Structure of the Bradykinin B₂ Receptors' Amino Terminus[†]

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ABSTRACT: The peptide hormone bradykinin exerts important biological functions by binding to and activating bradykinin B2 receptors. B2 receptors belong to the seven transmembrane domain (7TM) receptor family. Cloning of the cDNA sequences for the rat, human, and mouse bradykinin B2 receptor revealed several in-frame AUG triplets as potential initiation sites for translation. Due to "Kozak-like" consensus nucleotides, the AUG codon closest to transmembrane domain 1 was assumed the preferred initiation site for translation, but the real amino terminus of the B2 receptor protein was unknown. The amino terminus of several 7TM receptors has been shown to be essentially involved in receptor activation and/or ligand binding. Therefore we determined the amino terminus of the human and of the rat B2 receptor using domain-specific antipeptide antibodies, amino acid sequence analysis, and *in vitro* transcription/translation. We report that the human and rat B2 receptor protein start with the methionine which is translated from the first in-frame AUG. This start site extends the known amino terminus of the human and rat B2 receptors by 27 or 30 amino acid residues, respectively. Antibodies raised against a peptide of the initial 27 amino acids of the human B2 receptor stained B2 receptors on intact cells. This finding excludes the existence of a signal sequence for this receptor.

Receptors for the peptide hormone family of kinins (Müller-Esterl et al., 1986) are classified into B₁ and B₂ type. The receptors belong to the 7TM receptor family which have seven hydrophobic domains assumed to form α-helical structures (Schertler et al., 1993). They transmit their signal by activation of a G protein-mediated signal transduction cascade (Bascands et al., 1993; Jones et al., 1995). B₁ receptors bind carboxy-terminally-truncated derivatives of bradykinin, e.g., des-Arg9-bradykinin, desArg10-kallidin (Regoli & Barabé, 1988), whereas the agonists of B₂ receptors are kinins with intact carboxy terminus (Bhoola et al., 1992). The cDNA sequences of the rat (McEachern et al., 1991), human (Hess et al., 1992), and mouse (Yokoyama et al., 1994) B₂ receptors display several in-frame ATG triplets. Due to "Kozak-like" consensus nucleotides, the AUG closest to the beginning of transmembrane domain 1 was assumed to be the preferred initiation site for translation. According to this prediction the coding region of the rat (Pesquero et al., 1994), human (Ma et al., 1994a), and mouse (Ma et al., 1994b) B₂ receptor protein was localized entirely on the last exon, i.e., exon 3 for the human and mouse B2 receptor and exon 4 for the rat B₂ receptor. The amino terminus of various G protein-coupled receptors has been found important for ligand binding and/or signal transduction (Oppermann et al., 1993; Yokota et al., 1992). We analyzed the amino-terminal structure of denatured and native B₂ receptors using domain-specific antibodies, amino acid sequence analysis, and *in vitro* transcription/translation. In agreement with the scanning model developed by Kozak (1989), we found that the first in-frame AUG is used as start site of translation localized on exon 2 of the human and on exon 3 of the rat B₂ receptor gene without any evidence for context-dependent leaky scanning or the existence of a signal peptide.

EXPERIMENTAL PROCEDURES

Materials. The chemiluminescence detection kit and [35S]-methionine were from Amersham; [2,3-prolyl-3,4-3H]brady-kinin (specific activity 98 Ci/mmol) was from NEN Dupont; 1,5-difluoro-2,4-dinitrobenzene (DFDNB) was from Pierce; wheat germ agglutinin (WGA from *Triticum vulgaris*), *N*-acetylglucosamine, and fluorescein isothiocyanate (FITC)-conjugated goat anti-rabbit immunoglobulin were from Sigma; PVDF¹ sheets were from Millipore; Affi-Gel 10 and nonfat dry milk were from Bio-Rad; HOE140 was from Hoechst; the TNT reticulolysate kit was from Promega; the first strand cDNA synthesis kit was from Pharmacia; Vent-(exo+)DNA polymerase was from New England Biolabs; Centricon 30 filters were from Amicon. All other chemicals were of analytical grade.

