

Published in final edited form as:

*Mol Biol Rep.* 2014 April ; 41(4): 2067–2076. doi:10.1007/s11033-014-3055-3.

## **$\beta$ 3-Chimaerin, a novel member of the chimaerin Rac-GAP family**

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## **Abstract**

Chimaerins are a family of diacylglycerol- and phorbol ester-regulated GTPase activating proteins (GAPs) for the small G-protein Rac. Extensive evidence indicates that these proteins play important roles in development, axon guidance, metabolism, cell motility, and T cell activation. Four isoforms have been reported to-date, which are products of CHN1 ( $\alpha$ 1- and  $\alpha$ 2-chimaerins) and CHN2 ( $\beta$ 1- and  $\beta$ 2-chimaerins) genes. Although these gene products are assumed to be generated by alternative splicing, bioinformatics analysis of the CHN2 gene revealed that  $\beta$ 1- and  $\beta$ 2-chimaerins are the products of alternative transcription start sites (TSSs) in different promoter regions. Furthermore, we found an additional TSS in CHN2 gene that leads to a novel product, which we named  $\beta$ 3-chimaerin. Expression profile analysis revealed predominantly low levels for the  $\beta$ 3-chimaerin transcript, with higher expression levels in epididymis, plasma blood leucocytes, spleen, thymus, as well as various areas of the brain. In addition to the prototypical SH2, C1, and Rac-GAP domains,  $\beta$ 3-chimaerin has a unique N-terminal domain. Studies in cells established that  $\beta$ 3-chimaerin has Rac-GAP activity and is responsive to phorbol esters. The enhanced responsiveness of  $\beta$ 3-chimaerin for phorbol ester-induced translocation relative to  $\beta$ 2-chimaerin suggests differential ligand accessibility to the C1 domain.

## Keywords

Chimaerin; CHN2; Rac-GAP; C1 domain; Phorbol esters

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## Introduction

Rac, a small GTPase that belongs to the Rho family, controls numerous cellular functions, including actin cytoskeleton reorganization, motility, and cell cycle progression. Rac activation status is controlled primarily by guanine nucleotide exchange factors (GEFs) that promote GTP loading and thereby activate Rac, and by GTPase activating proteins (GAPs) that inactivate Rac by accelerating GTP hydrolysis. Among the several Rac-GAP families, chimaerins represent a unique class due to their direct regulation by diacylglycerol (DAG), a lipid second messenger that binds to the C1 domain in chimaerins which is highly homologous to C1 domains in protein kinase C (PKC) isozymes. It has been widely recognized that chimaerins play important roles in development, axon guidance, cell migration, and T-cell activation [1-4]. Early studies determined the existence of four chimaerin isoforms ( $\alpha 1$ ,  $\alpha 2$ ,  $\beta 1$ , and  $\beta 2$ ), reported to be alternative splicing products of the CHN1 ( $\alpha$ ) and CHN2 ( $\beta$ ) genes [5-8].

In addition to the C1 domain, all chimaerin isoforms have a C-terminal catalytic Rac-GAP domain. An SH2 domain in the N-terminal region of  $\alpha 2$ - and  $\beta 2$ -chimaerins is possibly involved in interactions with phosphotyrosine proteins, but its function remains essentially unknown. Binding of DAG or DAG mimetics (such as phorbol esters) to the C1 domain leads to allosteric activation of the protein which, in response to various stimuli, results in deactivation of the Rac GTPase [9-11]. The crystal structure of  $\beta 2$ -chimaerin revealed that the protein is in an autoinhibited state. The N-terminal region of the protein forms a 33 amino acid alpha-helix that rests against the lipid binding site in the C1 domain and occludes the Rac interaction surface in the GAP domain [12]. We have previously identified residues in  $\alpha 2$ - and  $\beta 2$ -chimaerins involved in intramolecular hydrophobic interactions that keep the protein in a “closed” conformation. When these residues are mutated, the protein becomes more sensitive to lipid and phorbol ester-induced activation [10, 12]. The fact that chimaerins activity and localization are controlled by different mechanisms as protein-protein or lipid-protein interaction, and phosphorylation [13, 14] strongly suggests that these Rac-GAPs are subject to complex regulatory mechanisms.

