

Co-Expression of P2X₁ and P2X₅ Receptor Subunits Reveals a Novel ATP-Gated Ion Channel

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ABSTRACT

P2X receptors are a family of ion channels gated by extracellular ATP. Each member of the family can form functional homomeric channels, but only P2X₂ and P2X₃ have been shown to combine to form a unique heteromeric channel. Data from *in situ* hybridization studies suggest that P2X₁ and P2X₅ may also co-assemble. In this study, we tested this hypothesis by expressing recombinant P2X₁ and P2X₅ receptor subunits either individually or together in human embryonic kidney 293 cells. In cells expressing the homomeric P2X₁ receptor, 30 μ M α,β -methylene ATP (α,β -me-ATP) evoked robust currents that completely desensitized in less than 1 sec, whereas α,β -me-ATP failed to evoke current in cells expressing the homomeric

P2X₅ receptor. By contrast, α,β -me-ATP evoked biphasic currents with a pronounced nondesensitizing plateau phase in cells that co-expressed both subunits. Further, the EC₅₀ for α,β -me-ATP was greater in cells expressing both P2X₁ and P2X₅ than in cells expressing P2X₁ alone (5 and 1.6 μ M, respectively). Heteromeric assembly was confirmed using a co-immunoprecipitation assay of epitope-tagged P2X₁ and P2X₅ subunits. In summary, this study provides biochemical and functional evidence of a novel channel formed by P2X subunit heteropolymerization. This finding suggests that heteromeric subunit assembly constitutes an important mechanism for generating functional diversity of ATP-mediated responses.

P2X receptors are ATP-gated ion channels that mediate a diverse array of physiological actions. They have been found in a variety of tissues, including smooth muscle, peripheral neurons, and the central nervous system (Bean, 1992). To date, seven P2X receptor subunits have been identified by cDNA cloning (Soto *et al.*, 1997). When expressed in either *Xenopus laevis* oocytes or mammalian cells, these cloned receptors form functional homomeric channels that conduct a nonselective cation current in response to extracellular ATP (Burnstock, 1997).

The phenotypes associated with activation of the individual recombinant P2X receptors display distinctive pharmacological and biophysical properties that can be grouped into four classes. First, P2X₁ and P2X₃ receptors desensitize rapidly and are sensitive to both the agonist α,β -me-ATP and the antagonist PPADS. Second, P2X₂ and P2X₅ receptors desensitize slowly in response to ATP and are not activated by α,β -me-ATP but are antagonized by PPADS. Third, P2X₄ and P2X₆ also desensitize slowly but are insensitive to both α,β -me-ATP and PPADS. Finally, P2X₇ is much less sensitive to

MgATP and is the only P2X receptor reported to be able to form a large ionic “super” pore.

All of these properties have been used to identify the presence of subunits in native tissues. For example, the properties of the native P2X response of rat salivary gland (i.e., slowly desensitizing receptors insensitive to α,β -me-ATP and PPADS) match that of the cloned P2X₄ receptor, which is in turn the only known P2X receptor expressed in this tissue (Buell *et al.*, 1996). However, in most cases, the phenotypes observed in native tissues do not closely resemble those reported for the cloned subunits (Edwards *et al.*, 1992; Edwards, 1994). These poor matches suggest that additional subunits might account for these responses. Alternatively, heteropolymerization of P2X subunits might occur in native tissues, as has been demonstrated for P2X₂ and P2X₃ (Lewis *et al.*, 1995). When co-expressed in HEK 293 cells, these subunits co-assemble to form a novel channel with distinct functional properties similar to those seen in sensory neurons (Khakh *et al.*, 1995; Lewis *et al.*, 1995).

Given the high amino acid homology among the members of the P2X family and the demonstration that several P2X subunits are expressed in the same tissues, it is tempting to speculate that heteromeric receptor complexes are a widespread phenomenon among the P2X receptor family. One possible combination suggested by *in situ* hybridization stud-

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ABBREVIATIONS: α,β -me-ATP, α,β -methylene ATP; PPADS, pyridoxal phosphate-6-azophenyl-2',4'-disulfonic acid; HA, hemagglutinin; HEK, human embryonic kidney; EGTA, ethylene glycol bis(β -aminoethyl ether)-N,N,N',N'-tetraacetic acid; HEPES, 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid; TBST, Tris-buffered saline/Tween 20.

ies is a complex of P2X₁ and P2X₅ that has overlapping patterns of expression in the ventral horn of the spinal cord (Collo *et al.*, 1996). In this report, we demonstrate that co-expression of P2X₁ and P2X₅ receptor subunits in mammalian cells results in heteromeric ATP-gated channels with unique pharmacological and biophysical properties.

