GIRK current responses via the XA1 receptor as compared with magnitudes of the responses via the endogenous adenosine receptor found here, suggesting that the differences in pharmacological characteristics between the endogenous adenosine receptor and the XA1 receptor were not caused by differences in receptor density expressing in oocytes. The present results suggest that the endogenous adenosine receptor found in defolliculated oocytes is different from the XA₁ and A₃ adenosine receptors.

Signal transduction mechanisms of a Xenopus oocyte adenosine receptor

Activation of various GPCRs opens GIRK channels via direct action of G protein $\beta\gamma$ -subunits (G $\beta\gamma$) released from

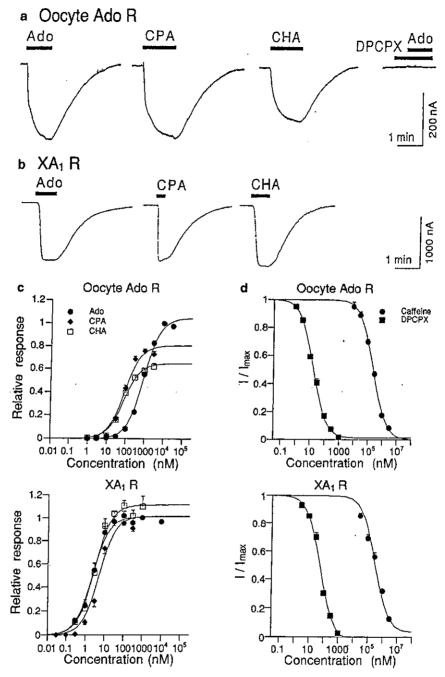


Figure 2 Effects of adenosine receptor ligands on an endogenous *Xenopus* oocyte adenosine receptor (Oocyte Ado R) and the cloned *Xenopus* adenosine A_1 receptor (XA₁ R). (a) In a defolliculated oocyte injected with GIRK1 and GIRK2 mRNAs, current responses to 3 μ M Ado, 1 μ M CPA, 1 μ M CHA and 3 μ M Ado in the presence of 1 μ M DPCPX are shown. (b) In a defolliculated oocyte injected with mRNAs for the XA₁ receptor and GIRK1/2 channels, current responses to 100 nM Ado, 100 nM CPA and 100 nM CHA are shown. Bars show the duration of application. (c) Concentration-response relationships for adenosine receptor agonists on Oocyte Ado R (top) and XA₁ R (bottom). The magnitudes of GIRK currents induced by adenosine receptor agonists were normalized to the magnitudes of 10 μ M Ado-induced currents, which were 355.9 \pm 36.7 nA (n = 25), in oocytes injected with GIRK1 and GIRK2 mRNAs and to the magnitudes of 1 μ M Ado-induced currents, which were 574.8 \pm 122.2 nA (n = 16), in oocytes co-injected with mRNAs for the XA₁ receptor and GIRK1/2 channels, respectively. (d) Concentration-dependent inhibition of adenosine-induced currents by adenosine receptor antagonists on Oocyte Ado R (top) and XA₁ R (bottom). I_{max} is the amplitude of GIRK currents induced by Ado at 3 μ M in Oocyte Ado R (563.1 \pm 91.2 nA, n = 12) and at 10 nM in XA₁ R (325.7 \pm 77.7 nA, n = 8), and I is the current amplitude in the presence of an adenosine receptor antagonist. Current responses were measured at a membrane potential of -70 mV in a high-potassium solution containing 96 mM K⁺. Each point and error bar represents the mean and s.e.mean of the relative responses obtained from 4-10 oocytes. Data points were fitted using a logistic equation.

G_{i/o} proteins, which are sensitive to PTX (Brown & Birnbaumer, 1990; Reuveny et al., 1994). To investigate the involvement of G protein-coupled mechanisms in activation of GIRK channels by the endogenous adenosine receptor found here, the responses to adenosine in oocytes expressing GIRK 1/2 channels were compared with and without PTX injection. The current responses to adenosine were almost completely abolished by injection of PTX (Figure 3a). The current responses to adenosine in the PTX-injected oocytes were significantly different from those in the sham-injected oocytes (Figure 3a). These results indicate that the endogenous adenosine receptor opens GIRK channels via activation of G_{i/o} proteins and is present on the oocyte membrane.

We next examined whether the receptor regulates intracellular cyclic AMP levels. In the defolliculated oocyte groups which showed the successful current responses to 3 um adenosine in oocytes expressed with GIRK channels, CPA significantly reduced cyclic AMP accumulation stimulated by forskolin, which produced a modest increase in the cyclic AMP content by 32% (Student's t-test, P < 0.01) in comparison with that of the untreated oocyte group (Figure 3b). Whereas CPA alone had no significant effect on cyclic AMP levels (Figure 3b). In contrast, the defolliculated oocyte groups which showed the unsuccessful current responses to adenosine in oocytes expressed with GIRK channels resulted in no significant change in cyclic AMP levels in any oocyte groups by addition of CPA (data not shown, five donors). The results suggest that the endogenous adenosine receptor inhibits adenylyl cyclase.

