

REVIEW ARTICLE

Neuroendocrine secretory protein 7B2: structure, expression and functions

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7B2 is an acidic protein residing in the secretory granules of neuroendocrine cells. Its sequence has been elucidated in many phyla and species. It shows high similarity among mammals. A Pro-Pro-Asn-Pro-Cys-Pro polyproline motif is its most conserved feature, being carried by both vertebrate and invertebrate sequences. It is biosynthesized as a precursor protein that is cleaved into an N-terminal fragment and a C-terminal peptide. In neuroendocrine cells, 7B2 functions as a specific chaperone for the proprotein convertase (PC) 2. Through the sequence around its Pro-Pro-Asn-Pro-Cys-Pro motif, it binds to an inactive proPC2 and facilitates its transport from the endoplasmic reticulum to later compartments of the secretory pathway where the zymogen is proteolytically matured and activated. Its C-terminal peptide can inhibit PC2 *in vitro* and may contribute to keep the enzyme transiently inactive *in vivo*. The PC2–7B2 model defines a new neuroendocrine paradigm whereby proteolytic

activation of prohormones and proneuropeptides in the secretory pathway is spatially and temporally regulated by the dynamics of interactions between converting enzymes and their binding proteins. Interestingly, unlike PC2-null mice, which are viable, 7B2-null mutants die early in life from Cushing's disease due to corticotropin ('ACTH') hypersecretion by the neurointermediate lobe, suggesting a possible involvement of 7B2 in secretory granule formation and in secretion regulation. The mechanism of this regulation is yet to be elucidated. 7B2 has been shown to be a good marker of several neuroendocrine cell dysfunctions in humans. The possibility that anomalies in its structure and expression could be aetiological causes of some of these dysfunctions warrants investigation.

Key words: chaperone, proprotein convertase, proteolytic processing.

INTRODUCTION

Limited proteolysis of precursor polypeptides is now recognized as a common biological mechanism for the production of bioactive proteins and peptides [1]. Neuroendocrine cells manufacture peptide hormones and neuropeptides through such a mechanism. The proprotein convertases (PCs) 1/3 and 2 are the principal mediators of prohormone and proneuropeptide processing in the secretory pathway of these cells [2,3]. PC1/3 and PC2 are themselves biosynthesized in the endoplasmic reticulum (ER) as inactive precursor proteins that are transported through the Golgi and the *trans*-Golgi network (TGN) into secretory granules, and are proteolytically activated along the way. The timing of this activation is a major determinant in the coordinated processing of prohormones and proneuropeptides. Thus in pituitary corticotrophs, PC1/3 mediates the initial processing of pro-opiomelanocortin (POMC) into corticotropin ('ACTH') and β -lipotropic hormone (β -LPH), and PC2 converts β -LPH into β -melanocyte-stimulating hormone and β -endorphin [4]. The autocatalytic conversion of proPC1/3 occurs in the ER and its activation takes place in the TGN and immature granules through secondary cleavages within the pro-segment and the C-terminal domain. Comparatively, proPC2 maturation into PC2 and the subsequent activation of the latter are delayed until the zymogen has reached the post-Golgi compartments [5]. Most neuroendocrine cells contain 7B2, an acidic protein of approx. 150 residues, whose cellular function has long remained un-

known. It was discovered in recent years that this protein binds PC2 and facilitates its transport and activation, thus defining an additional level of control of converting activities in neuroendocrine cells. This article reviews the biology of 7B2, from its structure to its function.

THE DISCOVERY OF 7B2

7B2 was discovered in 1982 by Seidah, Chrétien and their collaborators, while purifying the N-terminal glyco-segment of POMC from pig anterior pituitaries [6]. It eluted under a distinct peak in a reverse-phase HPLC profile of tissue extracts. The sequence of its first 50 amino acids showed a weak identity with duck proinsulin (30%) and pig secretin (26%) [6]. Soon after, the same investigators reported the purification of its human pituitary homologue, as well as the 77-residue N-terminal sequences for both the human and porcine proteins [7]. The two sequences differed by only one residue. This high evolutionary conservation suggested that 7B2 might be biologically relevant. The purified protein migrated with a molecular mass of 19–21 kDa, as determined by SDS/PAGE, and with a pI of 4.9 in an isoelectric focusing gel [6–8]. However, by gel permeation chromatography of tissue extracts, 7B2 immunoreactivity eluted with varying molecular masses, ranging from 11 to 50 kDa [8–10], an early indication that the protein might be processed and could associate with other proteins.

Abbreviations used: AP, activator protein; 7B2CT, C-terminal domain of 7B2; CPE, carboxypeptidase E; CRE, cAMP-responsive element; CRF, corticotropin-releasing factor; DTT, dithiothreitol; ER, endoplasmic reticulum; GH, growth hormone; IBMX, 3-isobutyl-1-methyl-xanthine; IGF, insulin-like growth factor; LHRH, luteinizing hormone-releasing hormone; β -LPH, β -lipotropic hormone; PACE, paired basic amino acid converting enzyme; PC, proprotein convertase; POMC, pro-opiomelanocortin; PWS, Prader-Willi syndrome; SH3, Src homology 3; TGN, *trans*-Golgi network; UTR, untranslated region; VP, vasopressin.

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7B2 PROTEIN AND GENE STRUCTURES

Over the years, the complete sequence of 7B2 was deduced from the sequence of cDNAs cloned in many species, organs and cell lines, including human anterior pituitary [11], mouse insulinoma [12], toad intermediate pituitary [13], rat insulinoma [14], pig adrenal medulla [15], fish hypothalamus [14], mollusc brain [16], nematode [17] and fruit fly [18]. An alignment between these sequences is shown in Figure 1. The overall residue identity is very high (90–96%) among mammals, relatively high (67–83%) between mammals and frog or fish, and low (17–22%) between vertebrates and invertebrates. The most conserved feature among all 7B2 sequences is a Pro-Pro-Asn-Pro-Cys-Pro motif corresponding to residues 90–95 in human 7B2 (hereinafter we will refer to the numbering of human 7B2 in Figure 1 to identify residues and domains). Among mammalian 7B2s, other conserved structural features include: clusters of basic residues (residues 139–140, 151–155 and 172–173), representing potential sites of processing by serine endoproteases of the PC family

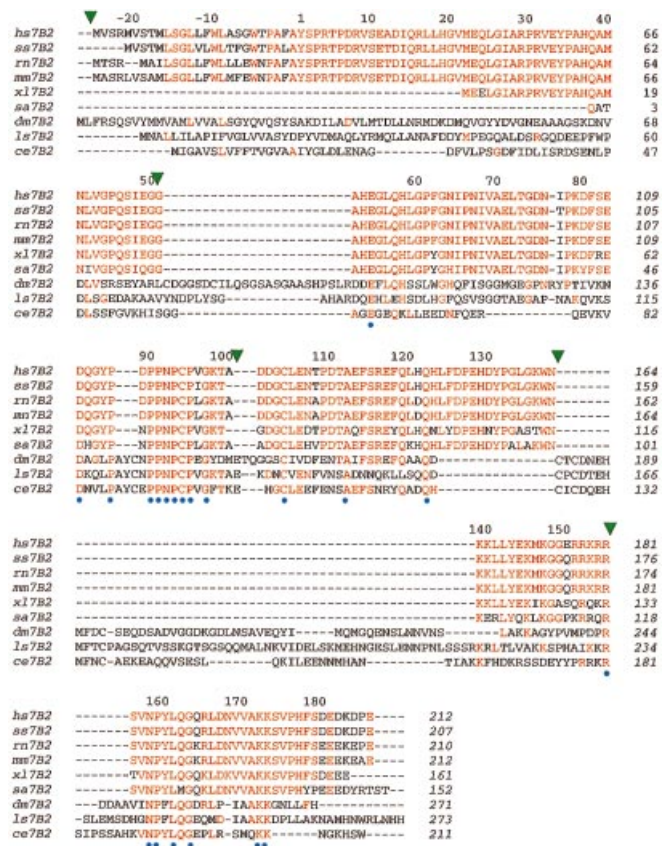


Figure 1 Alignment of known 7B2 sequences

The sequences were deduced from GenBank®-retrieved or published (see the text) cDNA sequences. The species (the scientific name, prefix and GenBank® accession numbers) are: man (*Homo sapiens*, *hs*, NM 003020); pig (*Sus scrofa*, *ss*, M23654); rat (*Rattus norvegicus*, *rn*, NM 13175); mouse (*Mus musculus*, *mm*, NM 009162); toad (*Xenopus laevis*, *xl*, X15608), salmon (*Salmo salar*, *sa*); fruit fly (*Drosophila melanogaster*, *dm*, AJ271974); snail (*Lymnaea stagnalis*, *ls*, U72702); and worm (*Caenorhabditis elegans*, *ce*). The human 7B2 sequence is numbered every ten residues on top of the aligned sequences, starting with the first residue after its signal peptide. For all sequences, the number of the terminal residue in each line is given to the right. Residues identical among all 7B2s are highlighted with blue dots. Those identical among or with mammalian sequences are highlighted in red. The genetic sequence encoding the human 7B2 is interrupted by introns at positions indicated with green arrowheads.