Cell Culture. Human foreskin fibroblasts, HF-15 (Roscher et al., 1983), were grown to confluency in Dulbecco's modified Eagle's medium containing 10% (v/v) fetal calf

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¹ Abbreviations: PVDF, polyvinylidenedifluoride; SDS-PAGE, sodium dodecyl sulfate—polyacrylamide gel electrophoresis; E64, *N*-[*N*-(L-3-transcarboxirane-2-carbonyl)-L-leucyl]agmatine; HEPES, 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid; PMSF, phenylmethanesulfonyl fluoride.

serum for 2-3 weeks and used at passages 8-15. Chinese hamster ovary cells (CHO) and CHO cells transfected with the rat B₂ receptor cDNA, rB2CHO12/3 (AbdAlla et al., 1996), were grown in Ham's F12 medium containing 10% fetal calf serum. Cells were kept in a humidified 5% $CO_2/95\%$ air atmosphere at 37 °C.

Reverse Transcriptase PCR. Different human B2 receptor cDNA fragments were obtained by reverse transcriptase PCR (RT-PCR). RNA was prepared from a human fibroblast cell line with the RNAzol B method (Wak Chemie, Germany). The following primers were used for cDNA synthesis: 5' nucleotide position [according to Hess et al. (1992)] and primer direction are in parentheses: BKR1exC, 5'-CAAAT-GTTCTCTCCCTGGAAG-3' (139, forward); BKR-18, 5'-ATGCTCAATGTCACCTTG-3' (223, forward); BKR-16, 5'-AAGCAACTGTCCCTCAATC-3' (1372, reverse). Primer BKR1exC directs DNA synthesis to start with the first inframe ATG whereas BKR-18 will amplify B2 receptor DNA beginning with the last, i.e., the third in-frame ATG. The reverse transcriptase-PCR products were cloned into the EcoRV site of the eucaryotic expression vector pcDNA3 (Invitrogen). Identity of the fragments created by PCR with the published human B2 receptor cDNA sequence was confirmed by DNA sequencing.

In Vitro Transcription and Translation. In vitro transcription and translation of the various human bradykinin B_2 receptor expression clones was performed with the TNT reticulolysate kit (Promega) including T7 polymerase according to the manufacturer's instructions. One reaction was performed using approximately 400 ng of purified DNA. The polypeptides were labeled by [35 S]methionine.

Membrane Preparation. HF-15 cells and CHO cells were washed twice with ice-cold phosphate buffered saline (PBS). Cells were harvested and homogenized in PBS containing protease inhibitors, 1 mM phenylmethanesulfonylfluoride (PMSF), 1 μg/mL N-[N-(L-3-transcarboxirane-2-carbonyl)-L-leucyl]agmatine (E64), and 2 μM leupeptin. After centrifugation (3000g, 15 min), membranes were recovered from the supernatant, sedimented by another centrifugation step (15000g, 30 min), and washed twice with PBS. Crude membranes (protein concentration 1 mg/mL) were stored at -80 °C until use. The binding activities of the membranes for [³H]bradykinin were 0.5-1 pmol/mg of protein for HF-15 cells and 1.5-3 pmol/mg of protein for rB2CHO12/3 cells.

Synthesis of Peptides and Production of Antipeptide Antibodies. Peptides derived from the rat or human B_2 receptor sequence were synthesized by solid phase peptide synthesis using the fluorenylmethyloxycarbonyl (Fmoc) or the *tert*-butyloxycarbonyl (tBoc) chemistry as described previously (AbdAlla et al., 1996). Peptides purified by high-performance liquid chromatography (HPLC) were routinely analyzed by Edman degradation and electrospray mass spectrometry. Peptides derived from extracellular domains $ED1_A$ and $ED1_B$ (Figure 1) were used for immunization in rabbit without prior coupling to a carrier protein. Antisera were tested for antigen specificity and cross-reactivity with human or rat peptides by the indirect enzyme-linked immunosorbent assay (ELISA) using microtiter plates (MaxiSorb, Nunc) coated with 2 μ g/mL of the peptide.

Purification of Antipeptide Antibodies by Affinity Chromatography. Purification of antibodies to the B₂ receptor

by affinity chromatography with the respective antigen was performed as previously described (AbdAlla et al., 1996).