Discussion

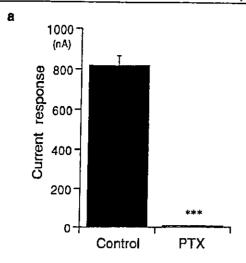
In the present study we demonstrated that an endogenous Xenopus oocyte adenosine receptor on the oocyte membrane can activate GIRK channels expressed in oocytes via interaction with PTX-sensitive G proteins. Furthermore, the receptor inhibited forskolin-stimulated cyclic AMP accumulation. These results suggest the existence of a $G_{i/o}$ protein-coupled adenosine receptor in the oocyte.

Among the cloned adenosine receptor subtypes, the A1 and A_3 adenosine receptors interact with $G_{i/o}$ proteins (Ralevic & Burnstock, 1998). We demonstrated that the adenosine receptor found here was sensitive to two A1 adenosine receptor agonists with EC50 values of moderate nanomolar concentrations, whereas the receptor was insensitive to A2A and A₃ adenosine receptor agonists tested (Figure 2c and Table 1). These results suggested that the receptor resembled an A₁ adenosine receptor. However, when compared with the cloned XA1 receptor (Figure 2 and Table 1), the pharmacological characteristics of the adenosine receptor found here were distinct from those of the XA1 receptor. Also, in the Xenopus oocyte system co-expressing the cloned rat A1 adenosine receptor and GIRK channels, the receptor was fully activated by CPA and CGS21680 with EC_{50} values of 7 nm and 2.6 μm, respectively (Pfaff & Karschin, 1997). Therefore, our results suggest that the adenosine receptor found in this study is different from the four subtypes of cloned adenosine receptors reported to date.

In addition to the cloned adenosine receptors, physiological, pharmacological and biochemical studies have suggested

the existence of additional adenosine receptors in the Xenopus oocyte and in several tissues in mammals. In Xenopus follicular oocytes (Lotan et al., 1982; 1985; Miledi & Woodward, 1989; Greenfield et al., 1990a, b) or defoliculated oocytes (Gelerstein et al., 1988), adenosine elevates cyclic AMP levels, and elicits cyclic AMP-mediated outward K+ currents with an EC₅₀ value of approximately 3 μ M, indicating that the receptors for adenosine stimulate adenylyl cyclase via Gs proteins and resemble A2 adenosine receptors. In addition, King et al. (1996) demonstrated that adenosine and ATP produced similar outward K+ currents in follicular oocytes with distinct pharmacological characteristics. The characteristics exhibited that adenosine and ATP were equipotent with EC₅₀ values of 1.9 and 1.7 μ M, respectively, whereas ATP and CGS21680 were 0.5 and 0.7 times as efficient as adenosine, respectively. However, we demonstrated that the adenosine receptor in defolliculated oocytes was coupled to $G_{i/o}$ proteins and inhibited folkkolin-stimulated cyclic AMP accumulation and that the receptor was activated by adenosine with an EC50 value of 917.3 nm but insensitive to ATP and CGS21680 at micromolar concentrations (Figures 1b, 2c and 3 and Table 1). Finidori et al. (1982) showed that adenosine inhibited adenylyl cyclase activity in the defolliculated oocyte membrane fraction, suggesting that the effect may be mediated by interaction with Gi/o proteins. However, only high micromolar concentrations of adenosine had such effect. Therefore, our results suggest that the Xenopus adenosine receptor found here is different from the Xenopus adenosine receptors described previously.

In the rat brain membrane, [3H]-CV 1808 binding study under anomalously low temperature suggested the existence of a novel high affinity component that could only partially be displaced by classical adenosine receptor ligands including CPA and a low affinity component with A1-like adenosine receptor characteristics (Cornfield et al., 1992). Also, [3H]-CV 1808 binding was not affected by 1 μM adenosine or GTP, and the IC50 values for NECA and DPCPX were greater than 10 μ M. Later, Luthin & Linden (1995) demonstrated that receptors on membranes prepared from both rat brain and COS cells transfected with rat A2A adenosine receptor took on either the unique binding characteristics of [3H]-CV 1808 or the characteristics of A_{2A} adenosine receptor, depending on temperature of the binding assay and the nature of the radioligand. We demonstrated that the receptor found here was sensitive to adenosine, NECA and DPCPX at nanomolar concentrations, and also coupled to Gi/o proteins, indicating that the characteristics of the receptor found here are distinct from those of [3H]-CV 1808 binding sites. Like the receptor found here, studies on the inhibitory effect on noradrenaline release in sympathetic nerves of the rat caudal artery (Shinozuka et al., 1988) and rat vas deferens (Forsyth et al., 1991) and in the rabbit brain cortex (von Kügelgen et al., 1992) suggested the existence of putatively novel receptors activated by adenosine and ATP, and antagonized by xanthine derivatives. In the sympathetic nerves, adenosine and ATP were equipotent with EC50 values of approximately 10 μ M, whereas in the brain, adenosine was more potent than ATP but both drugs were equally effective at 3 μ M. In this study, adenosine was more potent than ATP and adenosine at 3 μ M was much more efficacious than ATP, suggesting that the receptor found here is distinct from these receptors. In