Materials and Methods

DNA constructs. The P2X₁ receptor cDNA was cloned from a rat heart cDNA library provided by Dr. M. Tamkun (Vanderbilt University, Nashville, TN). P2X₅ receptor cDNA was a gift of Dr. G. Buell (Glaxo Institute for Molecular Biology, Plan-les-Ouates, Geneva, Switzerland). Epitopes were introduced into full-length P2X subunits immediately upstream of the stop codon using polymerase chain reaction. The FLAG epitope (DYKDDDDK) was inserted into P2X₁ (P2X₁-FLAG) and a HA epitope (YPYDVPDYA) was inserted into P2X₅ (P2X₅-HA). Epitope-tagged subunits were subcloned into pRK-5 and verified by oligonucleotide sequencing.

Cell culture and transfection. HEK 293 cells were transiently transfected with wild type or epitope-tagged P2X₁ and P2X₅ receptor cDNAs by incubating the cells with 1 μ g of total cDNA mixed with 6 μ l of Lipofectamine (GIBCO BRL, Grand Island, NY) in 1 ml of serum-free medium. After 5 hr at 37°, the medium was replaced with minimal essential medium. Transfected cells were analyzed 24–48 hr later. For co-transfections, 0.5 μ g of each plasmid was mixed and used in the transfection reaction.

Electrophysiology. A suspension of transiently transfected cells was made by agitating the solution bathing the cells attached to the bottom of a single culture dish using a fire-polished Pasteur pipette. Whole-cell voltage clamp was performed as described previously (Egan *et al.*, 1998; Torres *et al.*, 1998). Whole-cell current was recorded from single cells held at -40 mV using an AxoPatch 200A amplifier and low resistance electrodes (1–2 M Ω) (Axon Instruments, Foster City, CA). Recording pipettes were filled with the following intracellular solution: 150 mM CsCl, 10 mM tetraethylammonium-Cl, 5 mM EGTA, 10 mM HEPES, pH 7.4 with CsOH. The bath solution was 150 mM NaCl, 1 mM CaCl₂, 1 mM MgCl₂, 10 mM glucose, 10 mM HEPES, pH 7.4 with NaOH. Drugs were applied by manually moving the electrode and attached cell into the line of flow of solutions exiting one of an array of inlet tubes. Data averages are expressed as mean \pm standard error. Each experiment was repeated at least three times. Raw data were analyzed and plotted off-line using IgorPro (Wavemetrics, Lake Oswego, OR). The EC₅₀ and Hill slope values (and their 95% confidence limits) were determined from plots of peak current amplitudes versus agonist concentrations using InPlot (GraphPAD Software, San Diego, CA) and pooled data from separate experiments.

Immunoprecipitation and Western blotting. Confluent monolayers of HEK 293 cells in 35-mm dishes were washed three times with phosphate-buffered saline and incubated in solubilization buffer [phosphate-buffered saline (136 mM NaCl, 2.7 mM KCl, 12 mM Na₂HPO₄, 1.8 mM KH₂PO₄, pH 7.4), 1% nonidet P-40, 1 mM phenylmethylsulfonyl fluoride, 1 mM 4-(2-aminoethyl)benzenesulfonyl fluoride, 10 μ g/ml leupeptin] at 4° for 1 hr. Immunoprecipitation was carried out using the M2 anti-FLAG antibody (5 μ g/ml) in the presence of 50 μ l of Protein G Gamma-Bind agarose. Immunoprecipitates were washed five times with solubilization buffer and resuspended in protein sample buffer. Samples were boiled for 5 min and proteins were analyzed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis, followed by transfer to nitrocellulose filters. The filters were blocked overnight in TBST (20 mM Tris pH 7.6, 145 mM NaCl, 0.05% Tween 20) containing 2% bovine serum albumin, and incubated for 1 hr with primary antibody (M2 anti-FLAG, 10 μ g/ml, or anti-HA 1:1000). After several washes with TBST, filters were incubated with peroxidase-conjugated sheep anti-mouse antibody for 1 hr. Filters were washed extensively in TBST and immunoreactivity

was detected with the enhanced chemiluminescence detection kit following the manufacturer's suggestions.

