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ORIGINAL PAPER

Developmental Upregulation of an Alternative Form of pcp2 with Reduced GDI Activity

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Abstract The pcp2/L7 gene is characterized by its very cell type-specific expression restricted to cerebellar Purkinje cells and retinal bipolar neurons. Although remarkable progress as to the biochemical properties of the encoded protein has been made, knowledge on its physiological functions remains sparse. While characterizing a pcp2-driven transgenic strain, we observed the presence of a longer, so far unknown, pcp2 transcript. Different from another recently discovered splice variant, ret-pcp2, expression of this novel transcript is observed in bipolar as well as cerebellar Purkinje cells of mid-postnatal mice. The protein encoded by our novel variant appears to be less efficient in binding to Gα subunits compared to the original L7/pcp2 protein and it is also less inhibitory with respect to GTPγ binding. Its expression in the eye appears to be independent from eye opening in postnatal mice.

Introduction

A remarkable feature of the pcp2/L7 gene is its cell type-specific expression. Since its discovery in 1988 [20, 21], its protein and mRNA products have been repeatedly localized exclusively to cerebellar Purkinje cells (PC) and retinal bipolar cells in various species, including mouse and human [4, 5, 15, 16, 22, 27, 28, 35].

High conservation of protein and DNA sequence, restricted expression, and the relatively late appearance of the gene products after neurogenesis [20, 21, 26, 32, 35] suggested important roles for neuronal maturation. Besides a partial resemblance to platelet-derived growth factor [21], initial sequence comparison failed to provide functional insight. Surprisingly, two different targeted null mutant mouse strains lacked functional or morphological alterations [17, 27]. More detailed studies however found, that mice null mutant for pcp2 show enhanced motor learning abilities [11]. Studies into the cell biology of pcp2 revealed an interesting dissociation of mRNA and protein localization in PC, with the former accumulating in dendrites and the latter being more equally distributed within all cellular compartments [5, 28, 34, 35]. Moreover, the potential for activity-dependent regulation of pcp2 was demonstrated [29]. Insight into function was boosted with the discovery of interaction of pcp2 protein with Gα subunits [12–14, 18, 19, 22, 31], and the recognition of other Gα-interacting proteins sharing a structural feature, the GoLOCO motif, with pcp2 [23]. While characterizing a pcp2-driven

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transgenic strain [2, 3], we realized the presence of a longer pcp2 transcript. Subsequently, we determined its structure, expression pattern, activity-dependent regulation, and subcellular localization as well as key biochemical properties of the encoded protein. The alternative transcript characterized here is different from another recently published product [33, 35].

Material and methods

C57Bl/6 mice were used for all experiments. To determine the influence of light on pcp2 expression, adult mice or mothers with their litters were kept in darkness, and then sacrificed in the dark. Controls were housed under standard light conditions (12 h light/12 h dark). All animal holding and experiments were done in accordance with the national animal welfare regulations and institutional rules.

RNA isolation was performed as described elsewhere [8]. For reverse transcription, 1 μg of total RNA and 0.5 μg oligo-dT primer (GIBCO BRL) were mixed in 12 μl of Tris-EDTA (TE) buffer pH 7.4 and then incubated for 5 min at 90 °C, 10 min at 37 °C and 15 min at room temperature. Each sample was then incubated at 37 °C for 1 h with 4 μl 5× first-strand buffer (GIBCO BRL), 2 μl DTT (0.1 M), 0.5 μl of 0.25 mM dNTP mix, 0.5 μl RNAse inhibitor (40 U/μl, Boehringer), and 0.8 μl reverse transcriptase (200 U/μl, SuperScript, GIBCO BRL). Afterwards, 10 μl of TE buffer were added to obtain a total volume of 30 μl.

PCR (36 cycles) was carried out on 1 μl of cDNA in a reaction mixture containing 1× PCR buffer, 1.5 mM MgCl$_2$, 0.4 μM of each primer, and 0.625 U Taq polymerase (GIBCO BRL) according to the scheme: 5′95 °C [30″95 °C, 30″72 °C, 1′72 °C] 5′72 °C.

To control for sample loading, reverse transcription polymerase chain reaction (RT-PCR) for GAPDH (21 cycles) was carried out for all samples. The whole reaction mixture (25 μl) was loaded on 2 % agarose gels containing ethidium bromide.