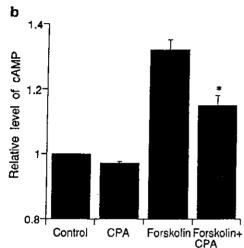


Figure 3 Interaction of an endogenous Xenopus oocyte adenosine receptor with $G_{i/o}$ proteins. (a) Effects of pertussis toxin (PTX) on adenosine-induced GIRK currents in oocytes expressing GIRK channels. The relationship of current responses to 3 µM adenosine (Ado) between the PTX-untreated group (817.9 \pm 48.0 nA; n=14; black bar) and PTX-treated group (8.46 \pm 2.65 nA; n= 22; open bar). Current responses were measured at a membrane potential of -70 mV in a high-potassium solution containing 96 mm K⁺. (b) Effects of CPA on forskolin-stimulated cyclic AMP accumulation in oocytes. Groups of 25 oocytes were exposed to either 1 μM CPA or 30 µM forskolin, or both drugs for 30 min. The results were obtained from four separate experiments. The basal cyclic AMP level in control group of untreated oocytes was 2389 ± 54 fmol oocyte⁻¹. The ratios of cyclic AMP levels in the oocyte groups treated with CPA, forskolin or forskolin and CPA to the control group were 0.97 ± 0.01 , 1.32 ± 0.03 and 1.15 ± 0.03, respectively. There was significant difference in cyclic AMP contents between the group treated with forskolin and the group treated with forskolin and CPA. Statistical analysis of differences between groups was carried out using Student's t-test. Asterisks indicate significant differences between groups (*P < 0.05; ***P < 0.001).

addition, a study on relaxation of smooth muscle in the porcine coronary artery suggested the existence of another type of adenosine receptor (Abebe et al., 1994). However, the receptor was insensitive to xanthines and the receptor-mediated vasorelaxation was independent of the effects mediated by CPA and CHA. Therefore, we propose the existence of an endogenous Xenopus oocyte adenosine receptor with unique pharmacological characteristics distinct

from those of known subtypes of adenosine receptors and other proposed adenosine receptors. The receptor may be considered an A₁-like adenosine receptor, although the nomenclature of the newly proposed receptors including the adenosine receptor found in this study remains tentative until identification of the adenosine receptors with the unique pharmacological characteristics.

The coronary vasodilatation mediated by 1 μ M adenosine was attenuated by antidiabetic sulfonylureas (Daut et al., 1990) and 10 μ M adenosine or 100 nM CHA activated the ATP-sensitive K⁺ channels, which are blocked by sulfonylureas, via $G_{i}\alpha$ proteins in rat ventricular myocytes (Kirsch et al., 1990), but the pharmacological characteristics of adenosine receptor agonists were not reported in these studies. The results suggested that an adenosine receptor sensitive to an A_1 adenosine receptor agonist couples to the ATP-sensitive K⁺ channels via G_i proteins. Further studies using cDNA clones for ATP-sensitive K⁺ channels (Ho et al., 1993; Inagaki et al., 1995a,b) may clarify whether the adenosine receptor found here can activate the K⁺ channels.

Endogenous Xenopus oocyte GIRK-related polypeptides (XIR) are also located on the oocyte membrane, although levels of XIR expression are low and variable among oocyte batches from different donors (Duprat et al., 1995; Hedin et al., 1996). As adenosine induced no significant current response in any of the naive defolliculated oocytes tested, the Xenopus adenosine receptor found here may hardly have XIR effect. However, the endogenous receptor was activated by adenosine at nanomolar concentrations, which are estimated to be in the physiological range of extracellular fluid (Fredholm, 1995). Therefore, other intracellular signal pathways via Gijo proteins may be involved in some effects in oocyte physiology.

Gelerstein et al. (1988) demonstrated in experiments using follicular oocytes and oocytes defolliculated by collagenase treatment and shaking periodically that 10 µM adenosine induced maturation, which was assessed by germinal vesicle breakdown, in stage VI oocytes and accelerated maturation of stage V and VI oocytes induced by approximately 3 μM progesterone. Also, adenosine increased cyclic AMP in defolliculated oocytes to the same extent as in follicular oocytes, suggesting interaction of an adenosine receptor located on the oocyte membrane with G_s proteins. In contrast, cyclic AMP is produced in follicle cells in response to NECA but no cyclic AMP accumulation can be detected in oocytes stripped by manual dissection after hypertonic treatment of collagenase-treated follicles, indicating that the receptor for adenosine appears to be located exclusively on follicle cells (Greenfield et al., 1990b). Despite localization of the endogenous G_s protein-coupled adenosine receptor, signal transduction by a Gi/o protein-coupled adenosine receptor found here as well as that by the Gs protein-coupled adenosine receptor may have some effects on numerous biochemical events in oocyte maturation. Recently, Lutz et al. (2000) demonstrated that Xenopus oocyte maturation induced by 50 nm progesterone was inhibited by $G\beta_1\gamma_2$, which can directly activate GIRK channels (Reuveny et al., 1994). Activation of GIRK channels by the adenosine receptor found in this study may be mediated by action of $G\beta\gamma$ released from Xenopus Gi/o proteins. The existence of the receptor may affect the signal transduction pathway induced by progesterone. Identification of the adenosine receptor

found here by molecular biological and genetic approaches may facilitate clarification of the functions and expression mechanisms of the receptor in *Xenopus* oocyte maturation.