It is well established that many eukaryotic genes possess alternative promoters regulating distinct expression patterns, probably because one single transcription start site (TSS) or regulatory region may not always be sufficient to accommodate all the required gene expression regulations (e.g. different tissues, different stages of development). Although alternative TSSs have been reported for many genes, this phenomenon still remains poorly understood. A recent report shows that more than 40 % of developmentally expressed genes in *Drosophila melanogaster* have at least two alternative promoters generally involved in distinct regulatory programs [15]. The usage of alternative promoters could generate protein variants, differentially regulated 5' UTRs, or a combination of both. In yeast, the 5' UTR in mRNAs can regulate translation efficiency, and this accounts for large changes in protein expression levels [16]. Regulation of mRNA localization and transport could also depend on 5' UTR sequences. At the present time there is no information on whether  $\beta$ -chimaerin isoforms could be generated as a consequence of alternative transcription mechanisms. Here we carried out a thorough analysis of the CHN2 gene, which led us to the identification of a novel  $\beta$ -chimaerin isoform,  $\beta 3$ -chimaerin, that is the product of an alternative TSS in the CHN2 gene.

## Methods

### Materials

Cell culture reagents were obtained from Invitrogen (Carlsbad, CA). Reagents for the expression and purification of recombinant glutathione S-transferase (GST) fusion proteins and Gammabind G-Sepharose were purchased from Amersham Biosciences, Inc. (Sunnyvale, CA). Phorbol 12-myristate 13-acetate (PMA) and GF109203X were purchased from LC Laboratories (Woburn, MA).

### Cloning of $\beta$ 3-chimaerin and plasmids

$\beta$ 3-Chimaerin was amplified by PCR using commercial cDNA from human brain and kidney (PrimerDesign, Southampton, UK) and a Labnet MultiGene™ 96-well gradient thermal cycler. As primers we used 5'-ctcggaggatccatgaccagaccacagg (sense) and 5'-acgcgtgcccggcggattagaataaaacgtcttcg (antisense) (Fig. 1c). The same primers were used to clone the entire  $\beta$ 3-chimaerin cDNA from A-172 and U-373 human cell lines.

PCR products were ligated into pCRII using the TA cloning kit (Invitrogen) or pCR2.1-TOPO using the TOPO TA cloning kit (Invitrogen). *EcoRI*–*Bam*HI or *Bam*HI–*Bam*HI fragments were isolated from these plasmids and subcloned into pEGFP-C3 or pEGFP-C1. All constructs were verified by sequencing.

### Cell culture and transfections

Cell culture reagents were obtained from Invitrogen (Carlsbad, CA). COS-1 cells were cultured in Dulbecco's modified Eagle's medium supplemented with 10 % FBS, 100 U/ml penicillin, and 100  $\mu$ g/ml streptomycin in a humidified 5 % CO<sub>2</sub> atmosphere at 37 °C. Cells in 6-well plates at 50 % confluence were transfected with different mammalian expression vectors (1–2  $\mu$ g) using polyethylenimine (CELLnTEC, Bern, Switzerland) according to the manufacturer's protocol.

### Determination of Rac-GTP levels

Rac-GTP levels were determined using a pull-down assay, as previously reported [17]. Briefly, cells were lysed in a buffer containing 8  $\mu$ g of GST-PBD domain, 20 mM Tris–HCl, pH 7.5, 1 mM dithiothreitol, 5 mM MgCl<sub>2</sub>, 150 mM NaCl, 0.5 % Nonidet P-40, 5 mM glycerophosphate, and protease inhibitors (5  $\mu$ g/ml 4-(2-aminoethyl) benzenesulfonyl fluoride, 5  $\mu$ g/ml leupeptin, 5  $\mu$ g/ml aprotinin and 1  $\mu$ g/ml pepstatin A). Lysates were centrifuged at 14,000 $\times$ g (4 °C, 10 min) and then incubated with glutathione-Sepharose 4B beads (4 °C, 1 h). After extensive washing, the beads were boiled in loading buffer. Samples were resolved in 12 % SDS-polyacrylamide gels and transferred to PVDF membranes for Western blot analysis using an anti-Rac1 antibody (Upstate Biotechnology, Lake Placid, NY).

### Translocation assays

Experiments were carried out as previously described [18]. Briefly, COS-1 cells ( $2 \times 10^5$ ) in six-well plates were transfected with pEGFP- $\beta$ 2-chimaerin or pEGFP- $\beta$ 3-chimaerin. After 24 h, cells were treated with different concentrations of PMA for 20 min. To avoid PKC activation by PMA, experiments were performed in the presence of the PKC inhibitor GF109203X (5  $\mu$ M), added 30 min before and during PMA stimulation. For fractionation assays, cells were harvested into lysis buffer (20 mM Tris–HCl, pH 7.5, 5 mM EGTA, and protease inhibitor cocktail for mammalian cell and tissue extract, 1:500, Sigma). Separation of cytosolic (soluble) and particulate fractions was performed by ultracentrifugation [19]. Equal amounts of protein were subjected to SDS-polyacrylamide gel electrophoresis,

transferred to PVDF membranes, and immunostained with an anti-GFP antibody (Santa Cruz Biotechnology, Dallas, TX). For fluorescence microscopy visualization, cells were washed with cold PBS, immediately fixed in 4 % PFA and visualized in a Olympus IX71 fluorescence microscope.