[2,3]; a serine phosphorylation consensus site (Ser¹⁷⁴); and a Glu- and Asp-rich acidic C-terminus (residues 180–186).

Interestingly, after the signal peptide, the only discontinuity among mammalian 7B2 sequences is the presence or the absence of an alanine residue following Thr⁹⁹ (Figure 1). Southern-blot analysis of cDNA clones randomly retrieved from a cDNA library with isoform-specific 7B2 oligonucleotide probes showed that five out of seven of these clones lacked the Ala¹⁰⁰ codon [19]. Their coexistence in other endocrine tissues and in different species was suggested by heteroduplex analysis of DNA amplicons by reverse transcriptase-PCR of their RNA [19]. The alanine residue was absent in the cDNA-deduced porcine 7B2 sequence [14], but was present in the amino acid sequence of the 7B2 protein purified from pig pituitary extracts [20]. A variety of models can be proposed to explain the presence of Ala¹⁰⁰ in the sequence of 7B2 protein purified from tissues and the prevalence of 7B2 transcripts without the Ala¹⁰⁰ codon among cloned mRNAs. On one hand, there is the possibility of preferential utilization of the Ala¹⁰⁰⁺-encoding mRNA isoform for translation coupled or not with its selective degradation. On the other hand, it is possible that the Ala¹⁰⁰⁻ protein may have a shorter half-life and may therefore be under-represented in tissue-extracted 7B2. There are naturally occurring precedents for all these possibilities. For example, differential translation has been observed between anglerfish prostanostatin mRNA I and its isoform, II, which contains three octanucleotide repeats in its 5'-untranslated region (UTR) [21]. Similarly, among the three insulin-like growth factor (IGF) mRNA isoforms of 6, 5 and 4.8 kb, differing by their leader sequence, the two shortest are preferentially utilized relative to the more abundant 6 kb isoform [22]. Although the structure of the 5'-UTR may be determining the efficiency of initiation in these two examples, theoretical computation of the structure of codon¹⁰⁰⁺ and codon¹⁰⁰⁻ mRNA using the MFOLD program [23] produced distinctive stem-loop structures in the region encompassing this codon (results not shown). Such structural differences may influence the relative unwinding, translatability and stability of the two isoforms. Preferential utilization of the codon¹⁰⁰⁺-7B2 mRNA may be associated with its selective degradation. Recruitment for translation is known to render some mRNAs susceptible to degradation by nucleases. The degradation is initiated by endonucleases and completed by exonucleases. Its extent may be partly determined by stabilizing or destabilizing RNA-binding proteins that recognize specific stem-loop structures in the mRNA [24]. Differential stability at the protein level is illustrated by the ΔK60 human α1 globin mutation in which a single codon deletion leads to the production of protein that lacks Lys⁶⁰ and is rapidly degraded [25]. Whether any of these models is applicable to 7B2 isoforms is surely amenable to experimental verification by a combination of ribosome-loading and pulse-chase studies using isoform-specific probes and antibodies. It should also be noted that the variation is located within a structural loop generated by the single and functionally important (as discussed later) disulphide bridge of the molecule. In view of the conservation of these isoforms across mammalian species, it is conceivable that the single-residue difference may subtly influence the cellular functions of 7B2.

The structure of the 7B2 gene in rat and human is known [14,26,27]. The human gene is more than 30 kb long and is made of six exons (Figure 2). Exon 1 specifies the 5'-UTR of the mRNA, exon 2 specifies the signal peptide and residues 1–50 of pro7B2, exon 3 specifies residues 51–101, exon 4 specifies residues 102–138, exon 5 specifies residues 139–155, and exon 6 specifies residues 156–186 (see Figure 1). The presence or absence of Ala¹⁰⁰ is probably due to alternative utilization of two different 3' splice sites that are three nucleotides apart at the end of the

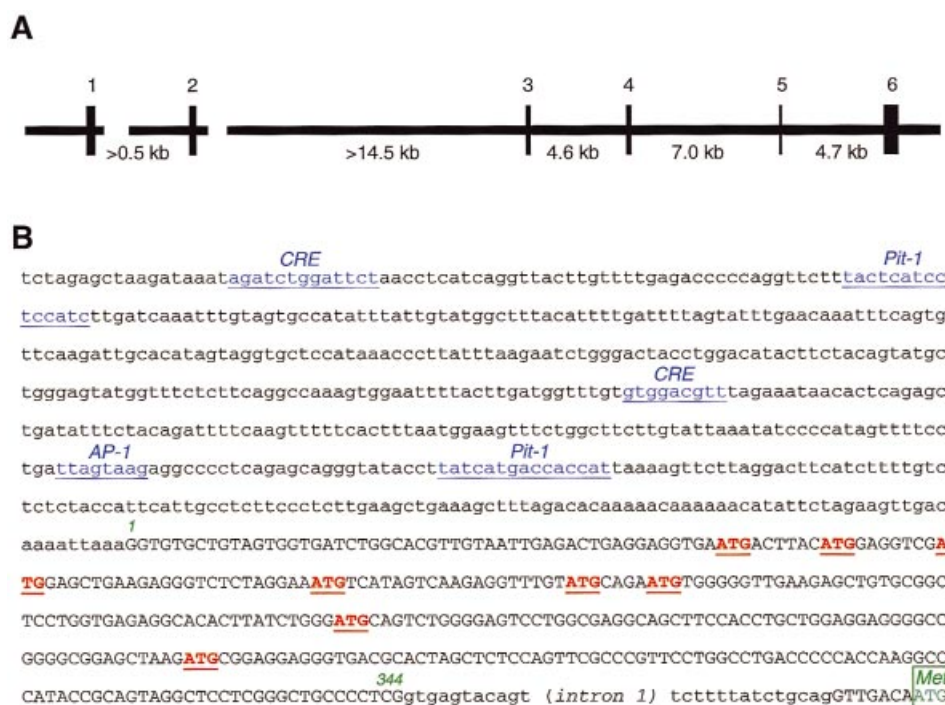


Figure 2 Structure and sequence of the promoter region of the human 7B2 gene

(A) Schematic representation of the gene based on GenBank® data (accession numbers: AC074201, AJ290437-41 and X94303). Exons are shown as vertical bars. The exact sizes of introns 1 and 2 have not been determined. (B) Sequence of the proximal promoter and the first exon. The exon sequence is shown in capital letters. Putative regulatory elements in the upstream sequence are underlined and the potential binding factors are indicated above in blue. Out-of-frame ATGs in the first exon are shown in bold red and are also underlined. The initiator ATG in the second exon is shown in green and boxed.

third intron [26]. Exons 4, 5 and 6 specify the two most important functional domains of 7B2 (see below). The human 7B2 locus (*SGNE1*) maps on human chromosome 15q [28]. In mouse, its homologue (*Sgne1*) maps on the E3-F3 region of chromosome 2 [26].