In conclusion, we demonstrate that an endogenous Xenopus adenosine receptor on the oocyte membrane couples to GIRK channels and adenylyl cyclase via interaction with $G_{i/o}$ proteins. Moreover, the unique pharmacological characteristics of the receptor may suggest the existence of a putatively novel adenosine receptor. As the receptor was activated by nanomolar concentrations of adenosine, which is a normal constituent of extracellular fluid, $G_{i/o}$ protein

signaling pathways via the adenosine receptor may have some effects in ovarian physiology.

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Degeneration of pontine mossy fibres during cerebellar development in weaver mutant mice

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Keywords: cerebellum, GIRK2, lobule formation, pontine nuclei

Abstract

In weaver mutant mice, substitution of an amino acid residue in the pore region of GIRK2, a subtype of the G-protein-coupled inwardly rectifying K⁺ channel, changes the properties of the homomeric channel to produce a lethal depolarized state in cerebellar granule cells and dopaminergic neurons in substantia nigra. Degeneration of these types of neurons causes strong ataxia and Parkinsonian phenomena in the mutant mice, respectively. On the other hand, the mutant gene is also expressed in various other brain regions, in which the mutant may have effects on neuronal survival. Among these regions, we focused on the pontine nuclei, the origin of the pontocerebellar mossy fibres, projecting mainly into the central region of the cerebellar cortex. The results of histological analysis showed that by P9 the number of neurons in the nuclei was reduced in the mutant to about one half and by P18 to one third of those in the wild type, whereas until P7 the number were about the same in wild-type and weaver mutant mice. Three-dimensional reconstruction of the nuclei showed a marked reduction in volume and shape of the mutant nuclei, correlating well with the decrease in neuronal number. In addition, Dil (a lipophilic tracer dye) tracing experiments revealed retraction of pontocerebellar mossy fibres from the cerebellar cortex after P5. From these results, we conclude that projecting neurons in the pontine nuclei, as well as cerebellar granule cells and dopaminergic neurons in substantia nigra, strongly degenerate in weaver mutant mice, resulting in elimination of pontocerebellar mossy fibres during cerebellar development.

Introduction

Among the ataxic mutant mice, the weaver mutant has been studied extensively (Herrup, 1996; Hess, 1996). The causal mutation was mapped in GIRK2 gene encoding an inwardly rectifying K+ channel subunit (Patil et al., 1995). Homomeric mutant channels lose their selectivity for K+ ions and regulation by G-proteins, while heteromeric channels with GIRK1 keep their original properties in their ion selectivity and activity regulation (Kofuji et al., 1996; Navarro et al., 1996; Slesinger et al., 1996; Hou et al., 1999). The mutation produces neuronal degeneration in the cerebellum and substantia nigra which, respectively, result in a strong ataxia and Parkinsonian-type deficiencies. Strong expression of the mutant gene induces neuronal cell death in 80-90% of the cerebellar granule cells during their postmitotic and premigratory stages, leading to a severe reduction in the size of the entire cerebellar cortex. In addition, along the rostrocaudal axis, clear transverse boundaries of the strong degeneration have been observed at the rostral face of lobule VI and the caudal side of lobule IX (Herrup & Kuemerle, 1997; Eisenman et al., 1998; Eisenman, 2000). Between these boundaries, the central region (lobules VI to IX) shows immature morphologies, i.e. smaller size and incomplete formation of sublobular structures.

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Cerebellar cortex is roughly separated to three regions, according to the origins of their major afferent mossy fibres (Voogd, 1995; Altman & Bayer, 1997). The anterobasal and anterodorsal lobes mainly receive afferents from the spinal cord, while the central and posterior lobes mainly receive the fibres from the pontine nuclei. The inferior lobe is a main recipient region of mossy fibres originating from the vestibular nuclei. Concerning the relationship between precerebellar systems and cerebellar cortex in weaver mutant mice, the mossy fibre systems and their origins have already been examined (Arsenio Nunes et al., 1988; Baurle & Guldin, 1998). From the results of WGA-HRP (wheat germ agglutinin-horseradish peroxidase conjugate) tracing experiments, almost normal topographic organization of the spinocerebellar projection was found in the mutant mice (Arsenio Nunes et al., 1988). In the vestibular nuclei, there were no significant changes in the number or morphology of neurons in weaver mutant compared to wild-type mice (Baurle & Guldin, 1998). On the other hand, no detailed analysis has been made of the mossy fibre afferents into the central region (the central and posterior lobes) and their origin, the pontine nuclei.

By in situ hybridization analysis, it has been shown that the GIRK2 gene is strongly expressed in pontine nuclei during all developmental stages of the cerebellum, starting at late embryonic days (E16–18) through to adult, while the expression of GIRK1 or GIRK3 is weak or starts later during development (Kobayashi et al., 1995; Chen et al., 1997; Wei et al., 1997). This expression pattern of GIRKs suggests

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the formation of homomeric GIRK2 channels in pontine nuclei during development. Considering this together with the relatively severe degeneration of the central region in the cortex, the main receptive field of the pontocerebellar projections, we examined structural features of pontine nuclei and their projections in weaver mutants.