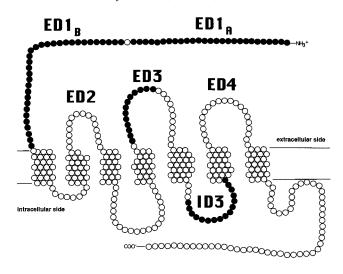
Western Blotting and Immunoprinting. Proteins were resolved by SDS-PAGE (Laemmli, 1970) and transferred to polyvinylidenedifluoride (PVDF) sheets using semidry blotting (Kyhse-Anderson, 1984). The sheets were treated with 50 mM Tris and 0.2 M NaCl, pH 7.4 (buffer A), containing 5% (w/v) nonfat dry milk and 1% (w/v) Tween 20 for 1 h. Antisera were diluted 1:1000 in buffer A containing 2% (w/v) bovine serum albumin (BSA). After a 30 min incubation at 37 °C, the PVDF sheets were washed 5× for 15 min each with buffer A and incubated for 30 min with peroxidase-labeled F(ab')₂ fragments of goat anti-rabbit antibody (Sigma, 1:5000). After extensive washing, bound antibody was visualized using the ECL chemiluminescence detection kit (Amersham).

Lectin Affinity Chromatography of B₂ Receptor. Enrichment of B₂ receptor from human foreskin fibroblasts by wheat germ agglutinin chromatography was done exactly as described (AbdAlla et al., 1996).

Immunoaffinity Chromatography and Amino Acid Sequence Analysis of the B₂ Receptor. Affinity-purified domain-specific antibodies were covalently coupled to Affi-Gel 10 according to the manufacturer's instructions (15 mg/ mL gel). Membranes of rB2CHO12/3 (100 pmol of B₂ receptor/40 mg of total protein) were solubilized with 1% (w/v) sodium deoxycholate in PBS including 1 mM PMSF, $1 \mu g/mL$ E64, and $2 \mu M$ leupeptin. The deoxycholate was diluted to 0.1% (w/v) by the addition of 20 mM HEPES, pH 7.4, containing 150 mM NaCl and 1 mM EDTA (buffer B). Human B₂ receptors of HF-15 cells (100 pmol of B₂ receptor/80 mg of total protein) were partially enriched by WGA-affinity chromatography. Eluates from the lectin affinity column were diluted by buffer B with protease inhibitors. Then 10% glycerol and 0.1% (w/v) Triton X100 were added to the solubilized rat or human B2 receptor preparation, and the solution was applied to the immunoaffinity matrix for an overnight incubation. The affinity matrix was extensively washed with buffer B, and bound proteins were eluted with 0.2 M glycine, pH 2.5, supplemented with 10% (v/v) 1,4-dioxane. The eluted protein fraction was neutralized with 1 M Tris, pH 8.0, and concentrated and desalted by Centricon filtration (exclusion limit 30 000 Da). The purity and identity of the enriched B2 receptor was assessed by SDS-PAGE followed by silver staining and immunoprinting. For amino-terminal sequencing, proteins from three experiments were pooled, applied to a ProSpin sample preparation cartridge, and sequenced on a 477 A Protein Sequencer equipped with an on-line 120A PTH Analyzer (Applied Biosystems).

Affinity Cross-Linking of the B₂ Receptor. B₂ agonist bradykinin or antagonist HOE140 were cross-linked to the B₂ receptor by 1,5-difluoro-2,4-dinitrobenzene as previously described (AbdAlla et al., 1993).

Fluorescence-Activated Cell Sorting (FACS) Analysis. Confluent HF-15 cells (1 pmol of B₂ receptor per mg of protein) were detached with PBS and 0.5 mM EDTA, pH 7.4, and washed twice with ice-cold RPMI 1640 medium containing 0.1% (w/v) bovine serum albumin and 20 mM Na⁺-HEPES, pH 7.4 (incubation medium). Cells (1 \times 10⁶) were suspended in the incubation medium containing the affinity-purified antibodies (10 μ g/mL) and incubated for 1 h at 4 °C. After washing three times, fluorescein isothio-



