Brief Report

The Transcriptional Coactivator CBP Interacts with β-Catenin to Activate Gene Expression

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Abstract. β-Catenin plays a pivotal role in the transcriptional activation of Wnt-responsive genes by binding to TCF/LEF transcription factors. Although it has been suggested that the COOH-terminal region of β-catenin functions as an activation domain, the mechanisms of activation remain unclear. To screen for potential transcriptional coactivators that bind to the COOH-terminal region of β-catenin, we used a novel yeast two-hybrid system, the Ras recruitment system (RRS) that detects protein–protein interactions at the inner surface of the plasma membrane. Using this system, we isolated the CREB-binding protein (CBP). Armadillo (Ar) repeat 10 to the COOH terminus of β-catenin is involved in binding to CBP, whereas β-catenin interacts directly with the CREB-binding domain of CBP. β-Catenin synergizes with CBP to stimulate the activity of a synthetic reporter in vivo. Conversely, β-catenin-dependent transcriptional activation is repressed by E1A, an antagonist of CBP function, but not by an E1A mutant that does not bind to CBP. The activation of Wnt target genes such as siamois and Xnr3 in Xenopus embryos is also sensitive to E1A. These findings suggest that CBP provides a link between β-catenin and the transcriptional machinery, and possibly mediates the oncogenic function of β-catenin.

Key words: X. laevis • CREB-binding protein • T cell factor/lymphoid enhancer factor • transcriptional activation • Wnt

Introduction

Wnt signaling pathways regulate a variety of processes including cell growth, oncogenesis, and development (Moon et al., 1997; Miller et al., 1999). Upon Wnt signaling, β-catenin accumulates in the nucleus, and binds to transcription factors of the TCF/LEF1 family, leading to transcriptional activation (Behrens et al., 1996). The TCF/LEF family members contain a single DNA-binding high mobility group (HMG) domain, whereas β-catenin provides transcriptional domains (reviewed by Barker et al., 2000). In the absence of nuclear β-catenin, the TCF/LEF transcription factors recruit the Groucho and CtBP corepressors to repress transcription (Roose et al., 1998; Brannon et al., 1999). An additional corepressor protein, the Drosophila melanogaster CREB-binding protein (dCBP), was shown to be involved in the repression of dTCF target genes in vivo (Waltzer and Bienz, 1998). In response to Wnt signaling, β-catenin somehow overcomes these repressive effects to activate transcription. Constitutive activation of downstream target genes, such as c-myc and cyclin D1 by the TCF/LEF-β-catenin complex is implicated in the development of cancer (He et al., 1998; Tetsu and McCormick, 1999).

β-Catenin and its Drosophila ortholog, Armadillo (Ar), are composed of 12 Ar repeats flanked by unique NH2 and COOH termini. Based on reporter gene assays, it has been suggested that two regions of β-catenin mediate transcriptional activation (Su et al., 1998; Hecht et al., 1999). In particular, the COOH-terminal activation domain was reported to be sufficient both for signaling and for oncogenic transformation (reviewed by Hecht et al., 1999). Genetic analysis has also demonstrated that the
corresponding region of \( \alpha \) rm is required for Wingless signaling in vivo (Cox et al., 1999). However, the underlying mechanisms for transcriptional activation by \( \beta \)-catenin are poorly understood.

In the present study, we have identified CBP as a transcriptional coactivator that binds to the COOH-terminal region of \( \beta \)-catenin. \( \beta \)-Catenin physically interacts with the CREB-binding domain of CBP. CBP then cooperates with \( \beta \)-catenin to activate transcription in mammalian cells and Xenopus laevis embryos.