Materials and methods

Mouse strains

For establishment of the C3H weaver mice used in the present experiments, original weaver mutant mice obtained from Jackson Laboratory (ME, USA) were mated with inbred C3H Heston N mice

(SLC, Japan) and backcrossed over three times (Kobayashi et al., 1999).

In situ hybridization of the whole brain and pontine nucleus

The probe for GIRK2 mRNA was oligo GIRK2A, as described in the previous report (Kobayashi et al., 1995). The probe was complementary to a 5' end part of the mRNA, which contained a unique sequence of the GIRK2 gene. The probe was 3' end labelled with [35S]-dATP (Amersham Pharmacia Biotech UK Inc., UK) using a terminal deoxyribonucleotidyl transferase kit (Takara Shuzo Inc., Japan). Tissue specimens were obtained from C3H/HeSlc mice and weaver mice at P7 and adult (2 months old) under deep diethyl-ether anaesthesia. Parasagittal and coronal sections of the specimens (15 µm in thickness) were prepared, prehybridized for 3 h at 42 °C in a prehybridization solution, and hybridized for 16 h at 42 °C. The

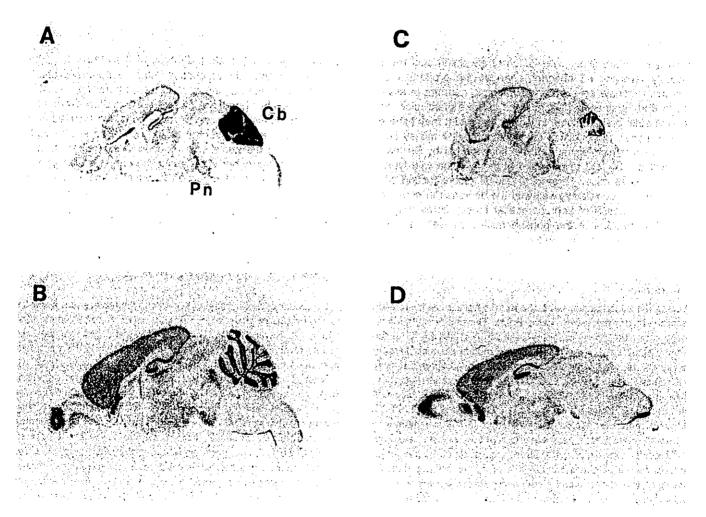
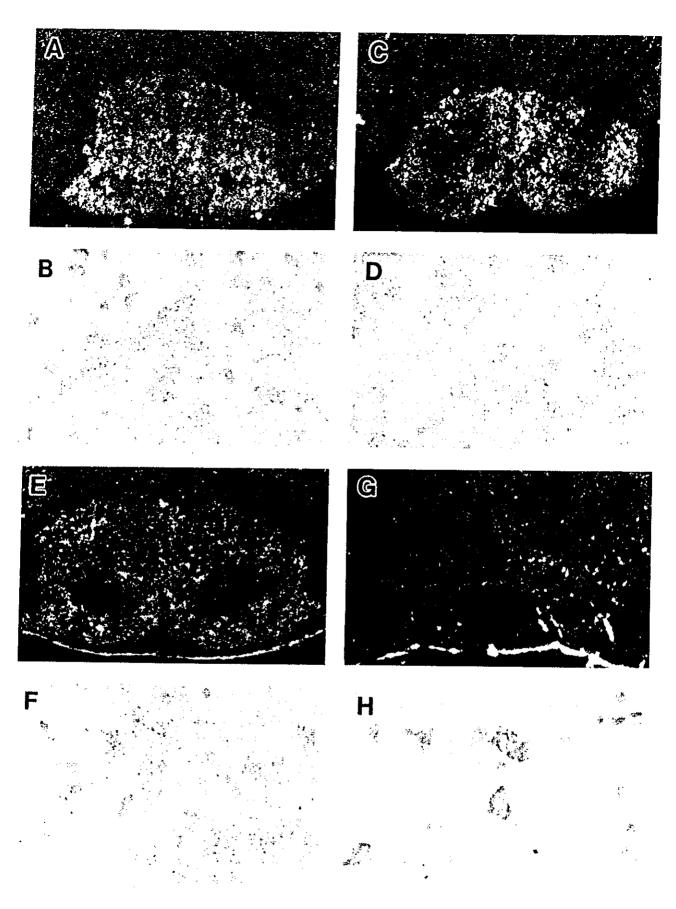


Fig. 1. Expression of GIRK2 mRNAs in P7 and adult mouse brains. Images were obtained after in situ hybridization of P7 and adult (2 months old) brain parasagittal sections of C3H wild-type and weaver mutant mice with probes specific for GIRK2 mRNA. (A) Wild type, P7. (B) Wild type, adult. (C) Weaver, P7. (D) Weaver, adult. The expression pattern of GIRK2 mRNA in the cerebellum and pontine nuclei of weaver mouse obviously differed from that of wild-type control. Cb, cerebellum; Pn, pontine nuclei.