Both splice variants were detected with primers: L7sense 5′-AAGGCTTCTTCAACCTGCTGA-3′ and L7anti 5′-GCTG TTCCTGCGGAAGCTGAG-3′. The new splice variant was specifically detected with primers: L7 sense (as above) and L73Aanti 5′-TCCCAGTACTCAAGAAACAGG-3′ (Fig. 1b). GAPDH expression was detected with primers: sense 5′-AC CACAGTCCATGCCATCAC-3′ and antisense 5′-TCCA CCACCCTGTTGCTGTA-3′.

To verify the PCR products, bands of interest were extracted from the gel, subcloned into the pCRII plasmid (TA Cloning Kit, Invitrogen) and sequenced on an ABI PRISM 377 DNA Sequencer (Perkin-Elmer). Sequence comparisons were performed using BLAST (NCBI, Bethesda, MD, USA).

Molecular modeling was performed using the SYBYL software, version 7.2 (Tripos Inc.). The model was generated, in part, by homology modeling with filamentous hemagglutinin secretion domain (Protein Data Bank, ID code 1rwr) as a template. The model was energy-minimized using a conjugate gradient method and subjected to repeating cycles of molecular dynamics using Kollman force fields and united atoms [30].

In situ hybridization for detection of the novel transcript was carried out at 38 °C according to a protocol described elsewhere [24]. The oligonucleotide DNA probe was complementary to base pairs 2,461–2,507 of the pcp2 genomic sequence (Fig. 1a; accession number S40022) [25]. The hybridization specificity was checked by competing with 100× excess of the cold probe.

As described later (see "Results" section), the novel longer transcript encodes a shorter protein variant than the known shorter transcript. We refer to the native proteins as long pcp2 and short pcp2 proteins, respectively.

For the generation of recombinant glutathione S-transferase (GST)–pcp2 fusion proteins, cDNAs corresponding to short and longer transcript were cloned into the EcoRI and XhoI sites of the pGEX-4T-1 vector (GE Healthcare) in frame with the glutathione-S-transferase/thrombin cleavage site. A single direct primer (L7Eco.d: AGG GCG AAT TCA TGG AGG AGC AGC GCT GTT C), containing an EcoRI site, was used to amplify both forms of pcp2 from mouse cerebellar cDNA. As reverse primers, both containing an XhoI restriction site, L7lgXho.r (TAG GAT CTC GAG AAC TCT CAA GGA GCT TGT G) provided specificity for the short transcript, while L7shXho.r (AAC AGG CTC GAG GAT TAT TTT GAG TTC AAA GC) amplified the long transcript only.

The resulting plasmids (GLL7 for the long form and GSL7 for the short form) were transformed into the JM109 $Escherichia coli$ to yield recombinant proteins (we refer to the GST-short pcp2 protein as SL7 and to the GST-long pcp2 protein as L7) as was the empty pGEX vector for the production of GST alone as a control. Proteins were obtained after 1 mM IPTG induction and purified by sepharose–glutathione affinity chromatography. Purity and integrity of the recombinant fusion proteins were verified by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE; not shown).