TISSUE DISTRIBUTION AND SUBCELLULAR LOCALIZATION OF 7B2

In addition to cloned cDNA probes, a number of polyclonal and monoclonal antibodies against defined domains of 7B2 have been raised [7,29–32]. This has permitted a detailed study of its tissue distribution, subcellular localization, biosynthesis and secretion. Table 1 describes the distribution of 7B2 in normal tissues as determined by various studies using radioimmunoassays, immunohistochemistry, immunocytochemistry or *in situ* hybridization. The mRNA or the protein are found in tissues that are either primarily neuronal (e.g. brain and adrenal medulla) or endocrine (e.g. pituitary, thyroid and pancreas), or are known to carry a sub-population of neuroendocrine cells (e.g. the gastrointestinal tract). In rat, in pg/mg of total proteins, the anterior lobe of the pituitary contains the highest amount of immunoreactive 7B2, followed by the neurointermediate lobe, the hypothalamus, the adrenal medulla, the thyroid gland and the pancreas. Other tissues contain relatively minor or undetectable amounts of the protein [8].

Within neuroendocrine cells, 7B2 is located inside secretory granules. This was initially determined by subcellular fractionation of porcine and rat neurointermediate lobes [8,33], and by immunocytochemistry on rat hypothalami and porcine chromaffin granules [10,33]. This localization was later confirmed

Table 1 Tissue distribution of 7B2

Abbreviations used: b, bovine; gp, guinea pig; H, human; ICC, immunocytochemistry; IHC, immunohistochemistry; ISH, *in situ* hybridization; p, pig; r, rat; RIA, radioimmunoassay; x, *Xenopus*.

Organs	Species	Methods	References
Brain	H, r	RIA, IHC, ISH	[9,34–36]
Hypothalamus	r	RIA, IHC, ISH	[8,34–37]
Supraoptic nucleus	r	IHC	[35,37]
Paraventricular nucleus	r	IHC	[35,37]
Median eminence	x	IHC, ISH	[38]
Basal ganglia	r	RIA	[34]
Spinal cord	r	RIA, IHC, ISH	[33,35,36,39]
Pituitary	r	RIA, IHC	[34,35]
Anterior lobe	r, x	RIA, IHC, ISH	[8,35,38]
Neurointermediate lobe	r, x	RIA, IHC, ISH	[8,38]
Thyroid	r	RIA	[8]
Adrenal medulla	b, r	ICC, RIA	[8,40]
Gastrointestinal tract			
Pancreas	H, gp, p, r	RIA	[8,41]
Antrum	H, gp, p, r	RIA, IHC	[41–43]
Fundus	r	IHC	[41,43]
Ileum	H, gp, p, r	RIA, IHC	[8,41–43]
Colon	H, gp, p, r	RIA, IHC	[41,42]
Duodenum	H, gp, p, r	IHC	[41,42]
Skin Merkel cells	p	IHC	[44]

for a variety of other neuroendocrine tissues and cells, where it often overlaps with that of resident hormones and neuropeptides (Table 2).

Table 2 Co-localization of 7B2 with hormones and neuropeptides

Abbreviations used: c, cat, ch, chick; FSH, follicle-stimulating hormone; H, human; h, hamster; ICC, immunocytochemistry; IHC, immunohistochemistry; ISH, *in situ* hybridization; m, mouse; MSH, melanocyte-stimulating hormone; PP, pancreatic polypeptide; r, rat; RIA, radioimmunoassay; TSH, thyroid-stimulating hormone; x, *Xenopus*.

Organs	Resident proteins	Species	Methods	References
Hypothalamus				
Supraoptic nucleus	VP	r	IHC	[37]
Paraventricular nucleus	VP	r	IHC, IHC	[37,45]
	Galanin	r	IHC	[46]
	Oxytocin	r	IHC, ISH	[45]
	Neuromedin B or U	H, r, m	IHC	[47]
Pituitary				
Anterior lobe	LH	r	ISH, IHC	[48,49]
	FSH	r	ISH, IHC	[48,49]
	TSH	r	ISH, IHC	[48,49]
	Corticotropin	r	ISH	[49]
	GH	r	ISH	[49]
	Prolactin	r	ISH	[49]
	Neurointermediate lobe	POMC	r, x	ISH, IHC
MSH		r	ISH	[49]
Posterior lobe	VP	r	IHC	[37]
Thyroid parafollicular cells	Calcitonin	H	IHC, ICC	[10]
Lung neuroepithelial bodies	Calcitonin gene-related peptide	c, r, h	IHC	[50,51]
Adrenal medulla	Somatostatin	ch	IHC	[52]
	Met-enkephalin	ch	IHC	[52]
	Neuropeptide Y	ch	IHC	[52]
Gastrointestinal tract				
Pancreas	Insulin	r	IHC	[53]
	Glucagon	r	IHC	[53]
	Somatostatin	r	IHC	[53]
	PP	r	IHC	[53]

BIOSYNTHESIS AND SECRETION OF 7B2

The first pulse-chase studies to examine the biosynthesis of 7B2 were conducted by Ayoubi et al. [54] using *Xenopus laevis* neurointermediate lobes, and by Paquet et al. [55] using mammalian cell lines. These studies showed that 7B2 is produced as an intracellular precursor of 25–29 kDa that gets converted into a secreted form of 18–21 kDa. The protein is not glycosylated [54], but is tyrosine-sulphated [55]. Two products of these post-translational modifications have been independently isolated from cell and tissue extracts, and have been characterized by protein sequencing: a 7B2^{1–150} protein purified from porcine pituitaries [20], and a 7B2^{174–186} phosphorylated peptide from bovine chromaffin granules [56]. The former was presumably generated by PC cleavage after the Arg¹⁵¹-Arg-Lys-Lys-Arg¹⁵⁵ basic quintuplet followed by carboxypeptidase E (CPE) removal of the basic residues; the latter by cleavage after Lys¹⁷²-Lys¹⁷³ (see Figure 1). In mammals, the PC most likely to be responsible for the endoproteolysis at the basic quintuplet is furin. This was determined by coexpressing pro7B2 and various PCs in mammalian cells using recombinant vaccinia viruses as vectors, and comparing the ability of these enzymes to process the precursor form of 7B2 to its smaller forms. Furin cleavage of pro7B2 occurs in the Golgi and requires Arg¹⁵² at the fourth residue before the cleavage site [55]. Other convertases, such as PC1, PC2, paired basic amino acid converting enzyme (PACE) 4-A, PC5 and PC7, can also cleave pro7B2 at this site *ex vivo* [57–59]. It is worth noting that in *Xenopus*, pro7B2 processing takes place after the Lys¹¹⁶-Lys¹¹⁷ pair preceding the furin cleavage site [54] (see Figure 1). Processing at such a pair may also occur in *Drosophila* and *Lymnaea* pro7B2s, which lack any furin recog-

nition site (see Figure 1). The enzyme mediating cleavage at this alternative site has not been determined.

After processing, 7B2 proteins are packaged into dense-core vesicles and are secreted upon exocytotic stimulation. This secretion was initially studied using primary cultures of rat anterior pituitary cells, because of the relative abundance of the molecule in these cells [8,60]. It was stimulated by plasma membrane depolarization with potassium ions and by treatment with luteinizing hormone-releasing hormone (LHRH) [60,61]. It was reduced by treatment with testosterone [61], and was unaffected by treatment with corticotropin-releasing factor (CRF) and growth hormone (GH)-releasing factor ('GRF') [60]. These observations suggested that, among pituitary cell types, gonadotrophs contain the largest amount of stored 7B2. This was confirmed by immunohistochemistry [48]. Regulated secretion was also demonstrated with bovine chromaffin granules [62], rat pheochromocytoma PC12 cells [63], and hamster pancreatic islets [64]. The packaging of 7B2 into secretory granules seems to depend on the integrity of its single disulphide bond, as suggested by its constitutive secretion by *Xenopus* intermediate pituitaries treated with dithiothreitol (DTT) [65].

REGULATION OF 7B2 EXPRESSION

7B2 gene expression is developmentally and hormonally regulated. It is induced in the mouse embryonic carcinoma cell line P19 following retinoic acid-promoted neuronal differentiation [66]. It is up-regulated by dexamethasone in the rat medullary thyroid carcinoma cell line rMTC [67], and by phorbol esters and forskolin in rat insulinoma and glucagonoma [14,68]. It is down-

regulated in rat adrenal medulla by adrenergic and cholinergic signals [69], and by light in toad intermediary pituitary [13].