Materials and Methods

Plasmids

An expression plasmid, pRas(61)\( \Delta F \)-\( \beta \)catR8-C, encoding the RRS bait was constructed by inserting cDNA sequences encompassing COOH-terminal region of \( \beta \) catenin (amino acids 425-781) in frame with activated Q63L c-Ha-Ras into the 350B-SRS (Isakov et al., 1998). The mouse CBP expression plasmid pRc/RSV-mCBP-HA and GST-CBP 451–682 fusion plasmid were gifts from R. Goodman (Vollum Institute, Portland, OR; Chrivia et al., 1993; K wok et al., 1996). Expression plasmids for E1A, E1A mutRB, and E1A mutCBP were provided by T. Kozarides (Welcome/CRC Institute, Cambridge, UK; Bannister and Kouzarides, 1995). \( \Delta nL\)EF-1 expression plasmid was a gift from J. Behrens (Max Delbruck Center, Berlin, Germany; Behrens et al., 1996). The \( \beta \)-catenin deletion constructs shown in Fig. 1 B were amplified by PCR with BamHI and subcloned into the BamHI site of 350B-SRS. To generate His-tagged \( \beta \)catR10-C expression plasmid and GAL4-\( \beta \)catR10-C fusion construct, an insert of the corresponding yeast expression plasmid was excised, and subcloned into pET-28c (Novagen) and pCMV-\( \beta \)D (Stratagene), respectively. GAL4 reporter plasmid pFR-Luc was obtained from Stratagene. For in vitro synthesis of RNA used in Xenopus injection experiments, the full-length mouse CBP cDNA from pRc/RSV-mCBP-HA was inserted into the HindIII and SacI sites of pXeX (Johnson and Krieg, 1994). A 5′ EcoRI fragment encoding E1A or E1A mutCBP was subcloned into pc52+.

RRS Screening

RRS screening in yeast was performed as described (Broder et al., 1998). In brief, cdc25-2 cells were first cotransformed with the pRAS(61)\( \Delta F \)-\( \beta \)catR8-C bait and mGAP expression plasmid (A ronheim, 1997), and then used to transform with HeLa cell cDNA library. The expression of library cDNA was controlled by a galactose-inducible promoter. Transformants were grown on selectable minimal glucose plates for 5 d at 25°C, followed by replica plating onto minimal galactose plates, and incubated at 37°C for 5–7 d. Positive colonies exhibiting efficient growth on galactose plates at 37°C were isolated and tested for galactose-dependent growth at 37°C. Library plasmids were extracted and further analyzed by DNA sequencing and retransformation of cdc25-2 cells to test the specificity of interaction.

In Vitro Binding Assays

2 μg of GST or GST-CBP 451–682 was incubated with 1 μg of bacterially expressed and purified His-tagged \( \beta \)catR10-C or c-myctagged \( \beta \)-catenin (Y ost et al., 1996) at 4°C for 1 h in 20 μl of protein-binding buffer (PBB: 20 mM Hepes-NaCl, pH 7.9, 20% glycerol, 0.5 mM EDTA, 60 mM NaCl, 6 mM MgCl,L, 0.1% NP-40, 5 mM 2-mercaptoethanol, 1 mM PMFS). A fter incubation, 2 μl of glutathione-Sepharose 4B (Pharmacia Biotech) in 20 μl of PBB was added, and the mixture was rotated at 4°C for 1 h. The beads were collected and washed with PBB, and then bound proteins were eluted for SDS-PAGE. His-tagged \( \beta \)catR10-C and \( \beta \)-catenin were detected on immunoblots by an anti-His antibody (Qiagen) and an anti-myctagged antibody, respectively.