Recombinant baculovirus expressed purified Gαo and Gαi1 [10] were kindly provided by Steve Graber (Morgantown West, VA, USA) and were preincubated at 1:1 M ratio (2.5 pmol) with purified noncleaved GST fusion proteins for AGS3 (cDNA provided by Steve Lanier, New Orleans, LA, USA), long pcp2, short pcp2, and GST alone in buffer A (20 mM HEPES, pH 8.0, 130 mM NaCl, 3 mM MgCl$_2$, 1 mM DTT, 1 mM EDTA, 10 μg/μl, bovine serum albumin, and 0.1 % Triton X-100) for 20 min at 25 °C in the presence of 1 μM GDP. At t=0, GTPγS^{35} (1 μM; specific activity, 1×10^5 cpm/pmol, New England Nuclear) was added for 60 min. Reactions were terminated by dilution into ice-cold phosphate-buffered saline (PBS) and rapidly filtered through 25 mm round nitrocellulose membranes (Millipore, Billerica, MA, USA; 0.45 μM HA), washed twice with 20 ml of cold PBS. Filters were placed in scintillation fluid and counted
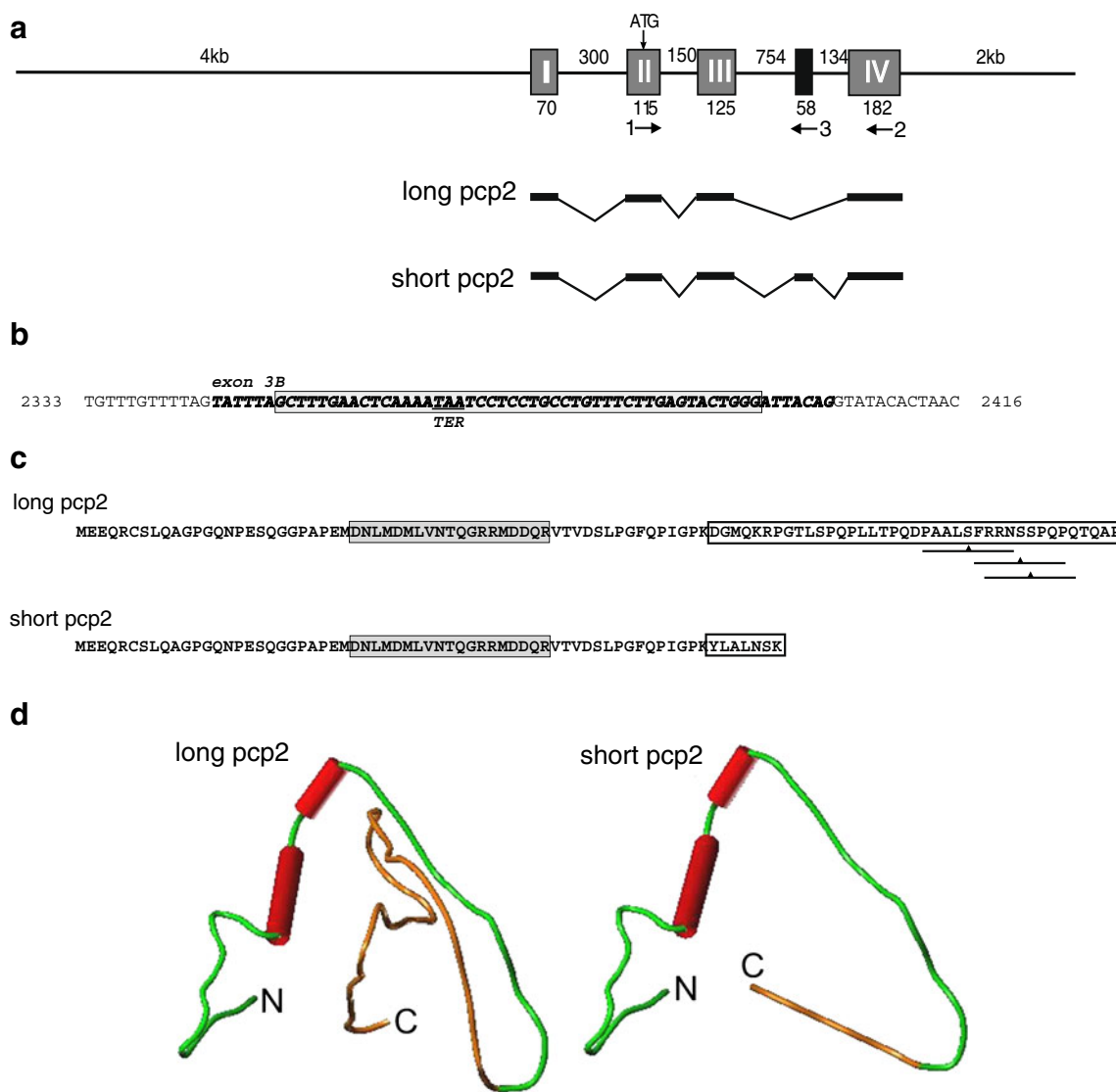
Fig. 1 Structure and sequence of the novel pcp2 transcript and protein. **a** Structure of the transcripts for long and short pcp2 (long and short refer to the protein and not to the mRNA). *Gray* and *black boxes* indicate previously known exons and the novel exon 3B, respectively. Lengths of exons and introns are indicated in base pairs. *Arrows* indicate primers used for RT-PCR. *1* L7sense, *2* L7anti, *3* L73Aanti. **b** Nucleotide sequence of exon 3B (*bold italic*) with intronic junctions. TER indicates the in-frame translation stop codon, and the *gray-shaded box* is the complement of the in situ hybridization probe. **c** Sequence of short and long pcp2 proteins. The *gray-shaded box* represents the GoLOCO motif. Sequences unique to either protein are *framed*, and predicted C-terminal phosphorylation sites are *underlined* with the phosphorylated serine being indicated by an *upward arrow*. **d** Computer-generated models of long and short pcp2. C-terminal domains that distinguish the two variants are indicated in *orange*. *Red cylinders* represent α-helical structures of the GoLOCO domain

in a Packard Tri-Carb A2200 liquid scintillation counter. Blank filters (no protein) were used to determine background and non-specific binding was determined with parallel filters incubated with excess (0.1 mM) cold GTPγS (Sigma).