The *cis* elements involved in this regulation have not been analysed. The sequence of the proximal promoter of the 7B2 gene is known in human and in rat [14,27]. It lacks obvious TATA and CAAT boxes, but contains several regulatory elements including binding sites for cAMP-responsive element (CRE) binding proteins, activator protein (AP) 1 and pituitary-specific transcription factor 1/growth hormone factor 1 ('Pit-1/GHF-1') (Figure 2B). The presence of multiple Pit-1/GHF-1 binding sites may contribute to the elevated expression of 7B2 in the pituitary. Uncharacterized elements located in the first intron of the rat gene appear to be important for the regulation of this gene by forskolin or phorbol esters [14,68].

7B2 expression may also be regulated at post-transcriptional levels. Temperature shift of the *Xenopus* intermediary lobes from 22 °C to 30 °C induces accumulation of the 18 kDa processed 7B2, but not of its mRNA, consistent with translational or post-translational regulation. In mouse corticotroph AtT-20 cells, exocytotic stimulation with CRF or KCl causes a 50–60% decrease in the level of 7B2 mRNA within 30 min, followed by a return to normal levels after 60 min (M. Mbikay, unpublished work). This observation suggests that degradation of its mRNA may be a mechanism of controlling the level of this protein in neuroendocrine cells. Translation regulation is also suggested by the intriguing case of the homozygous Brattleboro (*di/di*) rat. This rat suffers from severe diabetes insipidus due to a deficiency in vasopressin (VP) from the supraoptic and paraventricular nuclei of the hypothalamus. The VP gene of *di/di* rats carries a frameshift-causing single nucleotide deletion, which leads to the production of a C-terminally extended VP precursor that is retained in the ER. This extended precursor is the major form produced early in life. Later, however, some solitary neurons begin to produce a variant form of the prohormone from transcripts containing a dinucleotide deletion downstream of the original one. The variant prohormone can be transported through the secretory pathway and processed into VP. This leads to attenuation of the diabetes and a heterozygote-like phenotype. Interestingly, early in the life of *di/di* rats, 7B2 immunoreactivity is detectable in oxytocin neurons, but not in VP neurons [46], even though both neuronal types carry comparable levels of 7B2 mRNA [45]. With age, as the rats acquire a heterozygote-like phenotype, 7B2 immunoreactivity becomes detectable in some VP neurons too [46]. Blockage of pro7B2 biosynthesis due to the accumulation of the C-terminally extended VP precursor in shared ER compartments and competition between the two precursors for the translocation machinery have been suggested as possible explanations for this phenomenon [46,70].

Some sequence features of the 7B2 mRNA suggest that it may be a poor template for protein synthesis. Indeed, although moderately rich in G and C bases (58.57% in human 7B2), the 5'-UTR of 7B2 mRNAs is unusually long (> 300 nt, see Figure 2B). The average length of this region in mammalian mRNAs is approx. 80 nt. Long 5'-UTRs have been shown to form complex secondary structures that negatively affect translation initiation, by physical hindrance or through interaction with cytosolic regulatory proteins [71–73]. Secondary structure prediction using the MFOLD algorithm [23] indicates that the human 7B2 5'-UTR may form relatively stable stem-loop structures ($\Delta G = -126$ to -132 kcal/mol, where 1 cal \equiv 4.184 J), some of them located near the 5' end of the UTR. Such structures are likely to impede ribosomal scanning at translation initiation [74]. Moreover, this UTR is burdened by multiple out-of-frame AUGs (see Figure 2B). Such AUGs are often observed in the 5'-UTRs of mRNAs for tightly controlled proteins, such as growth factors

and oncogenes [75]. Because of these features, the 7B2 mRNA may not be efficiently utilized by the translation machinery when initiation factors are limiting. Differential translation may also explain why, out of the five cell types in the adenohypophysis, which all express 7B2 mRNA, only two appear to contain detectable levels of 7B2 protein [49]. The corollary to this hypothesis is that 7B2 production may be very sensitive to signals that affect the translational capacity of the cell, of the kind observed in glucose-stimulated pancreatic cells [76,77].

CELLULAR FUNCTIONS OF 7B2

Pro7B2 binds proPC2

A momentous breakthrough in the study of 7B2 came about in 1994 when Braks and Martens [78], led by structural similarities between the first 90-amino-acid sequence of 7B2 and a segment of human, wheat and *Escherichia coli* chaperonins, gathered experimental evidence showing that a recombinant 7B2, added to metabolically radiolabelled *Xenopus* pituitary extracts and immunoprecipitated, can retrieve the various forms of PC2 from these extracts. They also showed by pulse-chase studies that proPC2 is bound to pro7B2 in the early compartments of the secretory pathway and dissociates from it in later ones. They proposed that 7B2 serves as an intracellular proPC2 chaperone and prevents the premature activation of the zymogen during its transit in the regulated secretory pathway. The dynamic interaction between these two neuroendocrine molecules was further characterized in numerous other studies [65,79–86]. The results globally support the model of 7B2–PC2 interaction illustrated in Figure 3. Pro7B2 attaches to proPC2 in the ER. This attachment is facilitated by the relatively alkaline conditions of this compartment. The inactive complex is transported to the TGN where pro7B2 is cleaved into an N-terminal protein and a C-terminal peptide. ProPC2 then gets autocatalytically cleaved after the prodomain as the complex is transported into secretory granules. In the acidic environment of these organelles, the prodomain and the 7B2 fragments dissociate from the enzyme, which then becomes fully active. Depending on experimental cell systems and conditions, variations from this model have been observed and are discussed in the following sections.

Results from truncation, domain swapping and site-directed-mutagenesis experiments have implicated various 7B2 domains or residues in the binding and activation of proPC2. Major determinants of these effects are clustered within an internal segment extending from residues 86 to 131. They include the Pro⁹⁰-Pro-Asn-Pro-Cys-Pro⁹⁵ conserved motif, the Cys⁹⁴-Cys¹⁰⁴ disulphide bridge, the α helical sequence between residues 108 and 121, as well as the segment between residues 121 and 131, particularly Tyr¹³¹ [65,80,81,83,85]. The Arg¹⁵¹-Arg-Lys-Arg-Arg¹⁵⁵ primary processing site has also been implicated in the interaction [79], but is not indispensable, since the 7B2^{1–150} processed form has been shown to interact with PC2 [85]. Strangely, the 7B2^{1–90} sequence, whose similarity with chaperonin 60 spurred this line of investigation [87], has no PC2-binding activity [88].

Reduced or non-glycosylated proPC2 cannot attach to 7B2, suggesting that its proper folding is a prerequisite for this interaction [80]. The oxyanion hole Asp³⁰⁹ and Tyr¹⁹⁴ residues appear to be critical for both the binding of the zymogen to pro7B2 and its activation [79,82,84,89]. Interestingly, Tyr¹⁹⁴ is located in a polyproline region (D¹⁹²PYPXPY¹⁹⁹; where single-letter amino-acid notation has been used), which, like the one found in 7B2 (P⁸⁸DPPNPCP⁹⁹), bears some similarity with the Src homology 3 (SH3) domains [core motif PXXPX(R)]. On the basis of this similarity, an analogy was drawn between the

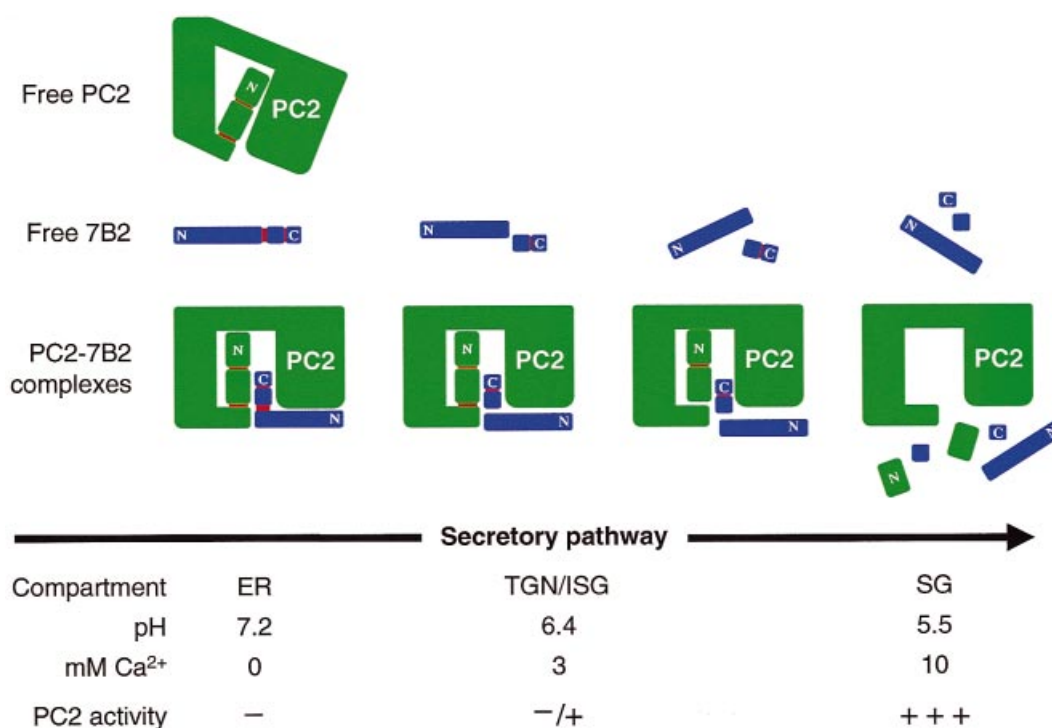


Figure 3 Schematic representation of 7B2 and PC2 transport in the secretory pathway

