

Genomic Organization of Human $\beta 3$ Subunit Gene of Voltage-Gated Calcium Channel

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= Abstract =

Voltage-gated calcium channel (VGCC) is composed of at least four ($\alpha 1$, $\alpha 2$, β , and δ) subunits. Among them β subunit accelerates the kinetics of activation (channel opening) and inactivation (channel closure), and regulates the channel activity by phosphorylation through PKA and PKC that are activated by various signal transduction mechanisms. Until recently four isoforms of beta subunits ($\beta 1$, $\beta 2$, $\beta 3$, $\beta 4$) have been identified. Our recent data shows that VDCC $\beta 3$ gene is expressed only in the nervous system and around the perinatal stage at high level. Alternative splicing was also observed at both 5'- and 3'- ends. To elucidate alternative splicing and cis-acting element of gene regulation of the $\beta 3$ subunit gene we isolated a 12.5kb-sized genomic clone encompassing $\beta 3$ subunit gene from human genomic library using the whole $\beta 3$ subunit cDNA from NG108-15 cell line as a probe. The genome was analyzed by Southern hybridization and sequencing. The $\beta 3$ subunit gene consists at least of 12 exons, and deduced amino acid sequence from the exons showed 98% similarity with that of rat gene. The $\beta 3$ subunit gene is not alternatively spliced at the middle of the gene, and has many possible phosphorylation sites, which may confer the regulatory role of the $\beta 3$ subunit gene.

KEY WORDS : Calcium channel · Human genome.

Introduction

Calcium ion in eukaryotes acts as a second messenger molecule like cAMP, inositol triphosphate, and diacylglycerol. Total intracellular concentration is regulated around $2\mu\text{M}$ in most nonexcitable cells but free calcium concentration is maintained around 0.05% of total calcium concentration, $0.1\mu\text{M}$, and minute change of free calcium ion mediates various phenomena. Entry of calcium ions into cells through voltage-gated calcium channels (VGCC) mediates a wide variety of physiological functions, including linking electri-

cal activity to neurotransmitter release, excitation-contraction coupling, and control of neuronal firing patterns¹⁾.

Traditionally VDCC was grouped into two major categories according to their voltage-dependent properties for activation of channels²⁾. Opening of low voltage-activated (LVA) calcium channels is triggered by small depolarizations under membrane holding potentials. Their function in vivo is supposed to be pacemakers, repetitive bursting. High-voltage activated (HVA) calcium channel can be open upon depolarization to relatively high potentials, and display diverse drug, toxin-binding and kinetic properties.

These channels are classified into L-, N-, and P-type channels based on their electrophysiological and pharmacological properties.^{2,3,4,5,6,7,8}

Molecular properties of L-type calcium channel were well known because this type of channel is rich at neuromuscular junctions, and has specific drug binding sites⁹. Biochemical studies show that skeletal dihydropyridine(DHP)-sensitive L-type VGCC is composed of five distinct subunits($\alpha 1$, $\alpha 2$, β , γ , and δ)^{2,3,10}. The $\alpha 1$ subunit of the calcium channel complex, which contain the binding sites for DHP, phenylalkylamine, and benzothazepine, can direct expression of functional calcium channels in *Xenopus oocyte*^{11,12,13}. Coinjection of skeletal muscle $\alpha 2$ - δ and β subunit mRNAs with the $\alpha 1$ subunit mRNA, however, drastically changed electrophysiological characteristics of the expressed calcium channels^{2,14}. These findings suggest that $\alpha 2$ - δ and/or β subunits of the calcium channel may play a modulatory role in regulating calcium channel function.

Beta subunit is a cytoplasmic protein and accelerates the kinetics of activation(channel opening) and inactivation(channel closure)^{14,15}, and regulates the channel activity by phosphorylation through PKA and PKC that are activated by various signal transduction mechanisms^{16,17,18}. Multiple possible phosphorylation sites were shown by cloning of β subunits from various sources. Four isoforms of beta subunits($\beta 1$, $\beta 2$, $\beta 3$, $\beta 4$) are known^{14,17,18,19,20,21}. Our recent data shows that VGCC $\beta 3$ subunit gene is expressed only in the nervous system, and alternative splicing was also observed at both 5'- and 3'- ends. To elucidate the spacial and temporal specificity of the $\beta 3$ subunit gene we isolated $\beta 3$ subunit genomic DNA from human genomic library and characterized.