Drugs and supplies. ATP and α , β -me-ATP were obtained from Sigma (St. Louis, MO). Enzymes for cloning and sequencing were obtained from Promega (Madison, WI). Vent DNA polymerase used for polymerase chain reaction-based mutagenesis was purchased from New England Biolabs (Beverly, MA), minimal essential medium, glutamine, fetal bovine serum, lipofectamine, and oligonucleotides were obtained from GIBCO BRL. Gel extraction kit, and plasmid DNA isolation kit were from Qiagen (Valencia, CA). Protein G Gamma-Bind agarose was from Amersham Pharmacia Biotech (Piscataway, NJ), and [³⁵S]dATP for sequencing, enhanced chemiluminescence detection reagents, and anti-mouse IgG/horseradish peroxidase conjugate were from Amersham (Indianapolis IN). M2 anti-FLAG monoclonal antibody was from Kodak (New Haven, CT), and mouse anti-HA antibody was from Babco (Richmond, CA).

Results and Discussion

In situ hybridization and Northern blot studies suggest that P2X₁ and P2X₅ subunits are possible candidates to co-assemble into functional ATP-gated channels. mRNA for

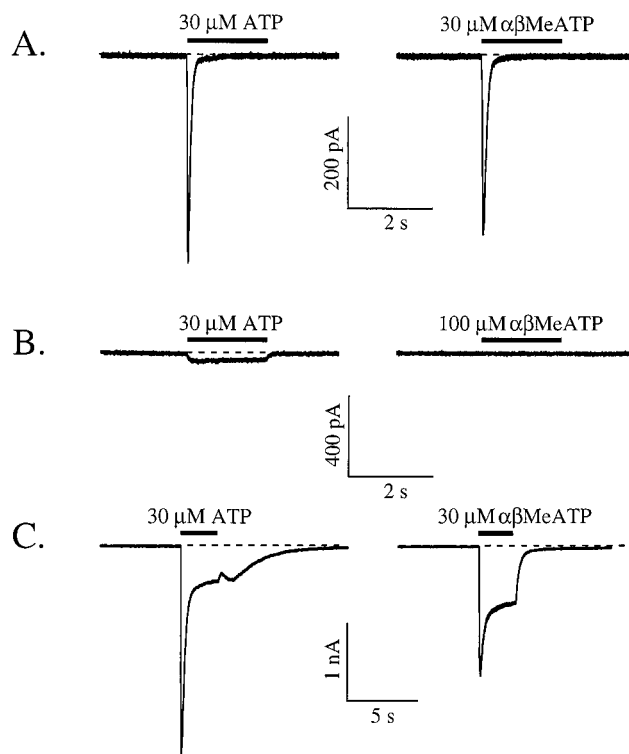


Fig. 1. Co-expression of P2X₁ and P2X₅ receptor subunits results in a unique phenotype. The agonists ATP and α , β -me-ATP were applied to cells expressing either or both P2X₁ and P2X₅ receptors. Typical responses are shown. A, A cell transfected with cDNA encoding P2X₁ alone showed rapidly desensitizing currents in response to application of either ATP or α , β -me-ATP. B, A different cell transfected with cDNA encoding the P2X₅ receptor gave a weak current in response to 30 μ M ATP but failed to respond to 100 μ M α , β -me-ATP. C, A cell transfected with both cDNAs showed biphasic currents in response to applications of either agonist. ATP caused rapid gating of inward current that quickly fell to a sustained plateau. Removing ATP was always accompanied by generation of an inward "bump" current that decayed slowly over a time course of about 5 sec. The cause of this current component is unknown. The response to 30 μ M α , β -me-ATP resembled that evoked by ATP, although this concentration of α , β -me-ATP never generated the bump current seen upon washout of ATP. The different response to α , β -me-ATP of these three typical cells demonstrates the existence of unique phenotypes for P2X₁, P2X₅, and heteromeric P2X₁/P2X₅.

both subunits are expressed in heart, sensory ganglia, and spinal cord tissue. Indeed, in cells of the cervical spinal cord, the expression pattern of P2X₁ matched that of P2X₅ (Collo *et al.*, 1996). Therefore, we examined the possibility that P2X₁ and P2X₅ subunits can co-assemble into functional channels when co-expressed in HEK 293 cells.