### Tissue arrays

96-Well TissueScan Human Major Tissue qPCR Array (HMRT102) and the TissueScan Human Brain Tissue qPCR Array (HBRT101) from OriGene (Rockville, MD) were used. Primers for  $\beta$ 3-chimaerin were as follows: 5'-cattcaggactacttgcaagccca (sense) and 5'-tcttcagcatcgctagt gcagc (antisense) (Fig. 1c). PCR was performed using the qSTAR SYBR Master Mix kit (OriGene) and an ABI Prism 7300 thermocycler.

## Results

### Identification of $\beta$ 3-chimaerin

Mammalian  $\beta$ 1- and  $\beta$ 2-chimaerins have been previously identified as important regulators of the small GTPase Rac. To investigate whether other products of the CHN2 gene might exist, we carried out a screening of EST databases. This led to the identification of a third gene product, which we named  $\beta$ 3-chimaerin.  $\beta$ 3-Chimaerin was cloned using a PCR approach from two different commercial human cDNAs samples (total brain and kidney) as templates. The PCR products were sequenced, and the full-length  $\beta$ 3-chimaerin sequence (Fig. 1a) was reported to GeneBank (accession ADK47390.1). The  $\beta$ 3-chimaerin cDNA was also cloned from A-172 cells (a human glioblastoma cell line) and U-373 cells (a cell line derived from human astrocytoma) (data not shown).

Sequence analysis revealed that  $\beta$ 3-chimaerin has a novel N-terminal domain that is encoded by two unique exons located 48 kb upstream from the  $\beta$ 2-chimaerin open reading frame (Fig. 1b). Comparison of protein sequences from  $\beta$ 1-chimaerin (NP\_001035025.1),  $\beta$ 2-chimaerin (NP\_004058.1) and  $\beta$ 3-chimaerin isoforms revealed in all cases unique N-terminal regions.  $\beta$ 1-chimaerin, an isoform only found in testis [5], is the product of an alternative TSS located on intron 6, ~250 kb downstream of the  $\beta$ 2-chimaerin TSS. This isoform lacks the SH2 domain and N-terminal  $\alpha$ -helix present in  $\beta$ 2-chimaerin, which are coded by a cluster of exons 160 kb downstream from the first exon and 80 kb upstream of the  $\beta$ 1-chimaerin TSS. On the other hand,  $\beta$ 3-chimaerin N-terminal region lacks key residues involved in autoinhibition of  $\beta$ 2-chimaerin GAP activity, as also reported for  $\beta$ 1-chimaerin [12], but maintains both SH2 domain and  $\alpha$ -helix. The Rac-GAP and C1 domains are encoded by a cluster of exons common to all  $\beta$ -chimaerins. The unique N-terminal region in  $\beta$ 3-chimaerin, coded by two exons exclusive of primates, is 91 amino acids long and does not share any sequence identity with other known proteins.

As indicated above, the unique N-terminal domain in  $\beta$ 3-chimaerin is encoded by two exons (1a and 2a) located 48 kb upstream from the  $\beta$ 2-chimaerin open reading frame, which are followed by exon 2b. Canonical donor sequence of exon 2a binds to the first available acceptor sequence that corresponds with exon 2b. The absence of the canonical acceptor sequence in exon 1b explains why this exon is excluded in  $\beta$ 3-chimaerin or other transcripts similar to  $\beta$ 3-chimaerin (ENSMBL transcript id: ENST00000539406, ENST00000474070; ENS00000439384). Therefore,  $\beta$ 2- and  $\beta$ 3-chimaerin cannot be alternative splicing products of the CHN2 gene, supporting the idea that alternate TSSs are responsible for the control of  $\beta$ 2-chimaerin and  $\beta$ 3-chimaerin expression.

As described previously [5], the testis-specific  $\beta$ 1-chimaerin isoform is the product of an alternative TSS located on intron 6. As shown in Fig. 1b, exon 7b is used as the first exon in  $\beta$ 1-chimaerin transcription. This is the seventh exon in  $\beta$ 2-chimaerin as a result of a

canonical splicing process due to an acceptor sequence located inside the exon which generates a shorter exon (exon 7a) (Fig. 1b) [20]. FirstEF software localized a non-CpG related promoter region 479 bp upstream of the exon 7b start site where a CCAAT box is localized. This CCAAT box in  $\beta$ 1-chimaerin is similar to the GGCCAATC box located at nucleotides -519 to -512 in  $\alpha$ 1-chimaerin. Point-mutation experiments revealed that this sequence is essential for  $\alpha$ 1-chimaerin expression, and its presence in  $\beta$ 1-chimaerin suggests that a similar mechanism to  $\alpha$ 1-chimaerin may control  $\beta$ 1-chimaerin transcription [20].