PC2 is presented as a folded green box with an extended bar at the N-terminus, and 7B2 is presented as a linear or bent blue box. Connecting red bars represent basic processing sites. According to the prevailing model of PC2 and 7B2 trafficking in the secretory pathway, free PC2 tends to misfold and to be retained in the ER, whereas free 7B2 or 7B2–PC2 complexes are more readily transported through the downstream compartments into secretory granules (SG). Affinity between the two molecules is influenced by, among other factors, the pH and the calcium concentration in the successive compartments of the secretory pathway. The pro7B2–proPC2 complex is formed in the alkaline and calcium-poor ER. It is enzymically inactive. Under the mildly acidic, calcium-rich conditions of the TGN and the immature secretory granules (ISG), pro7B2 is cleaved by furin, but its products remain attached to the PC2 zymogen, maintaining the latter in a maturation-conducive conformation. In the ISG, the zymogen self-activates by intramolecular cleavage after the prodomain, in a pH-driven calcium-independent manner. It is possible that the mature enzyme thus generated is transiently inhibited by the pro-region and the 7B2CT peptide. When the complex reaches the even more acidic and calcium-rich SG, these peptides are rapidly degraded by PC2 and CPE to non-inhibitory by-products, allowing the convertase to become fully active.

7B2–PC2 interaction with those mediated by SH3 domains [81,82]. The proregion and the P domain also contribute to the establishment and the stabilization of this interaction [84]. Sequence comparison between PC2 and PC1/3 has led to the identification within the catalytic domain of a unique seven residue (242–248) region of no homology. Substituting the PC1/3^{242–248} region into PC2 reduced the ability of this enzyme to bind 7B2, without affecting its processing activity on pro-enkephalin or POMC [86]. Figure 4 illustrates the 7B2 and PC2 domains currently known to be relevant for interaction between the two molecules.

7B2 binding facilitates PC2 transport in the secretory pathway

Pulse–chase studies of newly synthesized proteins have shown that pro7B2 is transported out of the ER faster than proPC2, suggesting that the former needs not interact with the latter for its trafficking in the secretory pathway. Newly made proPC2, on the other hand, exits the ER much more slowly [5,88,90–92] and must acquire a proper conformation to do so. This conformational change is also required for the zymogen to bind passing pro7B2. Through this association, the conformation is presumably rendered more stable, allowing a faster migration from the ER to the Golgi [80]. Reduction of the bonded half-cystines of pro7B2 with DTT or their mutation to alanine abrogates its

binding to proPC2 and causes retention of the zymogen in pre-Golgi compartments [65,80,81,83,85].

7B2 and PC2 proteins are both packaged into secretory granules. It is unclear whether proPC2 needs to be associated with 7B2 polypeptides to be sorted into these organelles. When 7B2 production was inhibited by antisense RNA in rat medullary thyroid carcinoma rMTC 6-23 cells, proPC2 could still convert into PC2 but was misdirected towards the constitutive secretory pathway [67], suggesting a need for 7B2 for the proper sorting of the enzyme. 7B2 binds PC2 with high affinity ($K_d \approx 7$ nM) [87,93]. Although not yet established, it may be a component of PC2 aggregates that are sorted into the secretory granules [94,95]. It has been shown to aggregate on its own in a calcium- and pH-dependent manner [96]. In part because of this property, it has been grouped with chromogranins and secretogranins into the so-called granin family of proteins, one of whose presumed functions is to facilitate the sorting of neuroendocrine proteins into secretory granules [97]. The strong affinity of 7B2 for PC2 is preserved when the whole molecule or its N-terminal fragment is fused to a heterologous protein. It has been ingeniously exploited by Rovère et al. [98] to deplete mouse corticotroph AtT-20 cells of PC2 by overexpression of a fusion 7B2 C-terminally tethered to the lysosomal cathepsin B. The depletion was due to PC2 binding to this chimaeric protein and to its misdirection towards the lysosomal degradation pathway.

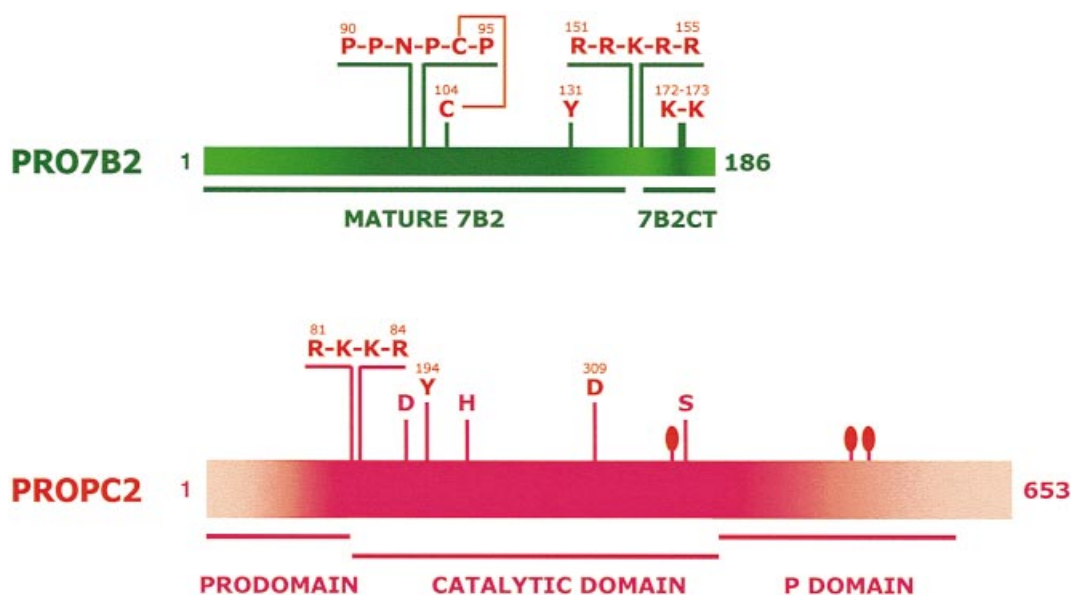


Figure 4 Graphical illustration of domains and residues involved in 7B2–PC2 interaction

Pro7B2 and proPC2 are represented linearly as coloured bars. The colour intensity reflects the relative importance of the various regions for effective interaction between the two molecules, as determined by deletional mutagenesis and site-directed mutagenesis. Residues that have been shown to be critical for the dynamics of this interaction (see the text) are indicated above the bars and are numbered. Most are located in the most intensely coloured regions of the bars. The major functional domains of the molecules are highlighted with lines below the bars and identified. For proPC2, glycosylation sites are indicated with small trees, and the aspartate, histidine and serine residues of the catalytic pocket are shown.

7B2 regulates PC2 activation

The interaction of proPC2 with 7B2 may be both facilitative and regulatory with regard to the maturation and activation of the enzyme. In some cells proPC2 is helped by, but does not absolutely require, 7B2 to proteolytically convert into PC2, as suggested in the above mentioned study with rMTC 6-23 cells expressing antisense 7B2 RNA [67]. In other cells, such as AtT-20/PC2 transfectants, transduced pro7B2 or 7B2¹⁻¹⁵⁰ clearly accelerates proPC2 maturation [88]. In the human neuroepithelioma SK-N-MCIXC cells, which express PC2 but not 7B2, the enzyme is secreted only as an inactive form of 71 kDa. Complementation of these cells with a 7B2 transgene led to the partial processing of endogenous proPC2 into the mature 68 kDa form [99], suggesting a need for 7B2 in proPC2 maturation.