Materials and Methods

1. Cloning of voltage-gated calcium channel $\beta 3$ subunit gene from human genomic library

Voltage-gated calcium channel $\beta 3$ subunit gene was isolated from human genomic DNA library (Stratagene 944201, W138 cell line from human lung fibroblast) using NG51 cDNA which has full coding

region of VDCC 3 subunit. About 7.0×10^5 plaques were screened with the cDNA probe which was labelled with ^{32}P -dCTP using random priming. The plaques were transferred onto nitrocellulose paper, immobilized, and hybridized with hybridization solution containing ^{32}P -dCTP labeled cDNA probe. The membrane was washed with $0.2 \times \text{SSC}/0.1\%$ SDS for 10 min three times at RT, followed by at 65°C for 10 min three times. The signal was visualized by exposure onto X-OMAT film overnight. The positive plaques were picked, and second screening performed as above. The resulting four plaques were cultured and their phage DNAs were isolated. Among them only one plaque, BHGx was positive for oligonucleotide from 5'-end of NG51 cDNA. The BHGx was digested with Sac I, and transferred onto Nylon membrane and Southern blot analysis was carried out with NG51 cDNA as a probe. The fragments positive for the probe was subcloned into pGEM 7zf(+), and their sequences were analyzed.

2. Sequencing

The Sac I fragments of the genomic DNA were subcloned into pGEM 7zf(+) vector. Basically the deletion mutants were prepared by manufacturer's manual(Promega). To get deletion mutants the restriction enzymes maps were made. The 5'-/3'-overhang DNA were made and digested with Exo III nuclease followed by S1 nuclease. The unidirectional deletion DNA was ligated and transformation was carried out. Resulting plasmids DNA from the deletion clones were prepared by Wizard miniprep kit(Promega). The sequencing template DNA was prepared by alkali denaturation-neutralization of the double-stranded plasmid. The sequencing was carried out by using the dideoxy-termination method of Sanger, the Sequenase v.2.0 (Amersham).

3. Data analysis

The sequencing data from the deletion mutants were assembled by using the Asseblign program from IBI Co. Exon sequences were analyzed by comparing the genomic DNA sequences with cDNA sequence from NG51 cell lines. The exon sequence was translated into amino acid sequence, and the possible phos-

phorylation and other motifs were analyzed using MacVector program (IBI)

Results

Calcium channel genomic DNA was isolated from genomic library of W138 cell line from human lung fibroblast (Stratagene 944201) which was cloned into λ Fix bacteriophage vector. The genomic DNA of $\beta 3$ subunit gene of VGCC was isolated by high stringency screening of the genomic library with NG51 cDNA, which encompasses whole coding region of $\beta 3$ subunit of VGCC. A phage clone, BHG, with 12.5kb-sized insert was isolated. The insert consists of 4 Sac I fragments, 5.8, 4.5, 1.3, and 0.8kb. Among them 5.8kb fragment was the most strong positive and 1.1kb

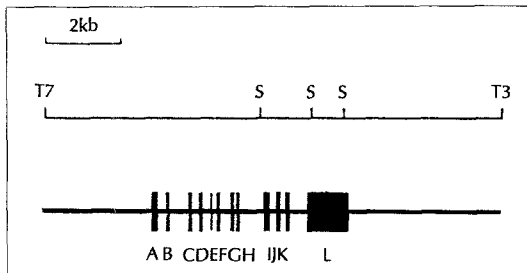


Fig. 1. Organization of the voltage-gated calcium channel $\beta 3$ subunit gene.

As indicated, the VGCC $\beta 3$ subunit gene consists of at least 12 exons from A to L in 12.5 kilobases. S denotes Sac I enzymes and T7/T3 indicates the promoter site in the λ Fix cloning vector. Closed rectangles in lower figure represent exons. The exon-intron junction sequences are depicted in Table 1.

fragment was positive for Southern hybridization using NG51 cDNA as a probe. All of above fragments were sequenced using the Exo III deletion kit from Progega. The sequencing data from deletion mutants were analyzed by using MacVector and Assemblign sequencing program.

The analyzed result disclosed that the genomic clone, BHG, has 12 exons from A to L as shown on Fig. 1. The order of Sac I fragment from 5' to 3' direction is 5.8kb, 1.3kb, 0.8kb, and 4.5kb. 5.8kb Sac I fragment has 8 exons, and 1.3kb Sac I fragment has 4 exons. The genomic clones do not have full cDNA sequences. The first exon observed started at 2864th bp which encodes the 16th amino acid of $\beta 3$ subunit gene. The 12th exon has termination codon.