The homomeric channels formed by either P2X₁ or P2X₅ have distinct pharmacological and biophysical properties. Fig. 1A shows P2X₁-mediated currents activated by either ATP or α,β -me-ATP. These currents activated rapidly and underwent fast and complete desensitization. By contrast,

ATP-gated currents desensitized slowly in cells that expressed P2X₅, and α,β -me-ATP was ineffective (Fig. 1B). We then compared the responses of the homomeric receptors to those seen in cells co-transfected with cDNAs encoding both subunits. In cells co-expressing P2X₁ and P2X₅ receptors, whole-cell recordings revealed an ion channel whose phenotype differed from those of either homomeric receptors. Like both P2X₁ and P2X₅, ATP evoked a quickly developing inward current in co-transfected cells held at -40 mV (Fig. 1C). The size of the current depended on the concentration of α,β -me-ATP applied (Fig. 2A). Superficially, the pattern of

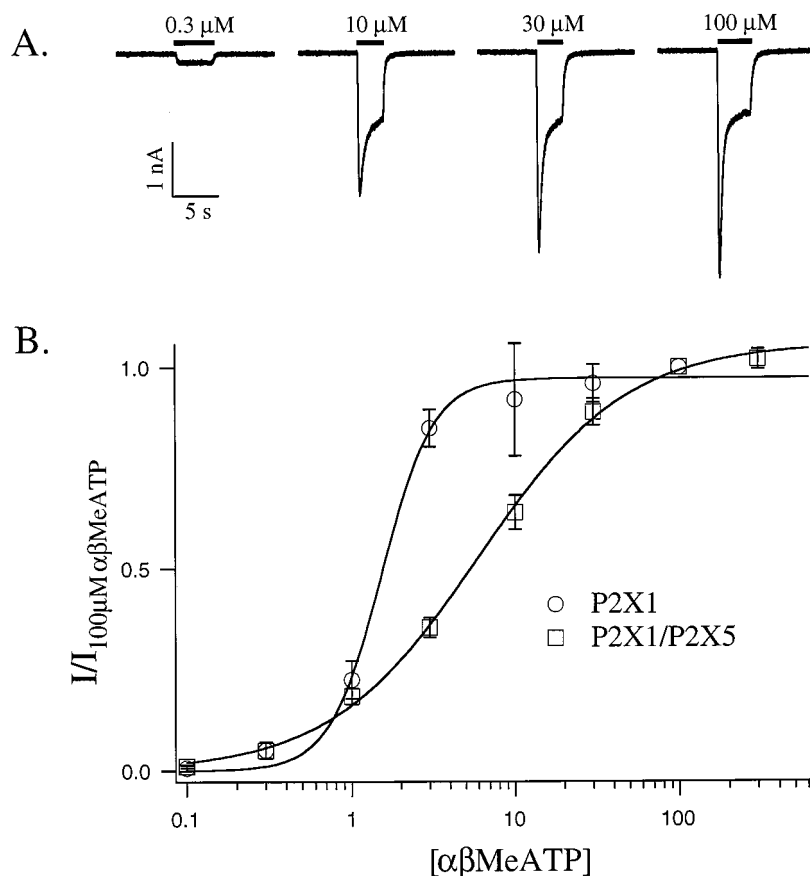


Fig. 2. Dose-response curves for homomeric P2X₁ and heteromeric P2X₁/P2X₅. A, Raw data traces for application of different concentrations of α,β -me-ATP to a cell expressing heteromeric P2X₁/P2X₅ receptors. B, Dose-response curves for P2X₁ and P2X₁/P2X₅ receptors. Plots, averaged data obtained from 24 individual cells. In each cell, peak currents evoked by a range of concentrations of α,β -me-ATP were normalized to that obtained with 100 μ M α,β -me-ATP. Points, average of at least three separate experiments. The solid line is the best fit of the average data to $I_{\text{max}} ([\alpha,\beta\text{-me-ATP}]^{n_H} / ([\alpha,\beta\text{-me-ATP}]^{n_H} + EC_{50}^{n_H}))$, where n_H is the Hill coefficient. Cells transfected with cDNA encoding P2X₅ receptor alone did not respond to 100–300 μ M α,β -me-ATP (three experiments, data not shown).