### Analysis of the CHN2 gene promoters

Although never formally proven,  $\beta$ 1- and  $\beta$ 2-chimaerins were proposed to be alternative splicing products of the CHN2 gene in chromosome 7 [5, 6, 8]. However, when we carried out bioinformatics analysis of mRNA, ESTs and genomic sequences available in public databases, we found that these  $\beta$ -chimaerin isoforms are products of alternate TSSs regulated by different promoter regions. Sequence comparison between  $\beta$ 1-chimaerin (NM\_001039936.1) and  $\beta$ 2-chimaerin (NM\_004067.2) mRNAs, revealed unique 5' untranslated regions (UTRs). Alternative TSSs are common features in protein-coding genes and frequently generate alternative N termini [21]. Alternative TSSs usually require distinct promoters that allow RNA polymerase to bind and initiate polymerization of ribonucleotides according to their regulation [21-24].

In order to determine if  $\beta$ 3-chimaerin is also a product of a new alternative TSS controlled by a new promoter, we used the encyclopedia of DNA Elements (ENCODE) to identify putative promoter regions flanking the  $\beta$ 2- and  $\beta$ 3-chimaerin TSSs. This analysis indicated that  $\beta$ 2- and  $\beta$ 3-chimaerins are the product of alternative TSSs rather than alternative splicing products. As shown in Fig. 2a (track 5), promoter prediction software FirstEF revealed a CpG-related promoter in the 5' UTR region of both  $\beta$ 2- and  $\beta$ 3-chimaerins [25]. We also found that both regions showed enrichment for enhancer- and promoter-associated histone marks (H3K4Me1, H3K4Me3, H3ac, H3K27Ac and H3 acetylation), which are usually linked to promoter regions [26] (Fig. 2a, tracks 2, 3, 4 and 9). In addition, binding sites for the promoter associated transcription factors USF1/USF2 and c-Myc located in  $\beta$ 2- and  $\beta$ 3-chimaerin promoters support our hypothesis (Fig. 2a, track 7, 8 and 9) [27, 28]. Moreover, Fig. 2a (track 6) shows that these regions presented high promoter activity in HepG2 human cells and poised state promoter in H1-hESC human cells. Finally, analysis of regulatory potential in these regions using ESPERR, an algorithm that discriminates between regulatory elements and neutral DNA, considered this DNA region as a regulatory element (Fig. 2a, track 11) [29]. Using the software methyl primer express (Applied Biosystems, Foster City, CA) we also identified highly dense CpG islands, which are typically associated with promoter regions and transcriptional regulation [30], in both  $\beta$ 2-chimaerin and  $\beta$ 3-chimaerin promoter regions (Fig. 2b). In addition, the Hudson Alpha Methyl-seq consortium reported that these CpG islands are methylated in several human cell lines (Fig. 2a, track 10). Taken together, results from CHN2 promoter analysis strongly support the idea that alternative TSSs, rather than alternative splicing, controls the generation of  $\beta$ 2- and  $\beta$ 3-chimaerins.

### Expression of $\beta$ 3-chimaerin

To determine the relative expression of  $\beta$ 3-chimaerin in tissues we used a commercial cDNA array (TissueScan Human Major Tissue qPCR Array) and specific  $\beta$ 3-primers. Although levels were generally moderate, most tissues expressed  $\beta$ 3-chimaerin. The highest levels of mRNA were found in epididymis, plasma blood leucocytes, spleen, and thymus (Fig. 3a). Given the important function of chimaerins in nervous tissues [1, 31], we also examined the expression pattern of  $\beta$ 3-chimaerin using a human brain cDNA array (Tissue Scan Human Brain Tissue qPCR Array). High  $\beta$ 3-chimaerin levels were detected in the

pituitary gland, gray cerebellum, white cerebellum and vermis (Fig. 3b).  $\beta$ 3-chimaerin expression was also detected in human cell lines A-172 (glioblastoma) and U-373 (astrocytoma) by RT-PCR (Fig. 3c) and by Western blot using a monoclonal anti-chimaerin antibody (Fig. 3d). Quantification of chimaerin expression by Western blot showed that  $\beta$ 2-chimaerin is  $3.1 \pm 0.6$  times more abundant than  $\beta$ 3-chimaerin in A-172 and  $1.4 \pm 0.3$  times more in U-373.