The exon-intron junction of $\beta 3$ subunit gene of VGCC was shown on Table 1. All introns began with 'gt' and ended with 'ag'. The codon phases were variable, from the first to third base of codon. The nucleotide sequence spliced from the exons is shown at Fig. 2 and the number of the nucleotide is 1410. The double asterisks indicates the spliced junctions of the exons.

The nucleotide sequences from the exons were translated into amino acid sequences (Fig. 3). Deduced amino acid sequences of human $\beta 3$ subunit of VGCC was compared with that of rat, which showed the 98% similarity, but it is less similar to $\beta 1$ or $\beta 2$ subunit of VGCC as 75% and 78% respectively (data not shown). The computer analysis of the amino acid sequence of the $\beta 3$ subunit reveals that $\beta 3$ subunit does not have

Table 1. Exon-intron junction sequences

A	cccaaccag	GGTTCAGCCG	AGGGCCAAGG	gtatacttc
B	aattctccag	CACAAACCTG	CATTAAGAG	gtgatcgacc
C	cctggctgg	GCATCAGTCT	CATGTCTGTC	gaagtgagca
D	ctgccccag	AAGTACAGCA	AGAAGGCCAG	gtgagagttg
E	ttcttctcag	GAGATCTGGG	CCATCTCTAG	gtagcctccc
F	ttcaaaaag	CCAAGCAGAA	GCAAAAGCAG	gtgagtcaag
G	cattctgcag	GCGGAACATG	AGGTTATGAG	gtgagaggag
H	cttccccag	GTACAGACA	TTGATGGCAG	gtaagctgcc
I	cccaccag	GATCTCCATC	TCCAGCATTG	gtgagaagtc
J	ccctccgtag	CGGAAGTGCA	CTACCAAAG	gtaagtgcag
K	ccccgctcag	GTA CTCCAGC	GTGCCCACCG	gtgagtgctt
L	ccctccccag	GAGTCATTG	CGGACTTCAG	gtaaccattt
M	tggccccag	AACCAGCAGC		

GGTTCAGCCGGCTCTACACCAGCCGCCA	TCTCTGGACTCAGCGTCTCCCTGGAGGAG	GACCCGGGAGAGTCCCGCGGTGAAGTAGAG	90
AGCCAGGCTCAGCAGCAGCTCGAAAGGGCC	AAGCACAACCTGTGGCATTGCGGTGAGG	ACCAATGTCAGCTACTGTGGCCTACTGGAT	180
GAGGAGTGCCCACTCCAGGNCCTGGAGTC	AACCTTGAGGCCAAAGATTTCTGCACATT	AAAGAGAAAGTACAGCAATGACTGGTGGATC	270
GGGCGGTAGTGAAGAGGGCGGGGACATC	GCCTTCATCCCCAGCCCCAGCCCTGGAG	AGCATCCGGCTCAACAGGAGCAGAAGGCC	360
AGGAGATCTGGGAACCTTCCAGCCTGAGT	GACATTGGCAACCGACGCTCCCTCCGCCA	TCTCTAAGCAAGCAGAAGCAAAAGCAGGCG	450
GAACATGTTCCCCATATGACGTGGTGCCC	TCCATGCGGCCTGTGGTCTGGTGGGACCC	TCTCTGAAAGTTATGAGGTCACAGACATG	540
ATGCAGAAGGCTTTCTCGACTTCTCAAA	CACAGATTGATGGCAGGATCTCCATCACC	CGAGTCACAGCCAGCCTCTCCCTGGCAAAG	630
CGATCTGTCTCAACAATCCGGCAAGAGG	ACCATCATTGAGCGCTCCTCTGCCCGTCC	AGCATTGCGGAAGTGTGAGTGAGATCGAG	720
CGCATATTTGAGCTGGCCAAATCCCTGCAG	CTAGTAGTTGGACGCTGACACCATCAAC	CACCCAGCAGCTCGCCAAGACCTCGTGTG	810
GCCCCATCATCGTCTTTGTCAAAGTGTC	TCACCAAAGGTA [▽] CTCCAGCGTCTCAITTCG	TCCCCGGGGAAGTCAGAGAAGCACCTG	900
GCCGTACAGATGATGGCATATGATAAGCTG	GTTCAGTGGCCACC [▽] GAGTCATTGATGTA	ATTCTGGATGAGAACCAGCTGGAGGATGCC	990
TGTGAGCACCTGGTGAGTACCTGGAGGTT	TACTGGCGGCCACGCACCACCCAGCCCT	GGCCCCGGAHCTTCTGGTCTCCCATGTGCC	1080
ATCCCCGGACTTCAGA [▽] ACCAGCAGCTGCTG	GGGGAGCGTGGCAGGAGCACTCCCCCTT	GAGCGGGACAGCTGTATGCCTCTGATGAG	1170
GCCAGC [▽] NNAGCTCCCGCCAAGCCTGGACA	GGATCTCACAGCGTACGTC [▽] CCGCCACCTG	GAGGAGhGACTATGCAGATGCCTACCAGGAC	1260
CTGTACCAGCCTCACCGCCAACACACCTCG	GGGCTGCCTAGTGTAACGGGCATGACCCC	CAAGACCGGCTTCTAGCCCAGGACTCAGAA	1350
CACAACCACAGTGACCGGA [▽] ACTGGCAGCGC	AACCGGCTTGGCCAAAGGATAGCTACTGA		1410