Cell Culture, Coimmunoprecipitation, and Luciferase Assays

HeLa and COS7 cells were maintained in MEM and DME with 10% FBS, respectively. SW480 cells were maintained in Opti-MEM I (GIBCO BRL) supplemented with 10% FBS. Transient transfections into HeLa cells were carried out by the calcium phosphate precipitation method.
SW480 and COS7 cells were transfected using lipofectamine Plus (GIBCO BRL). For coimmunoprecipitation experiments, COS7 cells were transfected with 0.5 μg of myc-tagged point-mutant (pt) β-catenin expression plasmid (Yost et al., 1996) and/or 1 μg of pRc/RSV-CBP-HA. Two days later, cells were washed and lysed in 1 ml of a lysis buffer (20 mM Tris-HCl, pH 8.0, 75 mM NaCl, 1.5 mM MgCl2, 1 mM EDTA, 0.5% NP-40, 10% glycerol, 1 mM PMSF, 10 μg/ml each of leupeptin and aprotinin). Cell lysates were cleared and incubated with anti-CBP polyclonal antibodies (A-22; Santa Cruz Biotechnology), followed by incubation with protein A-Sepharose beads (Sigma Chemical Co.). The beads were collected and washed three times with the lysis buffer before SDS 8% PAGE. Immunoblotting was subsequently performed with an anti-myc mAb. For luciferase assays, a β-galactosidase expression plasmid was included in each transfection as an internal control. Luciferase and β-galactosidase activities were measured 24 h after transfection, and luciferase activity was normalized to β-galactosidase activity. Each transfection was performed in triplicate and repeated at least three times.

**RNA Injections and Reverse Transcriptase PCR Analysis**

RNA injections and RT-PCR analysis were carried out as described previously (Brannon et al., 1999). **Results and Discussion**

To identify proteins that interact with the COOH-terminal region of β-catenin and that might be involved in transcriptional activation, we carried out an extensive screening using the RRS. Conventional yeast two-hybrid system was not suitable for our purpose because this region of β-catenin activates the reporter expression by itself when fused to a heterologous DNA-binding domain in yeast (Hecht et al., 1999). RRS is based on the ability of mammalian R as to rescue the growth defect of the yeast strain, in which the endogenous R as is inactive at the nonpermissive temperature (37°C) due to the lack of a functional Cdc25 guanyl nucleotide exchange factor (Broder et al., 1998). For RRS screening, a bait protein of interest is fused at the COOH terminus of mammalian activated Ras lacking its membrane localization (New et al., 1999). RRS is based on the ability of mammalian R as to rescue the growth defect of the yeast strain, in which the endogenous R as is inactive at the nonpermissive temperature (37°C) due to the lack of a functional Cdc25 guanyl nucleotide exchange factor (Broder et al., 1998). For RRS screening, a bait protein of interest is fused at the COOH terminus of mammalian activated Ras lacking its membrane localization signal [Ras(61)], whereas library cDNA s are fused to the v-Src myristoylation sequence targeted to the plasma membrane. A protein–protein interaction between the bait and library protein results in the recruitment of β-catenin to activate transcription.

We used the COOH-terminal region of X enopus β-catenin extending from Arm repeat 8 to the COOH terminus, βcatR8-C (Fig. 1 B), as a bait to cotransform cdc25-2 yeast cells with a myristoylated H eLa cell cDNA library. A fter screening ~2.5 × 106 colonies, a single clone encoding an NH2-terminal fragment of CBP (amino acids 153–822) was isolated. To confirm the specificity of the interaction, the plasmid encoding CBP was recovered, and retransformed into the same yeast strain with either an expression plasmid for Ras(61)ΔF-βcatR8-C or a negative control plasmid encoding Ras(61)ΔF alone. As shown in Fig. 1 A, cdc25-2 cells transformed with the CBP expression plasmid were able to grow at 37°C when coexpressed with Ras(61)ΔF-βcatR8-C, but not with Ras(61)ΔF, suggesting that the interaction is dependent on the βcatR8-C bait.