### Responsiveness of $\beta$ 3-chimaerin to PMA

In previous studies we established that the C1 domain in  $\beta$ 2-chimaerin binds phorbol esters with an affinity similar to C1 domains in PKC isozymes. The C1 domain is responsible for the redistribution of the protein from the cytosol to the plasma membrane where it binds its target Rac [9, 18, 19, 32]. As C1 domains in  $\beta$ 2- and  $\beta$ 3-chimaerins are identical, we expected that  $\beta$ 3-chimaerin should be responsive to phorbol esters. To address this issue we examined the intracellular redistribution of these chimaerins in response to different concentrations of the phorbol ester PMA using a subcellular fractionation approach. COS-1 cells were transfected with a  $\beta$ 3-chimaerin mammalian expression vector and treated with different concentrations of PMA. Cell lysates were prepared, and soluble (cytosolic) and particulate fractions were separated by ultracentrifugation. Western blot analysis revealed that PMA caused significant translocation of  $\beta$ 3-chimaerin to the particulate fraction (Fig. 4a). Densitometric analysis of the immunoreactivity in the soluble fraction allowed us to calculate the  $EC_{50}$  for PMA-induced  $\beta$ 3-chimaerin translocation ( $180 \pm 1$  nM,  $n = 6$ ). In comparison, the  $EC_{50}$  for PMA-induced translocation of  $\beta$ 2-chimaerin was approximately sevenfold higher ( $1202 \pm 1$  nM,  $n = 5$ ).

Translocation of  $\beta$ 3-chimaerin was also evaluated using fluorescence microscopy. COS-1 cells expressing GFP- $\beta$ 3-chimaerin, or GFP- $\beta$ 2-chimaerin as a control, were treated with vehicle, 0.3 or 30  $\mu$ M of PMA for 20 min, fixed and visualized for GFP localization. Figure 4b, shows that at 0.3  $\mu$ M  $\beta$ 3-chimaerin accumulates in the perinuclear region. Thus,  $\beta$ 3-chimaerin translocates more efficiently than  $\beta$ 2-chimaerin in response to activation via the C1 domain.

### Analysis of $\beta$ 3-chimaerin Rac-GAP activity

Next, we examined the ability of  $\beta$ 3-chimaerin to inactivate Rac. COS-1 cells were transfected with mammalian expression vectors for either  $\beta$ 2-chimaerin or  $\beta$ 3-chimaerin, and Rac-GTP levels were determined using a pull-down assay. Figure 5 shows that, although both  $\beta$ 2-chimaerin and  $\beta$ 3-chimaerin were able to reduce Rac-GTP levels,  $\beta$ 3-chimaerin was more efficient than  $\beta$ 2-chimaerin.

## Discussion

In this study we identified a novel product of the CHN2 gene,  $\beta$ 3-chimaerin. Like  $\beta$ 2-chimaerin,  $\beta$ 3-chimaerin has the SH2-C1-Rac-GAP domains tandem. The human CHN2 gene possesses at least three alternative TSSs with promoter regions driving the expression of  $\beta$ 1-,  $\beta$ 2- and  $\beta$ 3-chimaerins.  $\beta$ 1-Chimaerin, the smallest member of this family, lacking the SH2 domain, was originally described as a splicing variant in the rat testis [5]. However, our analysis showed that this chimaerin isoform is rather the product of an alternative TSS located on intron 6.  $\beta$ 2-Chimaerin is the most abundant product of the CHN2 gene. It is highly expressed in the cerebellum and ubiquitously expressed at low levels in various tissues. There are also reports that  $\beta$ 2-chimaerin is down-regulated in several cancer types, suggesting a potential role for this protein as a tumor suppressor [8, 17]. Transcription of  $\beta$ 2-chimaerin is driven by a promoter region located on intron 2a of the CHN2 gene.  $\beta$ 2-chimaerin possesses all three chimaerin domains, an SH2 domain presumably involved in

phosphotyrosine binding, a DAG/phorbol ester-responsive C1 domain, and a Rac-specific GAP domain [4, 6]. Additional 5' region present in  $\beta$ 3-chimaerin mRNA is encoded by two exons located 48 kb upstream of the  $\beta$ 2-chimaerin coding sequence. These additional exons generate a unique 5' UTR region and an additional N-terminus with no obvious sequence identity to any other protein. The sequence coding for this N-terminal region does not display any known domain or motif, and it was found only in primates, suggesting that it came late in the evolutionary process and that it may be involved in a highly specialized function.

Previous studies have assumed that  $\beta$ 1- and  $\beta$ 2-chimaerins represent alternative splicing products of the CHN2 gene. Although alternative splicing is responsible for a large fraction of protein variants, it is now recognized that other mechanisms exist, such as the usage of alternative TSSs or alternative polyadenylation signals. These mechanisms produce mRNAs with different 5' UTR or 3' UTR regions, respectively, which have differential mRNA stability, localization, or translation efficiency [33]. Additionally, these mechanisms could generate protein variants differing in their N- or C-termini. In this paper we show that the different isoforms encoded by the CHN2 gene ( $\beta$ 1-,  $\beta$ 2- and  $\beta$ 3-chimaerin) are not generated by alternative splicing, as suggested previously, but rather through alternative TSSs.