Peptides used for immunization in rabbit

ED1 _A	MFSPWKISMFLSVREDSVPTTASFSAD
ED1 _B	MLNVTLQGPTLNGTFAQSKCPQVEWLGWLNTIQ
ED3	KEYSDEGHNVTAC
ID3	RNNEMOKEKEIQTERR

FIGURE 1: Topology of the human B_2 receptor. A model of the B_2 receptor topology based on hydrophobicity plots and a transmembrane α -helix hypothesis is presented. Positions of the peptides from extracellular domain 1_A , 1_B , and 3 (ED1_A, ED1_B, ED3) or from intracellular domain 3 (ID3) used to raise antisera are marked in black. The amino acid sequence of these peptides is given in the lower panel. The single-letter code for amino acids is used.

cyanate (FITC)-conjugated goat anti-rabbit immunoglobulin (Sigma), diluted 1:80 (v/v), was added to the cells. The cells were incubated for 1 h at 4 °C, washed, fixed with 2% (v/v) formaldehyde, and analyzed on a FACScan (Becton Dickinson) using the Lysis program.

RESULTS AND DISCUSSION

Staining of Denatured Human B₂ Receptors by Anti-ED1_A and Anti-ED1_B Antibodies in Immunoprinting. To determine the structure of the B₂ receptor's amino terminus, we raised antibodies against a peptide corresponding to extracellular domain 1_B (ED1_B) which is the predicted amino terminus of the B₂ receptor and to a peptide corresponding to extracellular domain 1_A (ED1_A) which is a B₂ receptor sequence located on exon 2 of the human B₂ receptor gene (Ma et al., 1994a) (Figure 1). We first asked whether denatured human B2 receptors of human foreskin fibroblasts (HF-15) are recognized by the antibodies to ED1_A or to ED1_B. Human B₂ receptors partially enriched by wheat germ agglutinin affinity chromatography were separated by SDS-PAGE and transferred to PVDF membranes, and the Western blot was probed by antibodies to ED1_B and to ED1_A. Both antisera recognized a major protein band of 69 kDa (Figure 2, lanes 1 and 3), which is in good agreement with the apparent molecular weight of B2 receptors from HF-15 cells (AbdAlla et al., 1993). Preabsorption of the antisera on their cognate peptides abolished the staining, confirming the specific interaction of the anti-ED1_A and anti-ED1_B antisera with the denatured B2 receptors (exemplified for anti-ED1A antiserum: Figure 2, lane 2). As an additional control B₂ receptor was detected by anti-bradykinin antibodies after cross-linking of the agonist to B₂ receptors (Figure 2, lane 4). A 1000-

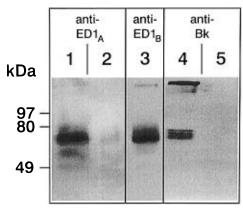


FIGURE 2: Immunoblotting of human B_2 receptors with domain-specific antisera to the amino terminus. Western blots of partially enriched B_2 receptors from HF-15 cell membranes were probed by antisera to $\mathrm{ED1}_A$ (lane 1) and to $\mathrm{ED1}_B$ (lane 3). As a control, the antiserum to $\mathrm{ED1}_A$ was preabsorbed on the cognate antigen (lane 2). For comparison, bradykinin was cross-linked to the B_2 receptor in the presence (lane 5) or absence (lane 4) of a 1000-fold excess of HOE140 and detected by anti-bradykinin (anti-Bk) antiserum. Antiserum dilution was 1:1000, and bound antibodies were visualized using the chemiluminescence detection method.

fold excess of the antagonist HOE140 suppressed the crosslinking of bradykinin to the B₂ receptor (Figure 2, lane 5).

Amino Acid Sequence Analysis of the Human B₂ Receptor. What is the amino-terminal sequence of the identified protein? We used a mixture of several domain-specific antibodies (AbdAlla et al., 1996) to isolate B2 receptor protein from human foreskin fibroblasts by affinity chromatography. The purity of the isolated protein was assessed by silver staining after SDS-PAGE (Figure 3A, lane 1), and B₂ receptor identity was proven in immunoprinting (Figure 3A, lane 2). The isolated B₂ receptor protein was submitted to amino acid sequence analysis. The amino-terminal sequence obtained in two independent experiments is shown in Figure 3B. The isolated protein is the B2 receptor. The aminoterminal sequence is derived from exon 2 of the B2 receptor gene indicating that the first in-frame ATG located on exon 2 of the human B₂ receptor gene is used (after transcription) as initiation site (Figure 3B,I). This ATG precedes the predicted initiation site, i.e., the third in-frame ATG on exon 3. The B₂ receptor sequence of run II amino-terminally lacks 16 amino acids. This is probably due to partial proteolytic degradation of the protein during the purification as was similarly observed with the purification of, e.g., the endothelin receptor protein (Hick et al., 1995), though we cannot completely rule out the possibility that the sequence of run II resulted from initiation of translation at the second inframe AUG.