In vitro translated Gα subunits were [S^{35}]-methionine labeled and prepared as previously described using the TNT coupled in vitro translation system (Promega) [9]. Similar amounts of translate (5–10 μl) were incubated with 0.3 μg of GST, AGS3, long pcp2, or short pcp2 for 2 h at room temperature in buffer A +0.1 % Triton X-100, 150 mM NaCl, and 20 μM GDP (binding buffer). Glutathione agarose beads were added for 30 min at room temperature, centrifuged, and washed three times with 1 ml ice-cold binding buffer. Samples were eluted in 2× SDS-PAGE sample buffer by heating at 100 °C for 5 min and analyzed by SDS-PAGE and autoradiography.

Results

RT-PCR on eye and cerebellar RNA using primers placed in exon 2 (L7sense) and 4 (L7anti) (Fig. 1b), consistently detected a novel 350 bp product together with the 300 bp band expected

Fig. 2 Developmental expression of the novel pcp2 transcript. Transcripts encoding short pcp2 protein were detected by transcript-specific RT-PCR at the indicated postnatal time points (*upper panel*)
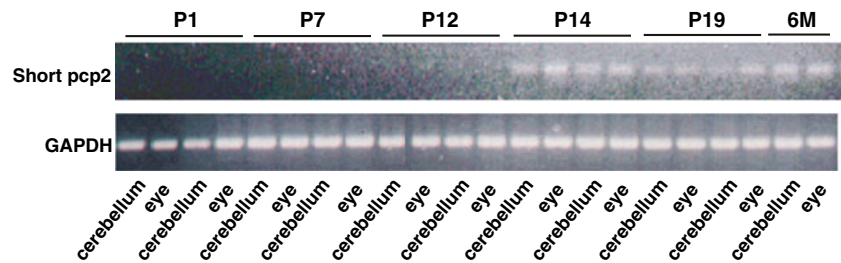
from the known pcp2 gene structure (Fig. 2). Sequencing and analysis of the RT-PCR product revealed a novel stretch of 58 bp between 2,455 and 2,513 bp within intron 3 (Fig. 1a). This analysis also revealed splice donor and acceptor sites flanking this exon. The novel exon, dubbed 3B, can be included or excluded resulting in two different pcp2 transcripts (Fig. 1b). In the following, we will refer to the originally published exon 3 as exon 3A. Interestingly, when included, exon 3B introduces an in frame stop codon. Thus, exon 4 does not contribute to the coding of this alternative product. As the translated product is 32 amino acids shorter than the originally published protein (here referred to as long pcp2 protein), we call it short pcp2 protein. The GoLOCO motif of long pcp2 is found between amino acids 27 and 45, and is entirely encoded by exon 3A. It is, therefore, not altered in short pcp2. The C-terminal, exon 4-encoded part of pcp2 contains a cluster of predicted phosphorylation sites (scores higher than 0.95; NetPhos 2.0, CBS Technical University of Denmark) [6]. These are a putative PKC site at serine 85 (PAALSFRNN), a CaM kinase II/PKA site around serine 90

(FRRNSSPQP), and a Cam kinase II/PKA/PKG site around serine 91 (Fig. 1c). Two of them are conserved between mouse, rat, and human [35]. With the exception of another predicted site at serine 18 (QNPSESQGGP), none of the putative phosphorylation sites of long pcp2 is present in the short pcp2.

Computer analysis of long and short pcp2 protein variants did not reveal many characteristic structural motives. Except for α-helical domains corresponding to the GoLOCO motif, the proteins are essentially characterized by an extended structure (Fig. 1d).

To study expression of the novel transcript, we designed a primer placed in the novel exon 3B (L73Aanti; Fig. 1b). RT-PCR using primers L7sense and L73Aanti confirmed the presence of the novel transcript in eye and cerebellum of adult mice (Fig. 2). During development, expression of the novel form is first detected between P12 and P14 in eye and cerebellum. The presence of the long form was observed already at P7 (data not shown).