Apparently, not all 7B2 molecular forms can promote this maturation. The precursor form, through its carboxy region (see below), may block, or at least interfere with, this maturation. Its prior processing might be required to allow proPC2 cleavage. Thus when supplemented to a cell-free translation lysate derived from *Xenopus* intermediate pituitary cells, mature 7B2, but not its unprocessed precursor, could stimulate PC2-mediated processing of POMC [100]. In the same vein, a processing-resistant mutant form of pro7B2, unlike the native form, was unable to promote the conversion of proPC2 into PC2 in mouse corticotroph AtT-20/PC2-transfectant cells [88]. This, however, may be due to the weaker affinity of the mutant pro7B2 for the zymogen [79] (leading to its retention in the ER), rather than to a direct maturation block. In a study with highly purified recombinant proPC2 obtained from CHO transfectant cells, neither pro7B2 nor its processing fragments were able to influence in any way the maturation of the zymogen, a process that appeared to be primarily pH-driven [101]. This study indicates that 7B2 may not facilitate proPC2 maturation in such a refined

system, but does not contradict the likelihood of it doing so under the more complex conditions of the cellular secretory pathway.

C-terminal domain of 7B2 (7B2CT) peptide, a specific inhibitor of PC2

The 7B2CT peptide that follows the basic quintuplet has been shown to strongly inhibit PC2 activity *in vitro* at nanomolar levels [87,93]. The Lys¹⁷²-Lys¹⁷³ pair is important for the binding and the inhibitory properties of the peptide [32,102,103]. These properties are conserved across species as they have been observed with *Lymnaea* and *Caenorhabditis elegans* 7B2 [16,17]. However, there is no clear-cut experimental evidence showing that the 7B2CT peptide has any PC2-inhibitory activity *in vivo*. One study has suggested that pro7B2 can prevent proPC2 conversion into PC2 and that its processing and subsequent dissociation are prerequisites for the maturation of the zymogen [92]. Other studies have contradicted this conclusion by demonstrating that the processed 7B2 products remain associated with the zymogen, protecting it from denaturation and allowing its conversion into PC2 [80,104]. Moreover, when the 7B2CT peptide was tethered at the carboxy end of proenkephalin and transduced in mouse corticotroph AtT-20/PC2 transfectants or in rat insulinoma Rin cells, it failed to block PC2 processing of the prohormone [105]. The difficulty to detect any 7B2CT peptide inhibition of PC2 in cells may be due to the fact that, once activated in the increasingly acidic conditions of post-Golgi compartments [5,80,101,106], PC2 would rapidly degrade the peptide to non-inhibitory by-products that are further inactivated by CPE removal of C-terminal basic residues [32].

Clearly, the *in vitro* conditions that have permitted the identification of the inhibitory activity of the 7B2CT peptide can hardly be construed to replicate those existing in the secretory

compartments of cells. The dynamics of the interactions between PC2 and 7B2 in these compartments may be influenced by other parameters, including the composition, the relative concentration and the subcellular distribution of resident and transient components. It remains possible that the 7B2CT peptide, within the pro7B2 context, may indeed interfere with proPC2 conversion into PC2, but only in pre-TGN compartments. Once it is processed by furin in the TGN, its products remain bound to the zymogen but can no longer prevent the latter from being matured, either autocatalytically [107,108] or by related PCs, such as furin and PACE4 [79]. The association, in fact, would allow the zymogen to maintain a maturation-conducive conformation. Once matured, the enzyme may become susceptible to inhibition by both its own propeptide and by the 7B2CT peptide. The need for the latter peptide may be explained by the fact the PC2 propeptide, compared with that of PC1 and PC7 [109,110], is a relatively less potent inhibitor [108]. Whether and how it cooperates with the 7B2CT peptide to maintain the complex enzymically inactive is yet to be demonstrated and clarified. In mature granules the complex may be further loosened. PC2, in conjunction with CPE, would rapidly degrade the propeptide and the 7B2CT peptide into non-inhibitory by-products, thus becoming fully active (see Figure 3).

7B2 function in evolution

The regulatory effect of 7B2 on PC2 biosynthesis and activity extends across evolutionary distances, but its efficiency appears to be determined by intraspecific cellular characteristics. This was made most evident by studying the effect of invertebrate 7B2s on mammalian PC2. For example, full-length *Drosophila* 7B2 was shown to increase the secretion of PC2 activity into the culture medium when transduced into CHO cells overexpressing mouse PC2, as determined by the 7B2CT-inhibitable cleavage of a fluorogenic substrate. It was also able to induce this activity when added as a recombinant protein to Golgi-enriched membranes extracted from these cells [18]. This activity, however, was consistently lower than that induced by rat 7B2. In the same vein, the mature form of *C. elegans* 7B2 was also shown to promote PC2 activation secretion when expressed in these cells or supplemented *in vitro* to their Golgi membrane preparations, but again less efficiently than mature mouse 7B2 [17]. It is very likely that the biogenesis of 7B2 and PC2, as well as their effective interaction, is most adapted to the cellular environment of each species. Thus it was recently reported that *Drosophila* PC2 could not be matured, activated and secreted when transduced in mammalian cells, irrespective of the presence of *Drosophila* 7B2 or mouse 7B2. In contrast, it underwent the processing and secretion when transduced into S2 insect cells, but only in the presence of either insect 7B2 or rat 7B2 [18]. The interspecific inhibitory activity of the 7B2CT peptide on PC2 has also been examined by *in vitro* analysis of PC2-specific cleavage of a peptidyl fluorogenic substrate. Thus human CT7B2 was shown to inactivate *Drosophila* PC2, but 100-fold less efficiently than it did mouse PC2 [18]. Similarly, a *Lymnaea* 7B2²³⁵⁻²⁷³ peptide was shown to inhibit mouse PC2, but 14-fold less potently than it did the orthologue PC2 activity contained in the neuroendocrine light green cell of the mollusc [16]. In the same vein, a full-length recombinant *C. elegans* 7B2 containing the CT region (but not its processed form lacking this region) was shown to inhibit purified mouse PC2 activity *in vitro*, but nearly 20-fold less efficiently than a full-length rat 7B2 [17].

Interestingly, *Lymnaea* and *C. elegans* 7B2 sequences contain more than one region of partial similarity with the VNPYL(Q/K)GKRLD-NVVAKKSVPH (conserved residues are

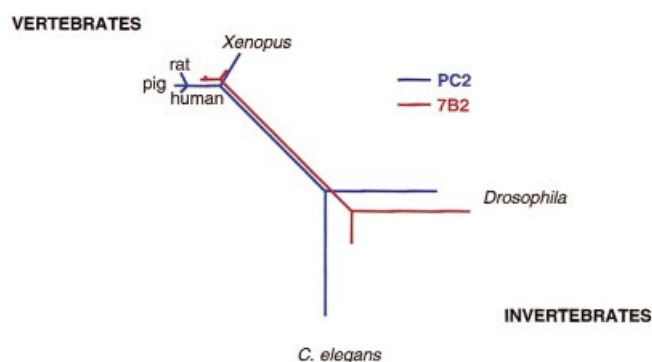


Figure 5 Co-evolution of pro7B2 and proPC2

To examine the evolution of pro7B2 and proPC2, phylum-representative species for which the complete protein sequences of both molecules have been elucidated were considered. These species include human, pig, rat, *Xenopus*, *Drosophila* and *C. elegans*. For each molecule, the sequences of the various species were aligned using the multiple alignment program CLUSTALW (<http://evolution.genetics.washington.edu/phylip/software.etc1.html#ClustalW>). The results were analysed using the neighbour-joining phylogeny program TREE (<http://igs-server.cnrs-mrs.fr/anrs/phylogenetics>) to derive the phylogenies shown. There are general branching similarities between the two trees, as would be expected of functionally linked proteins. However, differences in the length of the branches can also be observed. They probably indicate that, along branches, each protein evolved at a distinct rate. Note how, in mammals, 7B2 sequences can hardly be distanced, as predictable from their homology (see Figure 1), whereas PC2 sequences can. In contrast, between vertebrates and invertebrates, the differentiation of 7B2 sequences is greater than that of PC2 sequences. Visual examination of the aligned sequences (see Figure 1 for 7B2) clearly shows that invertebrate 7B2 sequences have incorporated many more additional sequences during evolution than PC2 sequences. The tree patterns thus suggest both phylogenetic links and differentiation in the functions of the two proteins.