Fluorescence-Activated Cell Sorting Analysis of Human B₂ Receptor's Amino Terminus. Do native B₂ receptors on the surface of intact cells also start with the first potential methionine or is the amino terminus identified in protein sequencing proteolytically cleaved as a signal peptide? A signal peptide has been hypothesized for a variety of G protein-coupled receptors, e.g., the endothelin (Sakurai et al., 1990) or the Ca²⁺ sensing (Brown et al., 1993) receptor. We stained B₂ receptors of intact HF-15 cells by antibodies to ED1_A and to ED1_B and did fluorescence-activated cell sorting (FACS) analysis. Anti-ED1_A antibodies bound to human B₂ receptors on intact HF-15 cells (Figure 4A). Internalization and/or sequestration of B₂ receptors by a 40 min preincu-

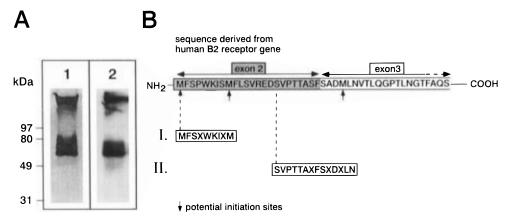


FIGURE 3: Amino acid sequence analysis of the human B_2 receptor. Human B_2 receptors of HF-15 cells were isolated by immunoaffinity chromatography. (A) Isolated proteins were separated by SDS-PAGE and visualized in silver staining (lane 1); enriched B2 receptors (10-20 fmol) were transferred to PVDF membranes and immunoblot was probed by anti-ED1_A antiserum (lane 2). (B) Amino acid sequence analysis of two different B_2 receptor preparations (I, II) and alignment of the sequences to the protein sequence translated from the B_2 receptor gene. The single-letter code for amino acids is used; X stands for unidentified residue.

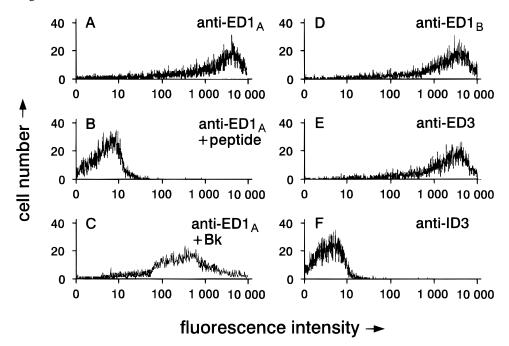
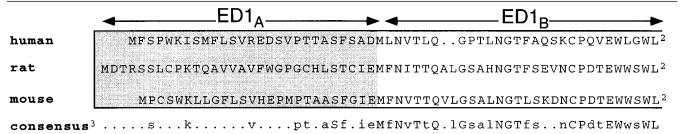


FIGURE 4: Fluorescence-activated cell sorting analysis of the B_2 receptor's amino terminus. Intact HF-15 cells containing about 1 pmol of B_2 receptor per mg of protein were labeled with affinity-purified antibodies to $ED1_A$ (A) and to $ED1_B$ (D). To internalize B_2 receptors, cells were pretreated with 1 μ M bradykinin at 37 °C for 40 min, cooled to 4 °C, and stained by anti- $ED1_A$ antibodies (C). As controls antiserum to $ED1_A$ preabsorbed on the cognate peptide (B) or antiserum to intracellular domain 3, ID3 (F) were used. Staining of HF-15 cells by antibodies to extracellular domain 3 (ED3) is presented (E) to compare fluorescence intensities between different domain-specific antibodies. The ordinate specifies the relative cell number and the abscissa gives the log of fluorescence intensity.