Fig. 2. Distribution of GIRK2 mRNA in the pontine nuclei. Coronal sections were obtained from both wild-type and weaver mutant mice. Expression patterns of GIRK2 mRNA in the pontine nuclei were detected by in situ hybridization. (A and B) Wild type, P7. (C and D) Weaver, P7. (E and F) Wild type, adult. (G and H) Weaver, adult. A, C, E and G show dark-field micrographs and B, D, F and H show bright-field micrographs. After hybridization with labelled probes, tissue sections were autoradiographed using NTB2 nuclear track emulsion. Hybridized sections were counterstained with pyronin-methylgreen. Distinct signals of GIRK2 mRNA were observed in large neurons.

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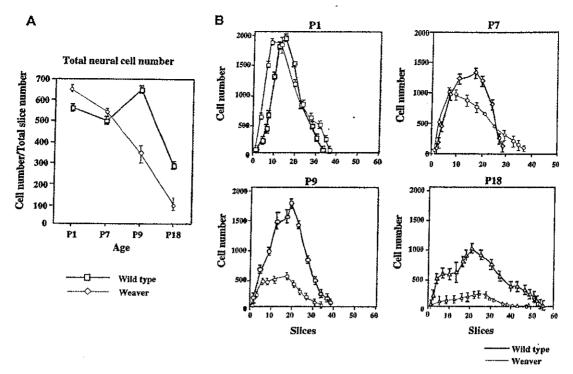


Fig. 3. Changes in the numbers of neurons in the pontine nuclei during development. The numbers of neurons were counted in 20-µm-thick serial sections of C3H wild-type and weaver mutant mouse brains during development (P1, P7, P9 and P18). Slices are numbered from rostral to caudal ends.

tissue sections were washed three times in $0.1 \times SSC/0.1\%$ Sarcosyl at 42 °C for 40 min, dehydrated and autoradiographed using Hyperfilm- β max (Amersham Pharmacia Biotech) for 2 weeks to obtain images. In some cases, the sections were dipped into NTB2 emulsion (Kodak, USA), kept in the dark for a month and counterstained by pyronin-methylgreen after hybridization.

Counting the number of neurons and 3-D reconstruction of pontine nuclei

Coronal sections of postnatal day (P)1, P7, P9 and P18 were prepared from wild-type and weaver mutant mice as serial sections of 20 μ m thickness and stained with pyronin-methylgreen. Neurons of pontine nuclei were plotted and counted using MD plot (Minnesota datametrics, MN, USA). Three-dimensional structure of the nuclei was reconstructed by using Strata Vision 3d (Strata Inc., USA).

Dil labelling of mossy fibres and tracing of the projection pattern

Under deep ether anaesthesia, developing mice (P0, P1, P3, P5, P7, P9, P14 and P18) were perfused with saline followed by a fixative containing 4% paraformaldehyde in 0.1 M phosphate buffer (pH 7.3). The brains were removed from skulls and immersed in phosphate-buffered 4% paraformaldehyde where they remained for 1–3 weeks. Then, with the aid of a small needle, pieces of crystals of DiI (a lipophilic tracer dye; Molecular Probes, Inc., OR, USA) were placed at the dorsal portion of the brachium pontis to label mossy fibres arising from the pontine nuclei. Following dye deposit the brains were returned to the fixative and stored in the dark at room temperature for 3 months before sectioning. Cerebellar cortices were sectioned in the parasagittal or coronal plane at 200 µm using vibroslicer (Microslicer DTK-1500, Dosaka EM Co. Ltd, Japan). The sections were collected in 0.1 M phosphate buffer and observed with a laser confocal microscope using YHS filter system (Bio-Rad Inc.,

CA, USA). The number of mossy fibre terminals was counted in weaver mutant and wild-type mice to make a map of the distribution on the cerebellar surface.

Experiments on animals

All animal experiments were carried out in accordance with the National Institute of Health Guide for the Care and Use of Laboratory Animals (NIH Publications no. 80-23) revised 1996, and all efforts were made to minimize the number of animals used.

Results

Expression intensity of GIRK2 gene in pontine nuclei was significantly reduced in adult weaver mutant mice

To observe the effects of the weaver mutation on the expression of its own gene, GIRK2, mRNA expression patterns were compared between the wild-type and mutant brains with the *in situ* hybridization method (Fig. 1). At P7, strong expression was found in the external and internal granular layers of wild-type cerebellum (Fig. 1A) while, in adults, the signals were detected only in the internal granular layer (Fig. 1B). In weaver mutant mice, however, the expression was observed only in the external granular layer at P7 (Fig. 1C), and no signal was detected in adult cerebellum (Fig. 1D). The absence of signals was consistent with the previous observation showing the granule cell death in the postmitotic stage before starting migration in the mutant (Rakic & Sidman, 1973a,b).