Fig. 2. Nucleotide sequence of VGCC β 3 subunit gene spliced from exons.

	1					51					100
b3h	MYDSSYVPGF	GSAGS	YTSRPSLDS	VSLEEDRESA	RREVESQAQQ	QLERAKHKPV	AFAVRTNVS	CGVLDEECPV	QGPVFEAK	DFLHIKEKYS	
beta3	MYDSSYVPGF	EDSEAGSAdS	YTSRPSLDS	VSLEEDRESA	RREVESQAQQ	QLERAKHKPV	AFAVRTNVS	CGVLDEECPV	QGPVFEAK	DFLHIKEKYS	
	101					151					200
b3h	NDWWIGRLVK	EGGDIAFIPS	PQRLESIRLK	QEQRARRSGN	PSSLSDIGNR	RSPPSLAKQ	KQKQAEHVPP	YDVVPSMRPV	VLVGP [□] SLKGY	EVTDM [□] MQAF	
beta3	NDWWIGRLVK	EGGDIAFIPS	PQRLESIRLK	QEQRARRSGN	PSSLSDIGNR	RSPPSLAKQ	KQKQAEHVPP	YDVVPSMRPV	VLVGP [□] SLKGY	EVTDM [□] MQAF	
	202					251					300
b3h	FDFLKH [□] RFDC	RISITRV [□] TAD	LSLAKRSVLN	NPGKRTI [■] IER	SSARSSIAEV	LSEIERIFEL	AKSLQLV [□] LD	ADTTNHPAQL	AKTSLAPI [□] IV	FVKVSS [□] PKVL	
beta3	FDFLKH [□] RFDC	RISITRV [□] TAD	LSLAKRSVLN	NPGKRTI [■] IER	SSARSSIAEV	LSEIERIFEL	AKSLQLV [□] LD	ADTTNHPAQL	AKTSLAPI [□] IV	FVKVSS [□] PKVL	
	301					351					400
b3h	QRLIRSRGKS	QMHLAV [□] QM	AYDKLVQ [□] CP	ESFDVILDEN	QLEDACEHLA	EYLEVYWRAT	HHPAPG [□] PGLL	GPPSAIPGLQ	NQQLGERGE	EHSPLERDSL	
beta3	QRLIRSRGKS	QMHLAV [□] QM	AYDKLVQ [□] CP	ESFDVILDEN	QLEDACEHLA	EYLEVYWRAT	HHPAPG [□] PGLL	GPPSAIPGLQ	NQQLGERGE	EHSPLERDSL	
	401					451		484			
b3h	MPSDEASESS	RQAWIGSSQR	TSRHLEEDAY	DAYQDLYQPH	RQHTSGLPSA	AQDSEHNHSD	R [□] NWQRNRPWP	KDSY			
beta3	MPSDEASESS	RQAWIGSSQR	TSRHLEEDAY	DAYQDLYQPH	RQHTSGLPSA	AQDSEHNHSD	R [□] NWQRNRPWP	KDSY			

Fig. 3. Deuced amino acid sequences of huamn VGCC β 3 subunit gene.

Alignment of deduced amino acid sequences of huamn VGCC β 3 subunit gene and rat β 3 gene. The human β 3 sequence is obtained by translation of sequence spliced together from exons. Identical sequences were shown as capital letter and nonidentical sequences were shown as lower cases. The conserved potential sites for phosphorylation are indicated with the following symbols : protein kinase C(\square), casein kinase II(\blacksquare). Underline shows the predicted a helices deduced from hydropathy profile(not shown).

typical membrane-spanning region and contains three major α helical domains. The $\beta 3$ subunit of VGCC has many possible phosphorylation sites. Potential protein kinase C(Ser/Thr-X-Lys/Arg) sites were found at 4 locations and 4 possible casein kinase II sites(Ser/Thr-X-X-Asp/Glu) were observed. No consensus site for cAMP-dependent protein kinase was found in $\beta 3$ subunit gene.