bation at 37 °C with 1 μ M bradykinin suppressed the staining of HF-15 cells by anti-ED1A antibodies (Figure 4C) confirming that anti-ED1_A antibodies specifically interact with native B₂ receptors on the surface of intact cells. Preabsorption of the antibodies on their cognate peptide abolished the staining of HF-15 cells (Figure 4B). Antibodies to ED1_B and to ED3 (AbdAlla et al., 1996) also bound to B₂ receptors of intact HF-15 cells (Figure 4D,E). The specific staining of B₂ receptors with anti-ED1_A, anti-ED1_B, or anti-ED3 antibodies was similar (cf. Figure 4A,D,E) indicating that equal amounts of B2 receptors are recognized by each antibody. Domainspecific antibodies to intracellular domain 3 (ID3) served as a negative control (Figure 4F). This experiment clearly demonstrates that extracellular domain 1A (ED1A) is accessible to antibodies on intact cells indicating that this receptor region is not a signal peptide but an additional receptor domain of 27 amino acids located on the extracellular side of the cell.

In Vitro Transcription/Translation. The third AUG triplet was assumed a preferred start site due to "Kozak-like" consensus nucleotides which would enable context-dependent leaky scanning (Kozak, 1995). We therefore asked whether the third methionine located on ED1_B closest to transmembrane domain 1 can act as start codon. To this end, we truncated the B₂ receptor cDNA thus that only the AUG closest to TM1 was available for translation initiation. We did *in vitro* transcription/translation and compared the product obtained with the truncated cDNA with a product of the full-length B₂ receptor cDNA. The ³⁵S-labeled proteins were separated by SDS-PAGE: The truncated cDNA was translated into a B₂ receptor of 35 kDa (Figure 5, lane 2); the full-length clone resulted in a single protein

Table 1: Sequence Comparison¹ of B2 Receptors' Amino-Terminal Domains Derived from Different Species



¹ The single letter code is used. ² Beginning of TM-1. ³ Identical residues between human, rat, and mouse (Yokoyama et al., 1994) sequences are indicated by uppercase letters, and identities between two of three species are given by lowercase letters.

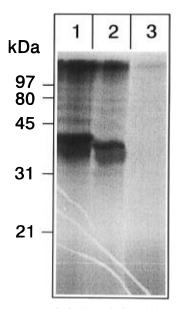


FIGURE 5: *In vitro* transcription/translation. The *in vitro* transcription/translation products of two different B₂ receptor cDNAs, which start three base pairs upstream of the first ATG in frame (lane 1) or with the third ATG in frame (lane 2) were labeled by [35S]methionine and separated by SDS-PAGE. The autoradiography of a 15% SDS-polyacrylamide gel is presented. As a control the pcDNA3 vector without insert (lane 3) was used.

band of 38 kDa (Figure 5, lane 1). For comparison, the calculated molecular mass of the additional 27 amino acids is 3.5 kDa. The major differences in the electrophoretic mobility of B_2 receptors expressed in HF-15 cells and of B_2 receptors expressed with the reticulocyte lysate (69 versus

38 kDa) points to the fact that the B₂ receptor protein on the surface of eucaryotic cells, similarly to other G protein-coupled receptors, is heavily glycosylated (AbdAlla et al., 1993). We conclude that the third methionine acts as the start site if the cDNA is truncated. With the full-length cDNA, translation starts with the first in-frame AUG (Figure 5, lane 1). Under the experimental conditions applied, there is no evidence for context-dependent leaky scanning, as suggested. The vector pcDNA3 without insert served as a negative control. It did not lead to a labeled polypeptide chain (Figure 5, lane 3).