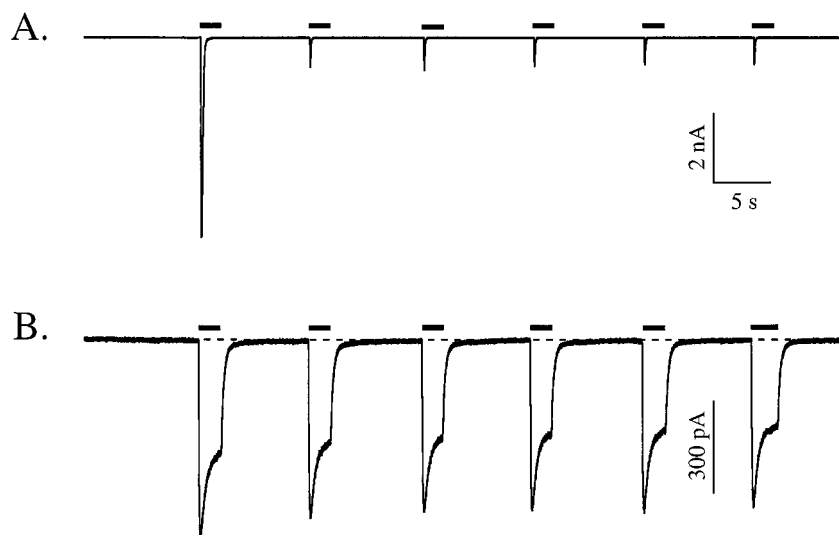


Fig. 3. Peak current amplitude decreases during repeated applications of α,β -me-ATP to cells transfected with P2X₁ but not P2X₁ and P2X₅ receptor subunits cDNAs. α,β -me-ATP (30 μ M) was applied for about 1–2 sec once every 10 sec in cells expressing either P2X₁ alone or both P2X₁ and P2X₅. Both traces are shown at the same time scale. A, In cells expressing only P2X₁, peak current amplitude was reduced by about 80% after the first agonist application. B, Remarkably less desensitization was seen in cells co-expressing both P2X₁ and P2X₅.

the response resembled that expected for a combination of currents through homomeric P2X₁ and P2X₅. That is, the response to ATP was biphasic and consisted of an initial current "spike" (as expected for a homomeric P2X₁ response) followed by a smaller sustained plateau current (as expected for a homomeric P2X₅ response). However, several lines of data suggest a unique phenotype. First, α,β -me-ATP also evoked a biphasic current, and this would not be expected for a combination of homomeric P2X₁ and P2X₅ because the latter receptor is insensitive to this drug. Second, cells co-transfected with both P2X₁ and P2X₅ were less sensitive to α,β -me-ATP than were cells expressing P2X₁ (Fig. 2B). Both the EC₅₀ (1.6 μ M, 1.3–1.9) and the Hill slope (2.6, 1.7–3.5) values of the pooled raw data from cells transfected with P2X₁ alone differed from those measured in cells co-transfected with both P2X₁ and P2X₅ (EC₅₀, 5 μ M, 4.3–6.2; n_H , 1.1, 0.9–1.3). This disparity in the Hill slopes could have several different underlying causes: there are fewer α,β -me-ATP responsive subunits than nonresponsive subunits present in the heteromeric assembly, heteromultimerization alters the cooperativity properties of α,β -me-ATP, or that there are different dose-response curves reflecting different subunit stoichiometries that are partially superimposed. In any event, the mechanism(s) involved do not alter the interpretation of the results. Third, the rate of recovery of peak current during repeated applications of α,β -me-ATP was quicker in cells expressing heteromultimeric P2X₁/P2X₅ re-

ceptors than in those expressing only P2X₁. This was shown by applying 30 μ M α,β -me-ATP repeatedly for approximately 1–2 sec followed by an 8-sec wash to cells expressing either P2X₁ alone or both P2X₁ and P2X₅ (Fig. 3). This protocol resulted in a profound reduction in peak agonist response after a single application in cells transfected with P2X₁ only (Fig. 3A), whereas the current after multiple applications of α,β -me-ATP to HEK 293 cells expressing both subunits were maintained at about 80% of the initial amplitude (Fig. 3B). This latter decrease could reflect either an inherent property of P2X₁/P2X₅ heteromers or the presence of a small population of homomeric P2X₁ receptors. Taken together, these three findings strongly suggest the formation of heteromultimeric P2X₁/P2X₅ receptors.