To further narrow down the CBP interaction domain in β-catenin, a series of Ras(61)ΔF-β-catenin fusion constructs spanning the COOH-terminal region were transformed into cdc25-2 cells, together with the CBP expres-

Figure 2. CBP synergizes with β-catenin to activate transcription. H eLa cells were transiently transfected with 1 μg of pTOPFLASH or pTOPFLASH reporter, indicated amounts of CBP expression plasmid, either with or without 1 μg of pt β-catenin-encoding plasmid. Transfections were carried out in triplicate and the means ± SD are shown. Where they are not evident, this is due to minimal variability between transfections.
variety of transcription factors to the basal transcription machinery (reviewed by Goldman et al., 1997). Additionally, CBP/p300 possesses histone acetyltransferase activity, suggesting that it potentiates transcription by loosening the chromatin structure (Ogryzko et al., 1996). On the other hand, in Drosophila dCBP acetylates dTcf in the Arm-binding domain, and lowers the affinity of dTcf for Arm, thereby negatively regulating Wingless signaling (Waltzer and Bienz, 1998). In an attempt to evaluate the physiological significance of the interaction between CBP and β-catenin, we performed transient transfections in HeLa cells with the TCF reporter plasmid pTOPFLASH containing three optimal TCF binding sites, or the mutant negative control plasmid pFOPFLASH (Korinek et al., 1997). A stabilized β-catenin was used in which four serine and threonine residues at NH₂ terminus were changed to alanine (ptβ-catenin; Yost et al., 1996). Fig. 2 shows that expression of ptβ-catenin resulted in about a threefold increase in luciferase activity compared with pTOPFLASH alone. The level of β-catenin was saturated under this condition since we did not observe a further increase in luciferase activity with a larger amount of ptβ-catenin expression plasmid (data not shown). The β-catenin-dependent transcription was further activated by cotransfecting a vector expressing CBP in a dose-dependent manner, more than doubling the activity observed with saturating levels of ptβ-catenin alone (Fig. 2). Similarly, the activation by wild-type β-catenin was also stimulated by CBP (data not shown). These data are consistent with the observation that the amount of CBP in cells is limiting (Kwok et al., 1994). In contrast, minimal stimulation by CBP was observed in the absence of β-catenin (Fig. 2). In separate experiments using human embryonic kidney 293 cells, we also observed that when we had reached saturating levels of β-catenin, and then cotransfected CBP, there was a greater than doubling of the luciferase activity (data not shown). As expected, the synergistic activation by β-catenin and CBP was not observed with the control pFOPFLASH (Fig. 2). These functional assays clearly indicate that CBP acts as a coactivator for β-catenin in mammalian cells.

The adenovirus E1A oncprotein is known to bind and inhibit the function of CBP (reviewed by Goldman et al., 1997). If our hypothesis that CBP is a coactivator with β-catenin were true, one would predict that E1A would inhibit pTOPFLASH expression in our assays. We tested this prediction, and found that E1A significantly inhibited transcription in a dose-dependent manner (Fig. 3 A). In contrast, expression of an E1A mutant that lacks the ability to interact with CBP (E1A mutCBP; Bannister and Kouzarides, 1995) even slightly enhanced reporter gene activity. To further demonstrate the cooperation between CBP and β-catenin, we carried out transfection assays with the human colon carcinoma cell line, SW480 (Fig. 3 B). In these cells, the level of β-catenin is increased as a result of inactivating mutations in the tumor suppressor gene APC, leading to constitutive transcriptional activation by endogenous β-catenin (Korinek et al., 1997). CBP is also limiting in SW480, since expression of CBP further increased pTOPFLASH activity (Fig. 3 B). Expression of E1A or E1A mutRB, which interacts with CBP like E1A, but is deficient in binding to the retinoblastoma protein (RB; Bannister and Kouzarides, 1995), resulted in a three- to fourfold decrease in reporter activity (Fig. 3 B). In contrast, E1A mutCBP did not significantly affect reporter gene expression. We also tested a dominant negative form of LEF-1 (dnLEF-1), which lacks β-catenin binding domain, and found that dnLEF-1 reduced reporter activity to an extent similar to E1A or E1A mutRB (Fig. 3 B). These observations suggest that endogenous CBP is required for
CBP had no repressive effect on reporter expression in our assays. Moreover, we could not detect an interaction between human LEF-1 and the C/H3 domain of CBP using RRS (data not shown), although the corresponding region of dCBP was shown to bind to mouse LEF-1 (Waltzer and Bienz, 1998). It is possible that dCBP functionally differs from its vertebrate orthologs. In vertebrates, CBP functions as a transcriptional coactivator through the interaction with β-catenin, whereas dCBP is recruited to a promoter by dTCF to repress transcription. A paradoxically, CBP may behave as a repressor in the absence of Wnt signaling, but it turns into a coactivator of β-catenin upon signaling.