shown in bold and - indicates a gap) region encompassing the functionally crucial KK pair of mammalian 7B2CTs. Thus besides the NPFLQGEQMD-IAAKK (*Lymnaea stagnalis* 7B2²⁴³⁻²⁵⁷) sequence found in the 7B2CT peptide, the *Lymnaea* 7B2 also contains the upstream similar sequence NPNLSSSRKRLTLVAKKS-PH (*L. stagnalis* 7B2²⁰⁹⁻²²⁹). Similarly, the *C. elegans* 7B2 contains the more remotely similar sequence LEENNMHANTIAKK (*C. elegans* 7B2¹⁵²⁻¹⁶⁵), in addition to the C-terminal VNPLYLQGEPLR-SMQKK (*C. elegans* 7B2¹⁹³⁻²⁰⁸). Functionally, a peptide encompassing the *L. stagnalis* 7B2²⁰⁹⁻²²⁹ region was shown to inhibit *Lymnaea* PC2 as well as mouse PC2, but less efficiently than the more C-terminal peptide *L. stagnalis* 7B2²³⁵⁻²⁷³. Collectively, these observations suggest evolutionary conservation of the regulatory function of 7B2 on PC2 biosynthesis and activation, as well as adaptive co-evolution of the two genes during speciation. This view is supported by the striking similarity between the PC2 and 7B2 phylogenetic trees derived from alignments of their respective sequences among human, pig, rat, *Xenopus*, *Drosophila* and *C. elegans* (Figure 5). These trees also suggest that 7B2 may have diverged more than PC2 after phylogenetic separation between vertebrates and invertebrates. This divergence may reflect structural changes needed for the PC2-regulation function or acquisition of new functions by gain or loss of functional domains. Both hypotheses can be supported by the size and number of gaps needed to align vertebrate versus invertebrate 7B2 sequences (see Figure 1). Concerning the presence of multiple PC2-inhibitory domains in *C. elegans* 7B2 and *L. stagnalis* 7B2 sequences, this may have occurred through intergenetic exon shuffling or by sequence duplication during insertional recombination events.

Co-regulation of 7B2 and PC2

The functional link between PC2 and 7B2 also implies that expression of their genes could be co-ordinately regulated. Except for CREs, specificity protein 1 ('SP1'), AP1 and AP2-binding sites, the proximal promoter sequence of these genes share no other obvious regulatory elements [27,111]. Although there are many studies in which the regulation of either PC2 or 7B2 has been individually examined [27,68,112–117], there are very few that have concomitantly analysed the regulation of both proteins in a single organ, tissue or cell line. A co-ordinated increase in the intracellular levels of immunoreactive 7B2 and PC2 has been observed in rMTC 6-23 cells treated with dexamethasone for 1–2 days [67]. In another study [99], the adrenal levels of mRNAs for both proteins were shown to significantly decrease 6 h after insulin-induced hypoglycaemic shock; however, the level of 7B2 mRNA remained reduced 72 h later, whereas that of PC2 mRNA significantly increased 24 h later and remained high for 72 h. This discordance was associated with reduced conversion of proPC2 into PC2, suggesting that down-regulation of 7B2 may be a cellular mechanism of limiting the amount of PC2 activity. Petit-Turcotte and Paquin [118] examined the levels of immunoreactive PC2 and 7B2 in differentiated P19 neurons treated with signal transduction modulators acting through the thyroid hormone receptor (3,3',5-tri-iodothyronine), the glucocorticoid receptor (dexamethasone), protein kinase C (PMA) and protein kinase A [dibutyl cAMP or 3-isobutyl-1-methyl-xanthine (IBMX)]. Both 7B2 and PC2 levels slightly (less than 2-fold), but significantly, augmented after treatment with PMA and dibutyl-cAMP. The increase was generally greater for PC2 than for 7B2. 3,3',5-Tri-iodothyronine and IBMX increased the levels of PC2 but had no apparent effect on that of 7B2. Although dexamethasone alone had no effect, it attenuated the effect of PMA and accentuated that of IBMX [118]. These results suggest that, although co-ordinately regulated, 7B2 and PC2 expression may be differentially sensitive to regulatory agents.

Other biological roles of 7B2

Helping in the trafficking of PC2 and controlling the temporal activation of PC2 may not be the only cellular function of 7B2. Indeed, *in situ* hybridization studies on rat brain have shown that whereas all cells containing PC2 transcripts also contained 7B2 transcripts, there were many cells containing the latter without the former [99]. In a study of *X. laevis* ontogeny, 7B2 mRNA was found in unfertilized eggs, as well as in the earliest developmental stages, whereas PC2 mRNA became detectable only after embryonic neurogenesis [119].

Expression studies in yeast have raised the possibility that 7B2 may effectively interact with other molecules. When the human pro7B2 was expressed in yeast (*Saccharomyces cerevisiae*) containing the endogenous proprotein convertase Kex2 (Kex2⁺ yeast), it remained unprocessed and was retained inside the cells, whereas a truncated 7B2 lacking the last 48 C-terminal residues was secreted. In pro7B2-expressing cells, Kex2 cleavage of a co-transduced proαfactor-IGF-1 fusion protein was inhibited, suggesting Kex2 inactivation by the C-terminal domain of 7B2. Interestingly, in Kex2-deficient (Kex2⁻) yeast, pro7B2 was processed by an alternative protease activity that is induced by the mutation. Yap3, an aspartyl protease that also cuts after pairs of basic residues, is probably this alternative convertase since its coexpression with pro7B2 in Kex2⁺ or Kex2⁻ yeast promotes the processing and secretion of 7B2 products [120]. A coexpression study was also conducted to determine whether 7B2 can exert a chaperone-like effect on the biogenesis and secretion of IGF-1 which, when expressed in yeast, is secreted in

multimeric form. 7B2 did not prevent the multimerization, but formed disulphide-linked complexes with IGF-1. However, when recombinant mature 7B2 was supplemented to the culture medium of recombinant yeast expressing IGF-1 alone, it promoted the formation of IGF-1 monomers in an ATP-dependent manner [121]. In a search for interacting proteins using a yeast two hybrid system, 7B2 was found to possess a potent intrinsic transcription-activating property, and to interact with the tumour suppressor protein p53 [121,122]. Since to date no 7B2-like molecule has been reported in yeast, these intriguing observations need to be confirmed and extended using cells that normally express 7B2.

The likelihood of other cellular roles for 7B2 has been made most evident by the remarkable phenotype of the 7B2 knockout mice generated by Westphal et al. [123]. Like in their PC2-knockout counterparts, PC2 activity is lacking in these mice and processing of pancreatic islet prohormones is severely impaired. However, unlike PC2 null mutants, which are viable, 7B2 null mutants die within weeks after birth from severe Cushing's disease due to excessive secretion of corticotropin by the intermediate lobe of the pituitary. It is unclear which of the various 7B2 peptides are involved in secretion regulation or whether they act in intracrine, autocrine or paracrine fashion. One of them, the C-terminal 7B2^{174–186} peptide, has been shown to induce membrane depolarization of VP and oxytocin of supraoptic nucleus neurons when applied to hypothalamic explants [124]. These observations need to be confirmed with other neuroendocrine systems.