Based on this study and our previous observations [13, 34, 35], and taking into consideration the information provided by the 3-D structure of  $\beta$ 2-chimaerin [12], we postulate that different members of the chimaerin family are subject to distinct mechanisms of control. Crystallo-graphic evidence points to the N-terminal region of  $\beta$ 2-chimaerin as a major determinant for autoinhibition. This region forms hydrophobic bonds with residues in the C1 domain that occlude the groove where ligands (DAG and phorbol esters) bind to induce allosteric activation. Specifically, Leu28 in the N-terminal region makes contact with Trp234 and Phe232 in the C1 domain, which prevents the access of ligands. In addition, hydrophobic amino acids in the Rac-GAP domain interact with residues in the C1 domain, thus contributing to the stabilization of the tertiary structure in the autoinhibited conformation. In support of this model, disruption of intramolecular contacts by site-directed mutagenesis (such as mutation of Leu28 to Ala) reduces the requirement for acidic phospholipids necessary for phorbol ester binding in vitro and sensitizes  $\beta$ 2-chimaerin translocation to plasma membrane by phorbol esters and its subsequent association with Rac [12]. Notably, somatic mutations in Leu20 in  $\alpha$ 2-chimaerin (equivalent to Leu28 in  $\beta$ 2-chimaerin), which leads to Rac-GAP hyperactivation, have been found in patients with Duane's retraction syndrome, arguing for a critical role of these internal contacts in keeping the protein in a closed conformation [36]. More importantly, these studies support the concept that the structurally related isoforms  $\alpha$ 2- and  $\beta$ 2-chimaerins are highly regulated proteins and possibly require modifications to destabilize the inactive structure and expose the catalytic Rac-GAP domain [10]. Unlike  $\beta$ 2-chimaerin,  $\beta$ 1-chimaerin lacks the N-terminal region and therefore is not subject to autoinhibition and allosteric activation. Consistent with this,  $\beta$ 1-chimaerin is more sensitive than  $\beta$ 2-chimaerin to PMA-induced translocation [32]. Chimaerins are responsible for the reduction in Rac-GTP levels after PMA treatment in the presence of PKC inhibitor GF 109203X [37]. Based on the data presented here,  $\beta$ 3-chimaerin resembles  $\beta$ 1-chimaerin in its hyper-sensitivity to PMA-induced translocation. As a potential explanation,  $\beta$ 3-chimaerin residues that mask the C1 domain, such as Leu28 in  $\beta$ 2-chimaerin, may be displaced or engaged in other interactions within the N-terminus domain, allowing a conformation that is energetically favorable for ligand binding to the C1 domain. Although the N-terminal domain in  $\beta$ 3-chimaerin may not be implicated in autoinhibition, we speculate that this region may be involved in some type of protein-protein as recently described for  $\beta$ 2-chimaerin N-terminus [38]. In fact, the atypic proline rich motif P(R/H)P(KR) implicated in the interaction with Nck1 is present in  $\beta$ 3-chimaerin. More over, the additional N-terminal region present in  $\beta$ 3-chimaerin may be subject to post-

translational modifications that modulate activation or intracellular localization. Further studies would be required to address this issue.

In summary, here we identified  $\beta$ 3-chimaerin as a novel member of the chimaerin family of Rac-GAPs. Our results suggest that individual chimaerin isoforms may be subject to different mechanisms of regulation. It remains to be determined if  $\beta$ 3-chimaerin has specialized functions in any given cell type or under different physiopathological conditions.

## Acknowledgments

This work is supported by grants PICT-2008-260 (ANCyP, Argentina), UBACyT 20020090200714 (UBA, Argentina), and PIP 11220110100573 (CONICET, Argentina) to Federico Coluccio Leskow., and Grants R01-CA74197 and R01-CA139120 (NIH) to Marcelo G. Kazanietz.