The mechanism by which CBP stimulates β-catenin-mediated activation is yet to be established. CBP might help to recruit the basal transcription machinery. In addition, CBP was shown to possess intrinsic histone acetyltransferase activity (Ogryzko et al., 1996), and to associate with multiple acetyltransferases, such as P/CaF (Yang et al., 1996). On the other hand, Groucho has been demonstrated to directly interact with the histone deacetylase Rpd3 in Drosophila, suggesting that Groucho-mediated repression may involve the modulation of local chromatin structure (Chen et al., 1999). Thus, it remains possible that the histone acetyltransferase activities are required for remodeling chromatin structure, alleviating the repression by Groucho factors.

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Figure 5. The activation of endogenous Wnt-responsive genes is sensitive to E1A. Both blastomeres of two-cell stage Xenopus embryos were injected with 20 pg of Xwnt-8, 0.5 ng of E1A mutCBP, or E1A, and 3.2 ng of CBP RNA as indicated. A nimal cap explants were dissected at stage 8 to 9 and analyzed for gene expression by RT-PCR.

Figure 4. Endogenous CBP is required for transactivation by GAL4-βcatR10-C fusion protein. HEK293 cells were transfected with 1 µg of GAL4 reporter construct, pFR-Luc, 50 ng of GAL4 1–147 or GAL4-βcatR10-C, and increasing amounts of E1A or E1A mutCBP expression plasmid (25 or 500 ng) in combinations as indicated.

β-catenin-mediated transcriptional activation. The experiments with E1A thus confirm the prior data supporting the hypothesis that CBP is a coactivator with β-catenin.

The previous finding that dCBP could bind to mouse LEF-1 in vitro (Waltzer and Bienz, 1998) raised the possibility that CBP might be recruited through the interaction with TCF/LEF factors, but not through β-catenin. To analyze the functional importance of the binding of the βcatR10-C domain to CBP more directly, we performed transient transfection assays in HEK293 cells using the βcatR10-C domain fused to the DNA-binding domain of the yeast GAL4 protein (GAL4-βcatR10-C). As previously reported (Hecht et al., 1999), expression of GAL4-βcatR10-C fusion was sufficient to activate the pFR-Luc reporter harboring five GAL4-binding sites (Fig. 4). Coexpression of E1A efficiently abrogated the reporter gene activity. In contrast, little effect was observed with coexpression of E1A mutCBP. These results clearly indicate that β-catenin cooperates with CBP to activate transcription.

To examine whether the activation of endogenous target genes by β-catenin also involves CBP, we analyzed the effects of E1A on the expression of Wnt target genes in Xenopus animal cap explants by RT-PCR (Fig. 5). Consistent with the results described above, coexpression of E1A strongly reduced the expression of siamois and Xnr3 induced by Xwnt-8 (Fig. 5, lane 5 compared with Xwnt-8 alone, lane 3), whereas E1A mutCBP showed a weaker inhibition (Fig. 5, lane 4 compared with lane 3). Furthermore, coexpression of CBP overcame the inhibitory effect of E1A (Fig. 5, lane 6 compared with lane 5). These data suggest that CBP is required for the activation of Wnt-responsive genes in Xenopus embryos.

Our results provide compelling evidence that CBP is a coactivator for β-catenin. In Drosophila, it has been shown that dCBP negatively regulates Wingless signaling (Waltzer and Bienz, 1998). However, overexpression of
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