To provide direct demonstration of the heteropolymerization between P2X₁ and P2X₅ subunits, we performed co-immunoprecipitation experiments. This assay is based on the specific affinity of an anti-tag antibody for an epitope-tagged protein. P2X₁ and P2X₅ were both tagged with different epitopes and transfected individually or in combination in HEK 293 cells. As seen in Fig. 4A, α,β -me-ATP-gated currents recorded from cells expressing the epitope-tagged P2X subunits alone or in combination were indistinguishable from those recorded from cells expressing the wild-type receptors. In addition, the anti-FLAG and anti-HA antibodies selectively immunoprecipitated P2X₁-FLAG or P2X₅-HA respectively. No detectable cross-reactivity was found between these two antibodies (Fig. 4B). We then

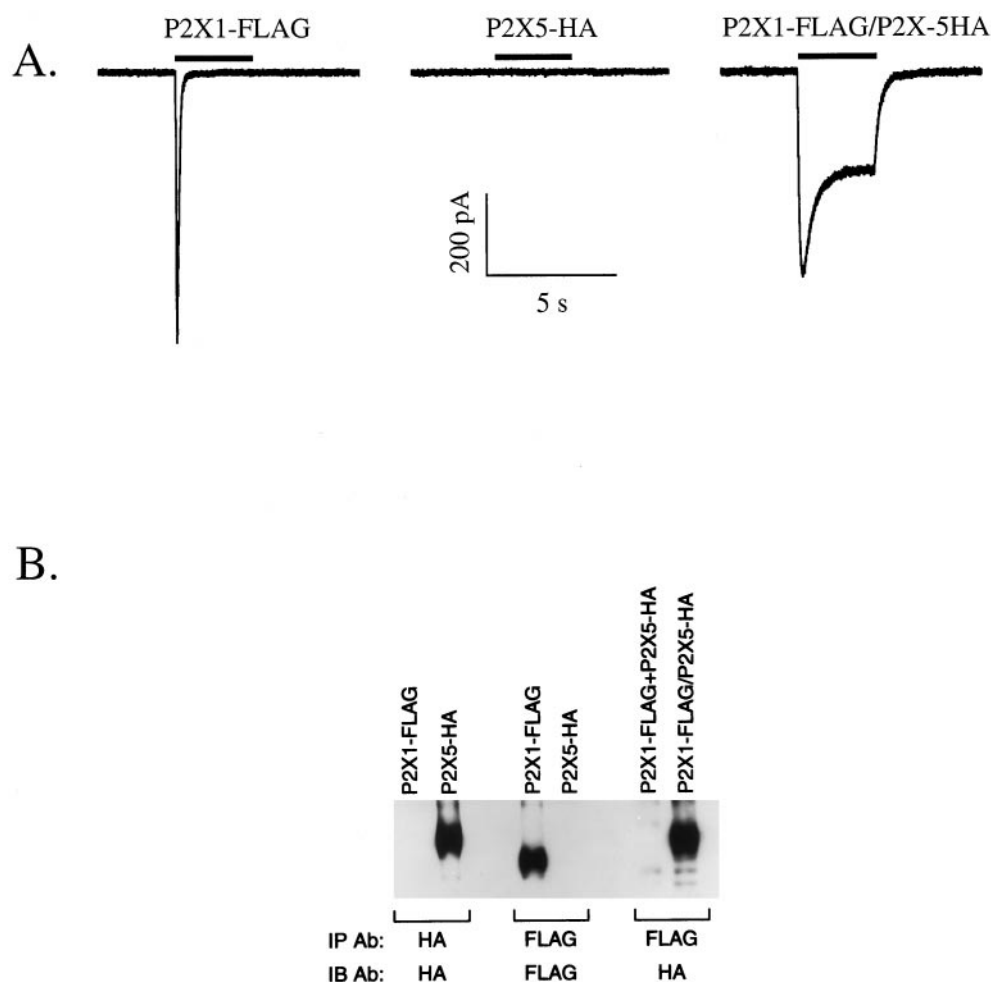


Fig. 4. Co-assembly between P2X₁ and P2X₅ receptor subunits. **A**, Functional expression of epitope-tagged P2X₁ and P2X₅ channels. Whole-cell recordings were obtained from HEK 293 cells transfected with the indicated constructs. The currents were elicited by 30 μ M α,β -me-ATP from a holding potential of -40 mV. **B**, Co-immunoprecipitation of epitope-tagged P2X₁ and P2X₅. Lysates from HEK 293 cells previously transfected with the indicated constructs were immunoprecipitated, separated on sodium dodecyl sulfate-polyacrylamide gel electrophoresis, and transferred to nitrocellulose filters. *Lanes 1 and 2*, lysates were immunoprecipitated and immunoblotted with the anti-HA antibody; *lanes 3 and 4*, lysates were immunoprecipitated and immunoblotted with the anti-FLAG antibody; *lane 5*, lysates from cells expressing individual subunits were mixed, immunoprecipitated with the anti-FLAG antibody, and immunoblotted with the anti-HA antibody; *lane 6*, lysates from cells co-expressing P2X₁ and P2X₅ were immunoprecipitated with the anti-FLAG antibody and immunoblotted with the anti-HA antibody.

immunoprecipitated one subunit (P2X₁-FLAG) and then detected the other subunit (P2X₅-HA) by Western blot. Fig. 4B shows the results of the co-immunoprecipitation experiment in cells co-expressing both P2X subunits. After immunoprecipitation of P2X₁-FLAG, a strong signal corresponding to P2X₅-HA was detected. When lysates from cells expressing either subunit were mixed, no interaction was detected. Although it is possible that the relatively high levels of expression for the two proteins in co-transfected cells promotes nonspecific assembly, these results, taken together with the functional data, support the hypothesis that the two subunits do co-assemble into heteropolymeric assemblies.