7B2 AS A NEUROENDOCRINE MARKER

7B2 is detectable in human plasma. Its mean plasma level in healthy adults ranges from 40–140 pmol/litre [9,125–136]. It is remarkably high (as high as 1 nmol/litre) in early childhood, gradually decreases to adult levels by 20 years of age and slowly rises with aging [126,128]. It is elevated in pregnancy, from the second to the fourth trimester, but sharply declines soon after delivery, and returns to normal by 4–6 weeks post-partum [129]. The source of this supplemental circulating 7B2 in pregnancy is unclear. It is apparently not the fetus as suggested by the absence of a gradient of 7B2 concentrations in fetomaternal circulation. Indeed, although 7B2 is particularly elevated in fetal pancreas [137] and in cord blood [129,132,138], it is found in comparable amounts in the umbilical artery and the umbilical vein, in lower amounts in the maternal vein and in negligible amounts in the placenta [129,138]. The remarkable increase in plasma 7B2 in patients suffering from chronic kidney failure and liver cirrhosis [126,127,132], suggests that these organs are involved in its clearance.

The variations of circulating 7B2 probably reflect the biosynthetic and secretory states of a variety of neuroendocrine cells. However, the 7B2 reserve seems to be greater in some neuroendocrine cells than in others, as suggested by treatments of healthy individuals with cell-specific hypophysial hormone-releasing hormones. Thus a significant increase in plasma 7B2 was observed in such individuals following treatment with LHRH, but not following treatment with corticotropin-releasing hormone, thyrotropin-releasing hormone or GH-releasing hormone [128,131,136], supporting the preferential storage with pituitary gonadotropins. A correlation between plasma 7B2 and plasma gonadotropins was also reported in menopause and patients suffering from Klinefelter's syndrome, as well as in patients with various human chorionic gonadotropin-secreting tumours of the gastrointestinal tract [134]. In the same vein, 7B2 was shown to be actively secreted by functionless pituitary

Table 3 Conditions associated with elevated circulating levels of 7B2

Condition	References
Infancy (< 2 years)	[128]
Old age	[126,132]
Pregnancy (second and third trimesters)	[129,132]
Menopause	[134]
Klinefelter's syndrome	[134]
Diabetes + oral glucose	[132]
Chronic renal failure	[126,127,132]
Liver cirrhosis	[126,132]
Pituitary tumours	
Gonadotropinoma	[136]
Somatotroma (with acromegaly)	[131]
Medullary carcinoma of the thyroid	[130,141]
Gastrointestinal tract tumours	[125,134]
Pheochromocytoma	[125,130,141]
Small-cell lung carcinoma	[133]

adenoma, which are often associated with gonadotropin production [139]. High levels of circulating 7B2 have been detected in patients with other specific tumours of neuroendocrine origin. Thus higher than normal plasma 7B2 levels have been observed in acromegalic patients affected by a GH-producing microadenoma. These levels were further increased when the patients were intravenously injected with GH-releasing hormone or thyrotropin-releasing hormone [131], but decreased following treatment with the somatostatin analogue SMS 201-995 [140]. Likewise, patients with medullary carcinoma of the thyroid or pheochromocytoma showed elevated plasma 7B2 levels [130]. In contrast, these levels were within normal range in patients affected by Cushing's disease, prolactinoma or medullary carcinoma of the thyroid even after cell-specific exocytotic treatment [131,141]. Table 3 summarizes conditions known to be associated with elevated levels of circulating 7B2.

No study of circulating immunoreactive PC2 under normal and disease conditions has been reported to date to allow quantitative correlation between the enzyme and 7B2. Even if that were possible, it would still be challenging to link the two molecules to correlative variations of PC2 enzymic activity in particular organs or cells. At best, an indirect correlation could be inferred from corresponding changes in the circulating levels of bioactive peptides derived from established PC2 substrates.

Other biological fluids have been studied for their content of 7B2. The normal concentration of 7B2 in cerebrospinal fluid is 10–100-fold greater than that found in the plasma (0.7–2 nmol/litre) [142–144]. It decreases slightly with age [142], but is not significantly altered in cerebrovascular diseases [143,144]. It is also elevated in pleural effusion, with a mean concentration of approx. 600 pmol/litre, but does not vary significantly in benign or malignant pulmonary pathologies [145].

Immunological analysis of pathological tissues has revealed more extensive association of 7B2 with neuroendocrine tumours than titration of its circulating levels. 7B2 has been detected in nearly half of pediatric peripheral neuroectodermal tumours of the bone [146], in a majority of benign and approx. half of malignant pancreatic tumours, mostly in insulin-producing ones [125,137,147,148]. Interestingly, insulinomas containing only proinsulin and not its active mature form were found also to lack 7B2 [147], suggesting a possible link between the absence of the latter protein and the lack of PC2 activity. 7B2 was also present in a small fraction of medullary carcinoma of the thyroid [10,125,148], and among pituitary tumours, in gonadotropinoma and corticotroma [47,136,148], in benign and malignant phaeo-

chromocytoma [125,148,149], in bronchial carcinoids and small-cell lung carcinoma [125,150,151].

Like 7B2, PC2 has been found to be a good marker of neuroendocrine tumours. It has been detected in pituitary adenomas [152,153], medullary thyroid carcinoma [154], pheochromocytomas [155,156], small-cell lung carcinomas [157,158], pancreatic islet tumours [159–161], and various carcinoids [161–163].

By examining neuroendocrine tumour samples, it has been possible to correlate expression of PC2 with the presence of peptides that this proteinase is known to generate from specific precursor proteins. Thus, in a study of POMC-expressing non-pituitary tumours, corticotropin-like intermediate lobe peptide ('CLIP'), a product of corticotropin cleavage by PC2, was found only in those tumours that express this convertase [148]. It can be assumed that these tumours also contained 7B2. A similar correlation involving both 7B2 and PC2 was drawn from the analysis of post-mortem hypothalamus samples from patients affected by the Prader–Willi syndrome (PWS), a neuroendocrine disorder associated with mutations on the paternal chromosome 15q11-q13 [164]. Because of the mapping of the 7B2 gene (*SGNE1*) in this region, it was considered to be a candidate gene for PWS [26]. In a semi-quantitative Southern-blot analysis of genomic DNA from a limited number of PWS patients, we observed no obvious anomaly of the 7B2 structural gene (M. G. Butler and M. Mbikay, unpublished work). However, in a post-mortem immunohistochemical study of supraoptic nuclei and paraventricular nuclei of five such patients, Gabreëls et al. [165] detected 7B2 in only three of the patients. The two patients lacking 7B2 in their hypothalamic nuclei also lacked PC2 and the processed form of VP [166], supporting the functional link between 7B2 and PC2 and the role of this enzyme in VP processing.

CONCLUDING REMARKS

The two-decade-long story of 7B2 has been marked by serendipitous turning points, which have made the importance of this molecule increasingly evident. It is still a matter of semantic debate whether 7B2 is an authentic molecular chaperone [78,80]. Its binding to proPC2, its stabilization of the zymogen in a transport-ready conformation, and its protective effect on PC2 against thermal- and pH-induced denaturation broadly meet some of the chaperone criteria [167]. However, its apparent lack of effect on proPC2 aggregation and folding puts it apart from classical chaperones, such as immunoglobulin heavy-chain binding protein ('BiP')/glucose-regulated protein of 78 kDa [168]. Like bacterial subtilisin [169], and mammalian furin [170], the folding of the PC2 zymogen primarily depends on its prodomain [107,108]. Pro7B2 binding may catalyse this folding towards a conformation that allows a faster exit from the ER. The co-operation between the prodomain and 7B2 may further extend to transient inhibition of PC2 activity, although this aspect remains to be convincingly demonstrated *in vivo*.

The PC2–7B2 model represents a novel neuroendocrine paradigm whereby endoproteolytic maturation of prohormones and proneuropeptides in the secretory pathway is spatially and temporally regulated by the dynamics of specific interactions between the PCs and resident binding proteins. The recent discovery of the proSAAS (where single-letter amino-acid notation has been used) molecule, which acts as a specific and potent inhibitor of PC1/3 [171–173] represents the first corroboration of this paradigm.

Involvement of 7B2 in the regulation of secretion is strongly suggested by the Cushing's disease of 7B2 knockout mice.

Whether, within the neuroendocrine system, this is a generalized or a cell-specific function, remains to be explored. Much is known about 7B2 biosynthesis and secretion, and little about the regulation of its expression at the levels of transcription and translation. Studies on the response of its mRNA and gene to physiological changes are likely to shed additional light on its other cellular functions. Finally, in view of the biological relevance of 7B2, it may be warranted to investigate whether structural or regulatory defects affecting its gene could be responsible for some human pathologies associated with abnormal processing and secretion of hormones and neuropeptides.

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