To localize the novel transcript at the cellular level, in situ hybridization was performed on cerebellar and retinal sections

Fig. 3 Localization of transcripts coding for the novel short pcp2 protein by in situ hybridization in adult C57BL/6 mice. **a** Dark field imaging of the cerebellar. *g* Granular cell layer, *p* Purkinje cell layer, *m* molecular layer. *Bar* 100 μm. **b** Control section. *Bar* 100 μm. **c** Bright field picture of Purkinje cells showing silver grains over cell bodies of Purkinje cells (*arrow heads*). *Bar* 100 μm. **d** Phase contrast image of mouse retinal layers. *PE* pigment epithelium, *R&C* rod and cone photoreceptors, *ONL* outer nuclear layer, *OPL* outer plexiform layer, *INL* inner nuclear layer, *IPL* inner plexiform layer, *GCL* ganglion cell layer. *Bar* 100 μm. **e** Dark field image of a hybridized retina section. *Bar* 100 μm. **f** Control section. *Bar* 100 μm
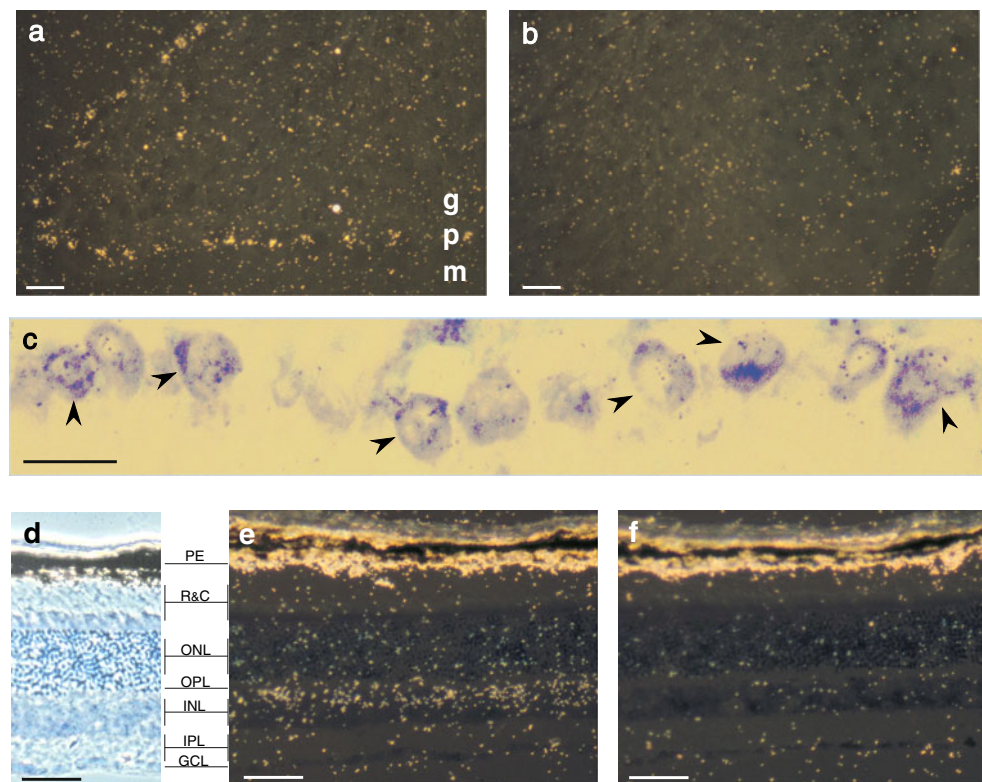
using an oligonucleotide probe corresponding to 46 bp of exon 3B. Microscopic analysis revealed specific signals within the cerebellar cortex at the level of the PC layer (Fig. 3a, b). Higher magnification microscopy revealed the presence of silver grains over the cell bodies of PC (Fig. 3c). In sections of the retina, labeling was detected in the outer part of inner nuclear layer, where bipolar neurons are localized (Fig. 3d, e). Specific signal was also found at the outer plexiform layer.