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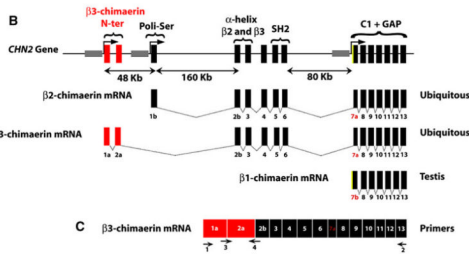
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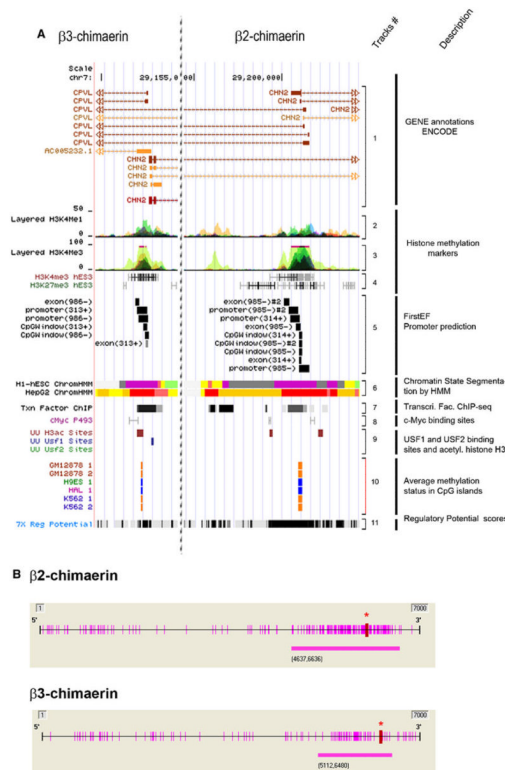
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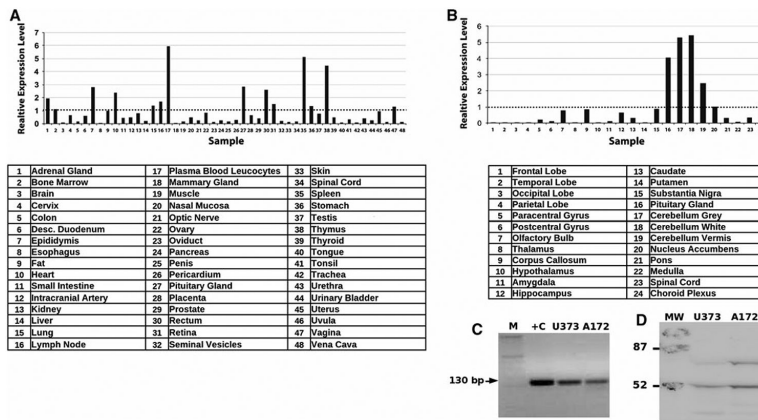
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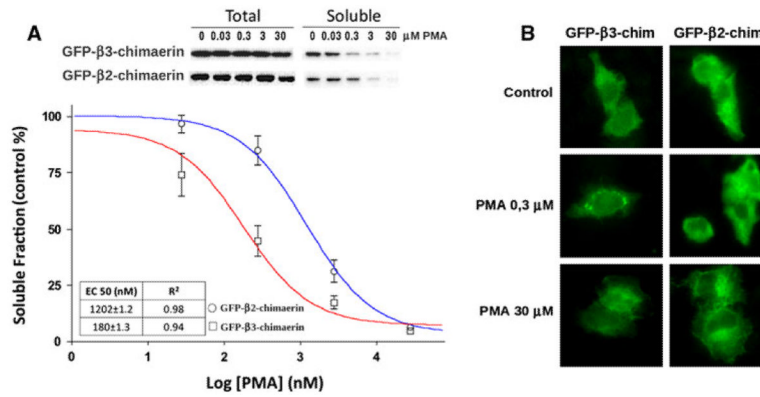
**Fig. 1.** CHN2 gene structure. **a**  $\beta$ 3-chimaerin sequence (accession no: ADK47390.1). *Red*, N-terminal region encoded by exons 1a and 2a; *green*, SH2 domain; *blue*, C1 domain; *yellow*, Rac-GAP domain. **b** Structure of the *CHN2* gene. The figure shows the exon arrangements leading to the different  $\beta$ -chimaerin isoforms. *Red*, exons that code for the  $\beta$ 3-chimaerin N-terminal domain; *green*, exon 1b that is specific for the  $\beta$ 2-chimaerin isoform. *Yellow*,  $\beta$ 1-chimaerin's exclusive 5' sequence on exon 7b; *gray*, promoter sequences for the different isoforms. **c** Schematic view of the primers used to amplify full-length (primers 1 and 2) or N-terminal region of  $\beta$ 3-chimaerin (primers 3 and 4). (Color figure online)