Heteropolymerization of channel subunits has been suggested as a means of generating functional and molecular diversity (Green and Millar, 1995). Indeed, the formation of heteromeric channels has been amply demonstrated for many members of the transmitter-gated ion channel family such as nicotinic (Ragozzino *et al.*, 1997; Yu and Role, 1998), and glutamate ionotropic receptors (Boulter *et al.*, 1990), as well as voltage-dependent K⁺ channels (Liao *et al.*, 1996; Wischmeyer *et al.*, 1997). In cells that co-express different channel subunits, the occurrence of heteromeric assemblies implies the existence of a variety of channel responses, each of which has potentially unique biophysical characteristics. This array of channel types might be critical for the regulation of cellular processes. ATP-mediated responses through the activation of P2X receptors are also affected by subunit co-assembly. P2X₂/P2X₃ and now P2X₁/P2X₅ heteromeric channels are good examples of such a heteropolymerization process. Because a wide variety of tissues and cell types express several P2X subunits, other combinations among P2X receptor subunits are likely to occur.

In summary, this report presents several lines of evidence supporting the notion that heteropolymerization occurs between P2X₁ and P2X₅ receptor subunits. First, whole-cell recordings in HEK-293 cells that co-express P2X₁ and P2X₅ subunits revealed an α,β -me-ATP-gated ion channel with unique biophysical properties that distinguish the channel from those observed in cells expressing either subunit alone. Second, receptors formed by P2X₁ and P2X₅ were less sensitive to the agonist α,β me-ATP compared with homomeric P2X₁ receptors. Third, peak current amplitude changed little during closely spaced repeated applications of α,β -me-ATP in cells expressing the P2X₁/P2X₅ heteromeric channel, which contrasts sharply with the profound decrease in peak current seen for the homomeric P2X₁ receptor. In addition, co-immunoprecipitation experiments provide biochemical evidence for

protein-protein interaction between these two subunits. Although the results presented in this report do not prove the formation of a heteromeric channel between P2X₁ and P2X₅ *in vivo*, our findings provide a new P2X phenotype that can be used as a template for elucidating the molecular identities of native P2X receptor channels.

Acknowledgments

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