Because expression of transcripts encoding the novel short pcp2 protein was first detected around the time of eye opening in mice (P12-14) [25], we wondered whether it would be modulated by maintenance of mice in the dark (Fig. 4). Pcp2 expression was analyzed in adult animals housed in the dark for 60 h or 6 days, respectively, and compared to animals kept under standard light–dark conditions (Fig. 4a). After the indicated time, animals were sacrificed in the dark, and tissue samples were immediately dissected for analysis. RT-PCR using the exon 2–exon 4 primer pair detected the presence of both transcripts in the eye and the cerebellum. It failed, however, to reveal any differences between groups. To investigate a possible induction of expression by light at the time of eye opening, P1 litters were maintained in the dark together with their mothers (Fig 4b). Pups were sacrificed in the dark at P15 and P19, tissues dissected and RT-PCR performed as above. Controls were pups kept under standard light–dark conditions. Again, both splice variants were detected in both tissues at levels apparently not influenced by dark rearing.
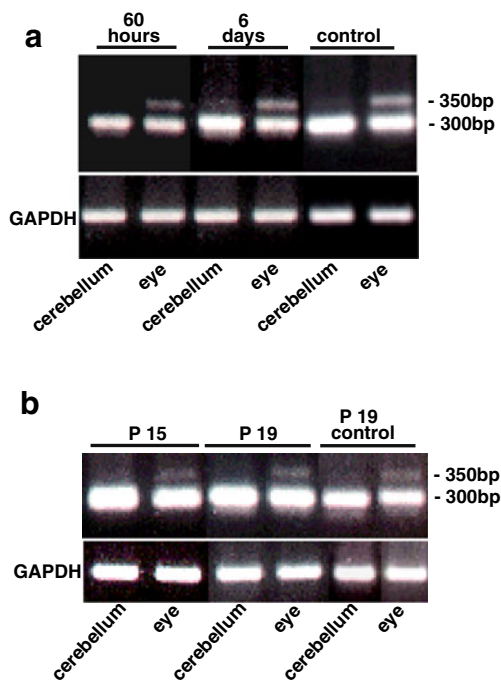

Fig. 4 Influence of dark breeding on expression of pcp2. **a** Adult C57Bl/6 mice were kept in darkness for 60 h or 6 days after which tissues were processed for RT-PCR common for both transcripts. **b** P1 pups were kept in darkness with their mothers until tissue dissection at P15 and P19. Controls were kept under standard light conditions. The length of the amplimers is given in base pairs

To investigate whether short pcp2 protein functions as a GDI for Gα subunits, we first examined whether short pcp2 interacts with Gα subunits. Figure 5a shows in vitro translated and [S^{35}]-methionine labeled Gαo, Gαi1, 2, and 3 used in GST pull-down experiments with GST (negative control), AGS (positive control), long pcp2 (L7), and short pcp2 (SL7). The GST proteins are shown in the Coomassie-stained gel below and the amount of labeled Gα subunit precipitating under each condition is shown in the autoradiogram. The relative interaction of SL7 and L7 with Gαi1, Gαi-2, Gαi-3, and Gαo is summarized in the bar graphs (Fig. 5b) relative to the AGS3 binding for this experiment. The experiment was repeated twice with similar results. It appears that for all four tested Gα subunits, the preferential binding was AGS>>long pcp2>short pcp2. Albeit, binding of SL7 was weak when compared to AGS3 it was higher than binding of GST alone. Importantly, binding of SL7 was clearly less than that of LL7. As expected from other reports [18], binding to Gαo was weak for all three GST fusion proteins in comparison with the Gαi family. There did not appear to be any preference for short pcp2 in comparison with long pcp2 for interacting with Gαo or any of the Gαi subunits.

We next examined the GDI potency of short pcp2 protein in comparison with long pcp2 and AGS3 (Fig. 5c). Baculovirus-purified Gαo and Gαi1 were used for these experiments and GTPγS$^{[35]}$ binding to each Gα subunit was compared in the presence and absence of GST (negative control and binding set to 100 %), GST-pcp2 long (L7), GST-pcp2 short (SL7), and GST-AGS3 under conditions very similar to those previously used to characterize differences between pcp2 and AGS proteins (e.g., [7]). The degree of GTPγS$^{[35]}$ inhibition in these conditions mirrored the binding results shown in Fig. 5a, b. There was a small but consistent inhibition of GTPγS$^{[35]}$ binding to purified Gαo (Fig. 5c) and there was no significant difference in inhibition for AGS3, short or long pcp2. However, the inhibition of GTPγS$^{[35]}$ binding to Gαi1 revealed relative potencies indicated already by the binding experiments; AGS3>long pcp2>short pcp2. There was no significant difference in inhibition of GTPγS$^{[35]}$ binding to Gαi1 for short or long pcp2, but short pcp2 protein was significantly different from control and AGS3. Taken together, the GST pulldowns and GTPγS$^{[35]}$ binding results are consistent with short pcp2 binding less avidly to Gαi1 and therefore being a slightly less effective GDI than long pcp2.