In the pontine nuclei, the signals were strongly detected at both P7 and adult in wild-type mice (Fig. 1A and B). However, the size of areas with positive signals was significantly reduced in adult weaver mutant mice compared with wild-type animals (Fig. 1C and D). The detailed distribution pattern of signals was observed in coronal sections of the nuclei from wild-type and weaver mutant mice

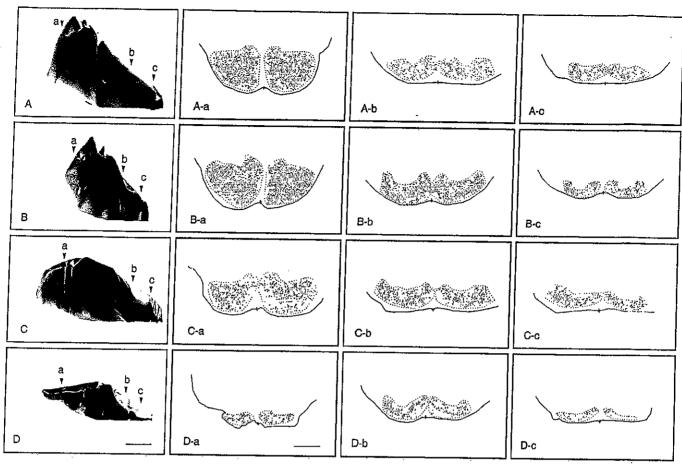


Fig. 4. Three-dimensional structure of the pontine nuclei and distribution of large neurons on sections. Coronal sections were prepared serially and stained with pyronin-methylgreen. After staining, the boundary of the pontine nuclei was traced with MD plot. Three-dimensional structure was reconstructed from the data of each section by using Strata Vision 3d software. Side views of the reconstructed pontine nuclei are shown in the left column. The rostrocaudal axis is orientated from left to right. (A) Wild type, P7. (B) Weaver, P7. (C) Wild type, P18. (D) Weaver, P18. Arrow heads (a-c) show position of each section in which distribution of neurons is shown. Scale bar, 300 µm.

(Fig. 2). Expression patterns of GIRK2 mRNA, intensity of the signals and size of the positive areas were similar in both wild-type and mutant mice at P7 (Fig. 2A and C). However, the signal was drastically reduced in adult mutant animals (Fig. 2G).

The number of neurons was significantly decreased in pontine nuclei of weaver mutant mice

To reveal the reason for the significant reduction of GIRK2 expression in the pontine nuclei of weaver mutants, distribution of neurons in the nuclei was examined in pyronin-methylgreen-stained sections (Fig. 2). A clear boundary was observed between densely stained nuclei and surrounding less stained regions (data not shown). This area contained two groups of cells: one with large cell bodies stained strongly by pyronin (red) and the other with small cell bodies stained strongly by methylgreen (green). The large cells are considered to be projection neurons and the small cells are interneurons and glial cells (Ruigrok & Cella, 1995). GIRK2 mRNA hybridization signals were found mostly in the large cell bodies, suggesting the expression of the gene in projection neurons (Fig. 2B, D and F).

To analyse the degenerating events in the pontine nuclei, we traced the boundaries of the nuclei and counted the number of large cells in every two sections cut at 20 µm thickness. The thickness was set to

avoid double counting of the neurons. In wild-type mice, the number of large cells peaked at P9 and then decreased during the later developmental stages (Fig. 3A). The decrement in the late stage might be related to neuronal death in the nuclei, possibly caused by failing to make correct connections with afferents or target cells. Until P7, the total numbers of large cells were similar in both the wild-type and weaver mutant mice. The number, however, decreased to half of the wild type at P9 and to one third at P18 in weaver mutants. Although no changes were detected in the total number of large cells at P7, the distribution of the cells in weaver mutants showed a clear difference from that in wild-type mice (Fig. 3B). At this stage, the number of cells on each slice was higher in the middle region of wild-type nuclei. On the other hand, the number of neurons in weaver mutant mice was decreased strongly in the middle region to shift the peak of neuronal distribution to the rostral side of the nuclei. In the later stages, the number was reduced throughout the whole pontine nuclei.

The changes in 3D structure reflected severe degeneration of the pontine nuclei in weaver mutant mice

The 3D structures of the nuclei were reconstructed based on the shape of boundaries on sections (Fig. 4). At P7 the total volume of the pontine nuclei, estimated from the sum of area size in sections, was