The Amino Terminus of the Rat B_2 Receptor. We demonstrated that the amino terminus of the human B₂ receptor is derived from the first in-frame AUG triplet. We asked whether, in analogy to the human B₂ receptor, it is also the first in-frame AUG which is the start site of the rat B₂ receptor. Two cDNA sequences for a rat B₂ receptor have been published differing in the absence (McIntyre et al., 1993) or presence (McEachern et al., 1991) of the nucleotides derived from exon-3 of the rat B₂ gene. These two cDNAs are probably derived from two different splice variants of rat B₂ receptor mRNAs (Pesquero et al., 1994). We stably expressed full-length rat B2 receptor cDNA which contains the sequence derived from exon 3 (McEachern et al., 1991) in CHO cells. Recombinant rat B2 receptor expressed in these cells is functionally active and displays characteristics similar to those of a B₂ receptor in primary cells (Quitterer et al., 1995). Antibodies to ED1_B of the rat B₂ receptor sequence (AbdAlla et al., 1996) recognized a protein of 69 kDa in immunoblots (Figure 6A, lane 1). This protein was absent on mock-transfected cells indicating

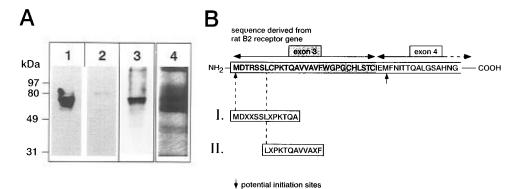


FIGURE 6: Rat B₂ receptor's amino terminus. (A) Immunoblot of rB2CHO12/3 cell membranes probed with anti-ED1_B antiserum (lane1). As a control, mock-transfected cells were applied (lane 2). For comparison, HOE140 was cross-linked to the rat B₂ receptor and detected by anti-HOE140 antiserum (lane 3). Silver staining of rat B₂ receptors isolated by immunoaffinity chromatography (lane 4). (B) Amino acid sequence analysis of two different B₂ receptor preparations (I, II) and alignment of the sequences to the protein sequence translated from the rat B₂ gene. The single-letter code for amino acids is used; X stands for unidentified residue.

specific staining of B₂ receptors (Figure 6A, lane 2). As an additional control, we cross-linked the B₂ antagonist HOE140 to rat B₂ receptors and detected the cross-linked receptor by anti-HOE140 antibodies. In the cross-linking experiment a protein of similar molecular weight was identified (Figure 6A, lane 3). To determine the rat B₂ receptor's amino terminus, we isolated B₂ receptors by affinity chromatography using a mixture of domain-specific antibodies. A major protein of 69 kDa was isolated (Figure 6A, lane 4), and additional protein bands may represent differentially glycosylated and/or aggregated B₂ receptors as was similarly observed for human B₂ receptors [cf. Figure 3A and AbdAlla et al. (1993)]. The amino-terminal sequence starts with a methionine corresponding to the first in-frame AUG (Figure 6B, I). In a second experiment a truncated B2 receptor lacking six amino acids was isolated (Figure 6B, II). Both experiments indicate that rat B₂ receptors expressed in CHO cells start with the first in-frame AUG. Thus additional 30 amino acids are added to the cloned sequence of the rat B₂ receptor protein (McEachern et al., 1991).

In analogy to the rat and human B₂ receptor, we postulate that for the mouse B₂ receptor it is also the first in-frame AUG that is used as start site for translation. We conclude that, in contrast to previous reports, the coding sequence of B₂ receptors from man, rat, and mouse is interrupted by an intron. Protein sequences encoded by different exons often constitute structural and functional entities (Go, 1981). Corresponding to the exon-intron boundaries of the B₂ receptor gene, we nominated the additional B2 receptor domain ED1_A. A sequence comparison of the aminoterminal ED1_A and ED1_B domains of the rat, human and mouse B2 receptor is given in Table 1. Compared to an overall sequence identity of more than 80% of the entire receptor sequences, the amino-terminal ED1_A domains of these three receptors share less than 20% sequence identity. It will be interesting to learn whether these major differences on the protein level of the B₂ receptors' amino termini are important for the observed differences in receptor function (Félétou et al., 1994) and/or ligand binding (Burch et al., 1993) of B₂ receptors derived from different species.

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REFERENCES

AbdAlla, S., Buschko, J., Quitterer, U., Maidhof, A., Haasemann, M., Breipohl, G., Knolle, J., & Müller-Esterl, W. (1993) *J. Biol. Chem.* 268, 17277–17285.