Discussion

Our study describes alternative splicing of the pcp2/L7 gene. The protein product encoded by the novel long transcript (short pcp2 protein) lacks most of the carboxy-terminal half of the originally described protein (long pcp2 protein), but still contains the N-terminal GPR motif. It is different from the
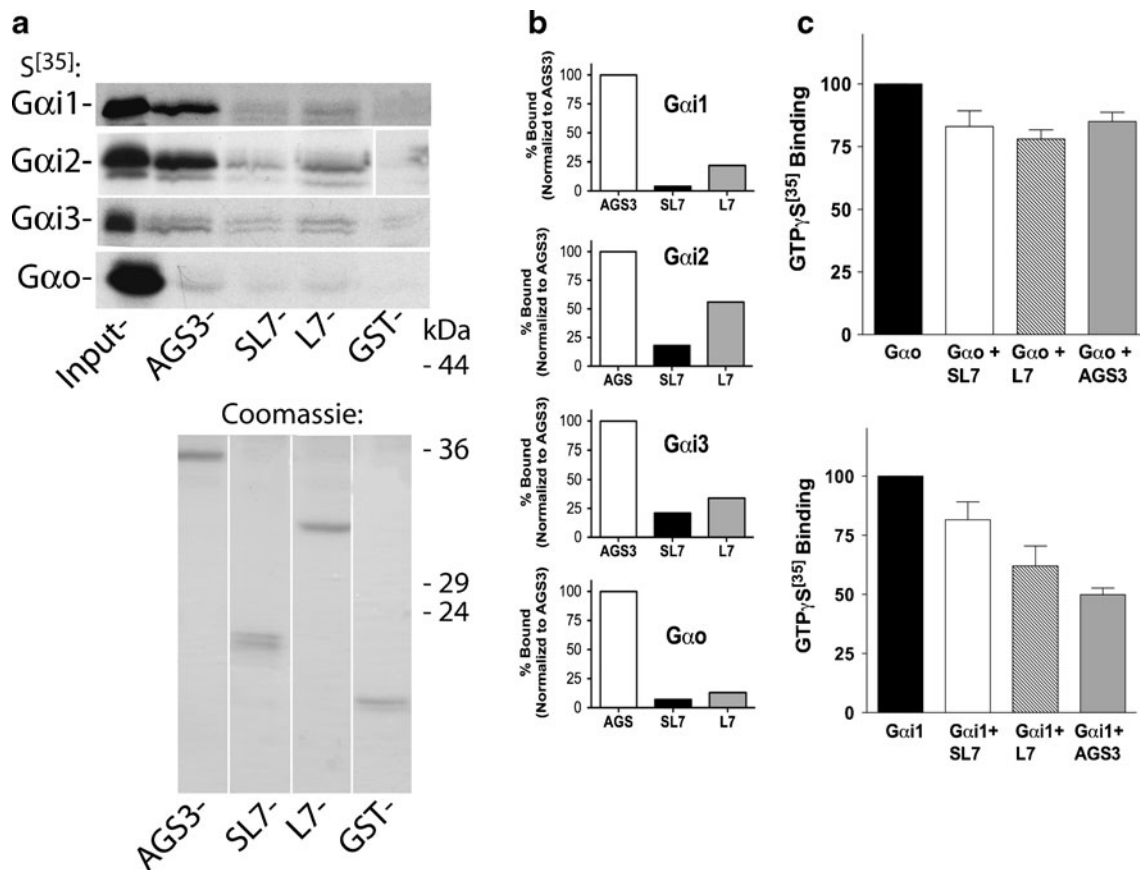
Fig. 5 Interaction with G protein α-subunits. **a** Interaction of Gα Subunits with short and long pcp2 protein. The indicated in vitro translated and S35-methionine labeled Gα subunits were incubated with recombinant GST fusions of AGS3, and short (SL7) and long pcp2 (L7), and GST alone, and then precipitates were analyzed by SDS-PAGE (see "Material and Methods" for details). *Top panel* the *left* lane is 5 % (Gαi2, Gαi3) or 10 % (Gαo, Gαi1) of input into the binding. Precipitated Gα subunits with each of the GST fusion proteins are shown in the subsequent lanes. The *bottom panel* shows Coomassie blue stained gel of the fusion proteins used in the binding experiments. Exposures are 24–48 h. **b** The binding of each Gα subunit to L7 and SL7 is shown relative to the AGS3 binding. **c** GTP binding to baculovirus-purified Gαo (*top*) and