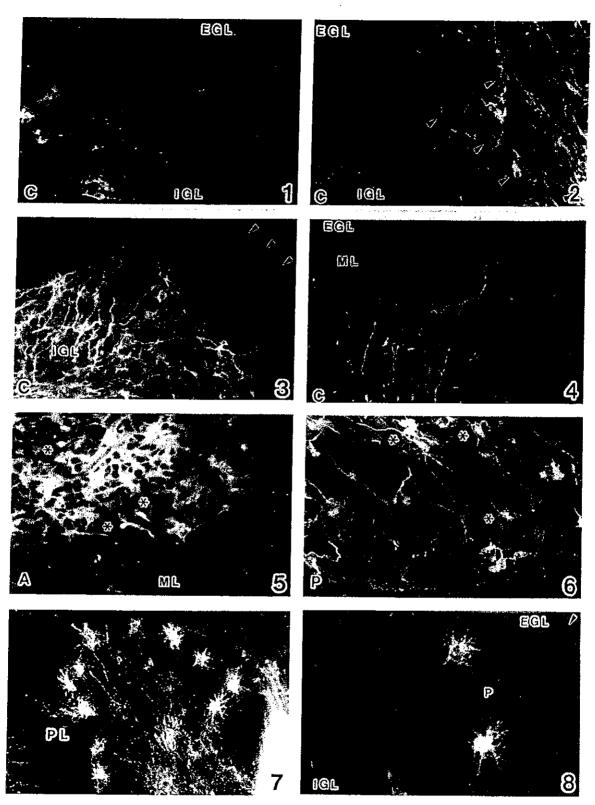


Fig. 5. Dil staining patterns of mossy fibre terminals in the wild type during development. After labelling of mossy fibres at each age in wild-type mice, the vermal part of the cerebellum was sagittally dissected at 200 µm thickness. (1) Central lobe, P1; (2) central lobe, P5, arrowheads indicate stained granule cells; (3) central lobe, P7, arrowheads indicate the surface of the cortex; (4) central lobe, P9; (5 and 6) anterior and posterior lobe, respectively, P14, asterisks indicate mossy fibre terminals; (7 and 8) overall distribution pattern of transiently stained Purkinje cells at P5 in a lobule and its enlarged view (P indicates stained Purkinje cells in panel 8); arrowhead indicates the surface of the lobule. EGL, external granular layer; IGL, internal granular layer; ML, molecular layer; PL, Purkinje cell layer; C, central lobe; A, anterior lobe; P, posterior lobe.

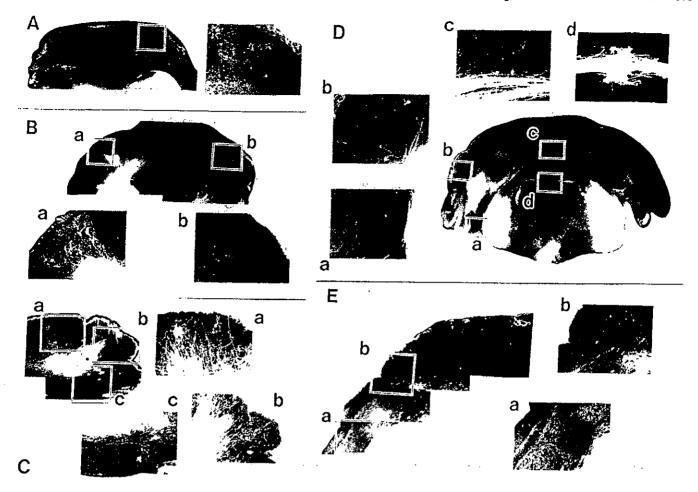


Fig. 6. Dil staining of mossy fibres in weaver mice during development. After labelling of mossy fibres at each age in weaver mutant mice, cerebellar cortices were coronally dissected at 200-µm thickness. (A) PO, (B) P3, (C) P5, (D) P7 and (E) P9. The areas indicated by rectangles are shown in enlarged views.

comparable in wild-type and weaver mice as expected from the similarity in the total number of large neurons (Fig. 4A and B). At P18, however, the volume of the nuclei in weaver mice was reduced to approximately one third of the wild type, whereas the length of the rostrocaudal axis of the nuclei was similar between wild-type and weaver mice (Fig. 4C and D). The reduction in the size in mutants at P18 was well correlated with the reduction in the total number of large-sized neurons, suggesting little change in cell density of the mutant, as was also directly observed in each section. This indicated that neuronal loss was not compensated for by glial cell proliferation in the total volume of the nuclei.

Innervating mossy fibres from the pontine nuclei were eliminated from cerebellar cortex in weaver mutant

Dil, a lipophilic tracer dye, was placed in the dorsal portion of the brachium pontis in order to observe correlation between the degeneration of pontine nuclear neurons and innervation of their axons, pontocerebellar mossy fibres, during development (Figs 5 and 6).

In the vermis of the central lobe of wild-type cerebellum, dotted staining of mossy fibre terminals were sparsely distributed at Pl (Fig. 5, part 1). At P5, a fibrous staining pattern was observed and some granule cells were labelled by DiI in the internal granular layer

(Fig. 5, part 2). Densly fibrous staining was observed in the internal granular layer at P7 and even in the molecular layer at P9 (Fig. 5, parts 3 and 4). At P14, the internal granular layer was stained with a mesh-like pattern in the anterior lobe, while densly fibrous staining with bulbous terminals was observed in the posterior lobe, corresponding to the development of glomerular structures at the terminal of mossy fibres and their connections with granule cells.

At PO and P3, we did not find obvious differences in the mossy fibre innervation pattern between wild-type and weaver mutant mice (Fig. 6A and B). At these stages a fibrous staining pattern was detected in the hemispheres, whereas there were no obvious innervating fibres in the vermis. At P5, however, there were several differences in innervation of mossy fibres between the wild type and the mutant. The density of stained fibres was decreased in the vermis of the mutants, in comparison with that of wild-type animals, whereas a fibrous staining pattern was still observed in the hemispheres (Fig. 6C). Interestingly, some portion of Purkinje cells were stained dispersedly from P3 to P5 in wild-type mice, suggesting transient interaction of pontocerebellar fibres with Purkinje cells during cerebellar development (Fig. 5, parts 7 and 8; Ozaki et al., 1999). In weaver mutant mice, however, it was hard to find staining of Purkinje cells through connection with mossy fibres. By P7, differences in innervation patterns of the fibres between wild-type