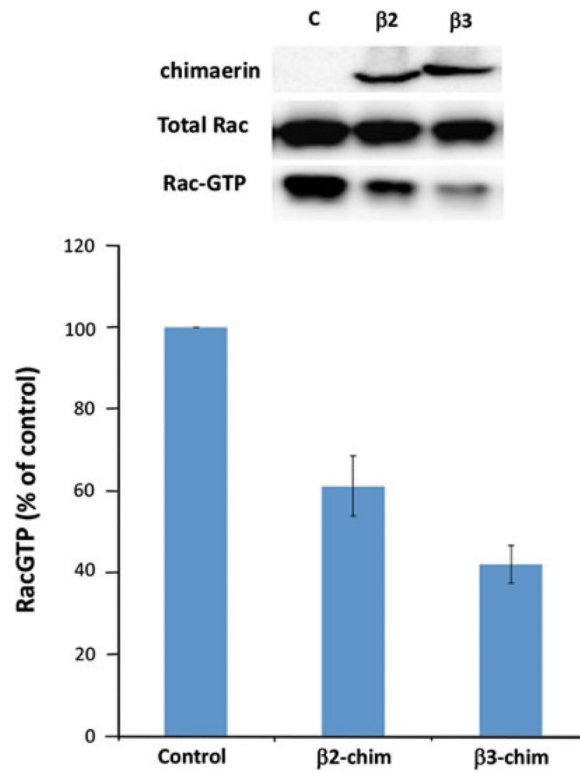
**Fig. 2.** Analysis of the CHN2 gene promoter. **a** Putative promoter regions of  $\beta 3$ -chimaerin (*left panel*) and  $\beta 2$ -chimaerin (*right panel*) (UCSC Genome Browser). Track #1 *CHN2* gene plot; Track #2, enhancer- and promoter-associated histones marks, H3K4Me1, from 9 human cell lines; Track #3, promoter-associated histones marks, H3K4Me3, from 8 human cell lines; Track #4, GIS ChIP-PET showing H3K4me3 and H3K27me3 histone modifications from 4 human cell lines; Track #5, first-exon promoter prediction; Track #6, ENCODE chromatin state segmentation by HMM from Broad Institute of 2 human cell types (*Bright Red* active promoter/*Light Red* weak promoter/*Purple* inactive-poised promoter/*Orange* strong enhancer/*Yellow* weak-poised enhancer/*Light Green* weak transcribed/*Gray* polycomb-repressed/*Light Gray* heterochromatin); Track #7, ENCODE transcription factor ChIP-seq; Track #8 GIS ChIP-PET: binding sites for c-Myc; Track #9, Uppsala University ChIP-chip Signal, showing localization of transcription factors (USF1 and USF2) and acetylated histone H3 (H3ac) in a liver cell line (HepG2); Track #10 ENCODE HudsonAlpha CpG methylation showing methylation status of specific CpG dinucleotides in 3 human cell types (*orange* = methylated; *blue* = unmethylated); Track #11 ESPERR regulatory potential (RP) compare frequencies of known regulatory elements and neutral DNA from 7 species. **b** CpG sites (*purple bars* along the axis) and CpG islands (*purple bars* below the axis) near  $\beta 2$ -chimaerin and  $\beta 3$ -chimaerin promoter regions. *Red asterisks* indicate translation start sites (ATGs). (Color figure online)



**Fig. 3.**  $\beta$ 3-Chimaerin expression analysis.  $\beta$ 3-chimaerin mRNA levels were determined by Q-PCR using cDNA arrays using specific primers against  $\beta$ 3-chimaerin. Expression levels are shown relative to the mean value of the array (indicated by the *dotted line*). **a** TissueScan human major tissue qPCR array. **b** TissueScan human brain tissue qPCR array. **c** RT-PCR showing expression of  $\beta$ 3-chimaerin in U-373 and A-172 cell lines. Molecular weight of the amplified insert and a positive control are shown. **d** Western blot showing relative expression of  $\beta$ 2-chimaerin and  $\beta$ 3-chimaerin in U-373 and A-172 cell lines (Molecular weight marker is shown in kD)



**Fig. 4.** β3-Chimaerin translocation after PMA treatment. **a** COS-1 cells expressing either β2-chimaerin or β3-chimaerin were treated with different concentrations of PMA for 20 min and subject to cellular fractionation. *Upper panel* representative western blots. *Bottom panel* densitometric analysis of immunoreactivity in the soluble fraction. Results are expressed as percentage of the values observed in control (non-treated) cells and represent the mean standard error of 5 (β2-chimaerin) or 6 (β3-chimaerin) independent experiments. The corresponding EC<sub>50</sub> values are shown in the *inset*. **b** GFP-β2-chimaerin or GFP-β3-chimaerin expressing cells were treated with vehicle, 0.3 or 30 μM PMA for 20 min, fixed and visualized by fluorescence microscopy



**Fig. 5.**  $\beta$ 3-Chimaerin has Rac-GAP activity. Rac-GTP levels were measured in COS-1 cells expressing either  $\beta$ 2-chimaerin or  $\beta$ 3-chimaerin. *Upper panel* representative experiment. *Bottom panel* densitometric analysis of Rac-GTP levels normalized to total Rac levels in each case. Values are expressed as % of control (C, non-transfected cells) and they represent the mean  $\pm$  SEM of seven independent experiments