Discussion

The first exon of the genomic DNA clone, BHG, as shown at Table 1. is GGTTCA---GCCAAG, from which other exon could not be found reaching 2.85kb upstream. The size of intron in the BHG genome ranges from 118 bp(between exon J and K) to 597 bp(between H and I). Deduced amino acid sequence of $\beta 3$ subunit gene from the exons starts with GSAD--, 16th amino acid of $\beta 3$ subunit protein¹⁸⁾¹⁹⁾²⁰⁾. The other effort should be done to find the exons encoding 5'-end of the $\beta 3$ subunit gene, where 3 alternatively spliced forms of $\beta 3$ subunit gene from rat were observed(unpublished data).

The deduced amino acid sequence from the exons has high degree of similarity with that of rat gene²⁰⁾ and identical to that of the human $\beta 3$ cDNA²²⁾. Alternatively spliced forms of $\beta 1$, $\beta 2$ subunit gene, which contribute to the functional diversity of the VGCC, were reported²³⁾. The genomic clones so far we have cloned does not have the exons which could be alternatively spliced in the middle of the gene as $\beta 1$ subunit²³⁾²⁴⁾.

The $\beta 3$ subunit protein is supposed to have theoretical 3 major α -helical domains. The $\beta 1$ subunit protein was known to have 4 α -helical domains, and first two α -domains was proposed to be a binding domain to the $\alpha 1$ subunit of skeletal muscle type VGCC²⁵⁾. Missing the second α -helical domain in the $\beta 3$ subunit might contribute to the different binding patterns with various $\alpha 1$ subunits.

Calcium currents through the cardiac and skeletal muscular VGCC are modulated by phosphorylation mediated by several protein kinases, protein kinase C, cAMP-dependent protein kinase, etc¹⁶⁾¹⁸⁾¹⁹⁾. Although

it has been demonstrated that preferred substrate for protein kinases are the $\alpha 1$ subunits, β subunits have several potential phosphorylation sites²¹⁾⁸⁾¹⁹⁾. Among them possible phosphorylation sites for protein kinase C were the most abundant, but possible phosphorylation sites for cAMP-dependent kinase and cGMP-dependent kinase could not be found. These suggest that phosphorylation through the activation of the protein kinase C system might be important regulatory machinery in calcium signalling.

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Genomic Organization of Human $\beta 3$ Subunit Gene of Voltage-Gated Calcium Channel

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전압의존성 칼슘이온통로는 $\alpha 1$, $\alpha 2$, β , 및 δ 등 적어도 네 개 이상의 아단위로 구성되어 있다. 이중 β 아단위는 칼슘채널의 활성화(Activation; 이온통로의 열림) 및 비활성화(Inactivation; 이온통로의 닫힘)를 크게 강화시키며, 또한 여러 신호전달 체계를 통해 활성화된 PKA 혹은 PKC 등에 의해 인산화됨으로서 칼슘채널의 활성도를 조절한다. β 아단위는 여지껏 $\beta 1$, $\beta 2$, $\beta 3$, $\beta 4$ 의 네가지 아형이 알려져 있는데 이중 $\beta 3$ 형이 신경계에 특이적으로 발현되며 칼슘채널을 조절하는 $\beta 3$ 형 칼슘채널의 유전자조절을 알아보고자 게놈수준에서 조사하였다. $\beta 3$ 형 게놈 유전자는 사람 폐에서 유래한 섬유아세포의 게놈으로부터 만든 유전자은행으로부터 NG108-15세포주에서 분리한 $\beta 3$ 형 cDNA를 탐색자로 이용하여 분리하였다. 이 게놈 DNA의 크기는 12.5kb였으며 12개의 exon을 포함하며, 이 유전자 단백질의 16번째 아미노산으로부터 끝 아미노산까지를 포함하고 있으며 흰쥐 cDNA 유전자에서 밝힌 아미노산 서열과 비교하면 98% 동일하였다. Exon들로부터 유추한 아미노산서열에는 인산화될 수 있는 많은 아미노산들이 발견되어 이 전압의존성 칼슘이온통로의 $\beta 3$ 아단위 유전자가 칼슘이온의 흐름조절에 중요함을 알 수 있다.