Gαi1 (*bottom*) in absence or presence of recombinant GST fusions of AGS3, short pcp2 (SL7), and long pcp2 (L7) (see "Material and Methods" for details). Specific binding of GTPγS to Gα subunits was determined in triplicate and set to 100 %. Results are the mean values± SEM (Gαo, $n=8$; Gαi1, $n=6$ independent experiments). In comparison to Gαo alone, all three fusion proteins had small but significant reductions in GTPγS binding (SL7, $p=0.017$; L7 and AGS3, $p<0.001$). For Gαi1, $p=0.036$ for SL7 and $p<0.001$ for L7 and AGS3. The differences between short and long pcp2, and long pcp2 and AGS3 did not reach statistical significance, but short pcp2 was significantly different from AGS3 ($p=0.003$)

product of a recently described alternative splicing of 5′ exons [35]. Several additional features distinguish long from short pcp2 protein. First, there seem to be differences as to the developmental time course of expression. The novel transcripts appear to occur later although more detailed expression analysis is needed to exclude misleading effects of its low expression level. Our data on short pcp2 together with previous work [35] suggest that, at least in the cerebellum, both forms co-exist in the same cell. Its expression in retina and cerebellum distinguishes our transcript from a previously described splice variant, coined ret-pcp2, which is exclusively expressed in retinal bipolar cells and accelerates light responses [33]. Thus, generation of our short form could be readily explained by assuming that the alternative form depends on maturation of the splicing apparatus and is cell autonomous, or is induced by extrinsic systemic

factors, e.g., hormones. It is of interest in this context, that expression of the transcripts encoding long pcp2 protein is transcriptionally activated by thyroid hormone during the second and third week of cerebellar development in the rat [1]. Earlier transcriptional activation by thyroid hormone appears to be repressed by a DNA-binding protein. Similar mechanisms, e.g., blockade of *cis*-acting splicing enhancers, could explain the developmental pattern of alternative splicing observed here. In contrast, use-dependent activity in the retina as initiated by eye opening is not a major factor regulating this process.

Second, biochemical properties of short and long form differ. When recombinant Gα subunits are used, both forms act as GDI, with long pcp2 protein being more potent. The meaning of increased amounts of a weaker GDI during development is unclear at present. Short pcp2 might replace long forms at some,

but not all, specific intracellular sites. Transfection experiments so far failed to reveal such specific intracellular targeting (data not shown). This might be due to masking caused by overexpression of the protein. Alternatively, the upregulation of the short form might tune the interaction of the long form in homo- or heteromeric molecular complexes. Our data indicate that relative expression of short to long variant is stronger in retina than cerebellum. This might suggest that retinal bipolar cells, which are known to express an additional specific pcp2 isoform [33], might be particularly dependent on fine tuning of pcp2 and G-protein function. It is interesting to speculate on the differing potencies of GDI activity of long and short pcp2. Both proteins contain a single GoLOCO motif, so the differences are likely to result from important other conformational or structural differences between the isoforms. Further differentiation in the biochemical properties of the short variant might depend on the use of the alternative exon 1B, which would introduce a second GoLOCO motif [35]. We cannot exclude that functional differences between both forms are stronger when additional Gα subunits are tested. In addition, there are intriguing differences in putative post-translational modifications of short and long pcp2.

A cluster of phosphorylation sites predicted in the C-terminus of long pcp2 is lost in the short variant. This includes a site for phosphorylation by protein kinase G, which is abundantly expressed in PC, and possibly also in retinal bipolar cells. Further experimentation has to be awaited to see whether pcp2 is indeed a substrate for G kinase, and subsequently, how hyperphosphorylation would interfere with the developmental function of pcp2.

As indicated by the work on ret-pcp2 [33], pcp2 splice variants subserve delicate and important biological roles. These might depend on the proportion of the different splice forms and their products. Future progress in understanding the biological function of pcp2 will require a careful comprehensive analysis of the expression of all its different splice variants.

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