- AbdAlla, S., Quitterer, U., Grigoriev, S., Maidhof, A., Haasemann, M., Jarnagin, K., & Müller-Esterl, W. (1996) *J. Biol. Chem.* 271, 1748–1755.
- Bascands, J. L., Pecher, C., Rouaud, S., Emond, C., Tack, J. L., Bastie, M. J., Burch, R., Regoli, D., & Girolami, J. P. (1993) Am. J. Physiol. 264, F548-556.
- Bhoola, K. D., Figueroa, C. D., & Worthy, K. (1992) *Pharmacol. Rev.* 44, 1–79.
- Brown, E. M., Gamba, G., Riccardi, D., Lombardi, M., Butters, R., Kifor, O., Sun, A., Hediger, M. A., Lytton, J., & Hebert, S. C. (1993) *Nature 366*, 575–580.
- Burch, R. M., Kyle, D. J., & Storman, T. M. (1993) in *Molecular Biology and Pharmacology of Bradykinin B*₂ *Receptors*, pp 19–32, CRC Press, Boca Raton, FL.
- Félétou, M., Germain, M., Thurieau, C., Fauchère, J.-L., & Canet, E. (1994) *Br. J. Pharmacol.* 112, 683–689.
- Go, M. (1981) Nature 291, 90-92.
- Hess, J. F., Borkowski, J. A., Young, G. S., Strader, C. D., & Ransom, R. W. (1992) Biochem. Biophys. Res. Commun. 184, 260-268.
- Hick, S., Heidemann, I., Soskic, V., Müller-Esterl, W., & Godovac-Zimmermann (1995) Eur. J. Biochem. 234, 251–257.
- Jones, S., Brown, D. A., Milligan, G., Willer, E., Buckley, N. J., & Caulfield, M. P. (1995) Neuron 14, 399-405.
- Kyhse-Anderson, J. (1984) J. Biochem. Biophys. Methods 10, 203-209
- Kozak, M. (1989) J. Cell. Biol. 108, 229-241.
- Kozak, M. (1995) *Proc. Natl. Acad. Sci. U.S.A.* 92, 2662–2666. Laemmli, U. K. (1970) *Nature* 227, 680–685.
- Ma, J.-X., Wang, D.-Z., Ward, D. C., Chen, L., Dessai, T., Chao, J., & Chao, L. (1994 a) *Genomics* 23, 362–369.
- Ma, J.-X., Wang, D. Z. Chao, L., & Chao, J. (1994b) Gene 149, 283–288.
- McEachern, A. E., Shelton, E. R., Bhakta, S., Obernolte, R., Bach, C., Zuppan, P., Fujisaki, J., Aldrich, R. W., & Jarnagin, K. (1991) *Proc. Natl. Acad. Sci. U.S.A.* 88, 7724–7728.
- McIntyre, P., Phillips, E., Skidmore, E., Brown, M., & Webb, M. (1993) *Mol. Pharmacol.* 44, 346–355.
- Müller-Esterl, W., Iwanaga, S., & Nakanishi, S. (1986) *Trends Biochem. Sci.* 11, 336–339.
- Oppermann, M., Raedt, U., Hebell, T., Schmidt, B., Zimmermann, B., & Gotze, O. (1993) *J. Immunol.* 151, 3785–3794.
- Pesquero, J. B., Lindsey, C. J., Zeh, K., Paiva, A. C., Ganten, D., & Bader, M. (1994) *J. Biol. Chem.* 269, 26920–26925.
- Regoli, D., & Barabé, J. (1988) *Methods Enzymol.* 163, 210–230.
- Roscher, A. A., Manganiello, V. C., Jelsema, C. L., & Moss, J. (1983) *J. Clin. Invest.* 72, 626-635.
- Quitterer, U. Schröder, C., Müller-Esterl, W., & Rehm, H. (1995)
 J. Biol. Chem. 270, 1992–1999.
- Sakurai, T., Yanagisawa, M., Takuwa, Y., Miyazaki, H., Kimura, S., Goto, K., & Masaki, T. (1990) *Nature 348*, 732–735.
- Schertler, G. F., Villa, C., & Henderson, R. (1993) *Nature 362*, 770–772.
- Yokota, Y., Akazawa, C., Ohkubo, H., & Nakanishi, S. (1992) EMBO J. 11, 3585–3591.
- Yokoyama, S., Kimura, Y., Taketo, M., Black, J. A., Ransom, B. R., & Higashida, H. (1994) *Biochem. Biophys. Res. Commun.* 200, 634–641.

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