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Article

A novel LIM protein Cal promotes cardiac differentiation by association with CSX/NKX2-5

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The cardiac homeobox transcription factor CSX/NKX2-5 plays an important role in vertebrate heart development. Using a yeast two-hybrid screening, we identified a novel LIM domain–containing protein, named CSX-associated LIM protein (Cal), that interacts with CSX/NKX2-5. CSX/NKX2-5 and Cal associate with each other both in vivo and in vitro, and the LIM domains of Cal and the homeodomain of CSX/NKX2-5 were necessary for mutual binding. Cal itself possessed the transcription-promoting activity, and cotransfection of Cal enhanced CSX/NKX2-5–induced activation of *atrial natriuretic peptide* gene promoter. Cal contained a functional nuclear export signal and shuttled from the cytoplasm into the nucleus in response to calcium. Accumulation of Cal in the nucleus of P19CL6 cells promoted myocardial cell differentiation accompanied by increased expression levels of the target genes of CSX/NKX2-5. These results suggest that a novel LIM protein Cal induces cardiomyocyte differentiation through its dynamic intracellular shuttling and association with CSX/NKX2-5.

Introduction

CSX/NKX2-5 is a member of NK homeobox gene family that is conserved in evolution and acts as a DNA-binding transcription activator (Komuro and Izumo, 1993; Lints et al., 1993; Akazawa and Komuro, 2003). During embryogenesis, *CSX/NKX2-5* is expressed predominantly in the heart progenitor cells from the very early stage. Targeted disruption of murine *CSX/NKX2-5* resulted in embryonic lethality due to the arrested looping morphogenesis of the heart tube (Lyons et al., 1995). In addition, mutations of *CSX/NKX2-5* cause human hereditary cardiac malformations associated with atrioventricular conduction disturbance (Schott et al., 1998). These results indicate that *CSX/NKX2-5* plays a pivotal role in normal heart development in mammals.

To understand the mechanisms of how *CSX/NKX2-5* controls cardiac development, it is necessary to elucidate the molecular framework of fine-tuned transcriptional regulation of its distinct target genes. Recently, protein–protein interactions have been recognized to be important in many biological processes. Protein complexes consisting of transcription factors and cofactors are responsible for transcriptional regulation, and its composition is thought to be the key determinant of specificity and intensity of the reaction. Transcriptional activity of CSX/NKX2-5 is modulated through physical interaction with other transcription factors such as GATA-4 (Durocher et al., 1997; Lee et al., 1998; Shiojima et al., 1999), SRF (Chen and Schwartz, 1996), and Tbx-5 (Bruneau et al., 2001; Hiroi et al., 2001). Here, we isolated a novel CSX/NKX2-5–associated protein by a yeast two-hybrid screening using *CSX/NKX2-5* as a bait. The protein was a novel LIM domain–containing protein, which we named CSX-associated LIM protein (*Cal*). The LIM domain is a double-zinc finger motif and functions as a module for protein–protein interactions (Dawid et al., 1998; Bach, 2000). Nuclear LIM proteins such as LIM homeodomain proteins and LIM only proteins are directly involved in transcriptional regulation during cell differentiation (Dawid et al., 1998; Bach, 2000). Cytoplasmic LIM proteins are involved in divergent biological processes such as regulation of cytoarchitecture, protein trafficking, and specification of cell polarity (Dawid et al., 1998; Bach,

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Key words: cardiogenesis; homeobox transcription factor; LIM domain; nucleocytoplasmic transport; transcriptional regulation

Abbreviations used in this paper: ANP, atrial natriuretic peptide; Ca^{2+}, calcium; Cal, CSX-associated LIM protein; CRP, cysteine-rich protein; LMB, leptomycin B; LPP, lipoma preferred partner; NES, nuclear export signal; SERCA2, sarcoplasmic reticulum Ca^{2+}-ATPase 2; trip6, thyroid receptor interacting protein 6.

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2000). In regard to muscle development, the roles of cysteine-rich protein (CRP) 3/MLP, which is primarily cytoplasmic, have attracted much attention (Arber et al., 1994). Overexpression of CRP3/MLP in C2C12 myoblasts promoted skeletal myogenesis, whereas inhibition of CRP3/MLP activity by antisense oligonucleotide interrupted terminal differentiation of these cells. Mice homozygous for CRP3/MLP mutation exhibited dilated cardiomyopathy resulted from disrupted cytoarchitecture in cardiomyocytes (Arber et al., 1997). These results indicate the possibility that cytoplasmic LIM proteins regulate cell differentiation as well. Recently, some cytoplasmic LIM proteins have been reported to show nuclear localization. For example, CRP3/MLP associates with nuclear LIM proteins Lmo1 and Apterous (Arber and Caroni, 1996) and basic helix-loop-helix transcription factor MyoD (Kong et al., 1997) as well as cytoskeletal proteins, Zyxin, and α actinin (Louis et al., 1997). However, the molecular mechanism by which the cytoplasmic LIM proteins are involved in nuclear events remains largely unknown.

Here, we show that Cal functions as a coactivator for CSX/NKX2-5 and fulfills its cooperative function based on its dynamic intracellular shuttling mechanisms. Consistent with the notion that the LIM domains function as an interface of protein–protein interactions, the LIM domains of Cal are required for binding to the homeodomain of CSX/NKX2-5. Cal itself has the transcription-promoting activity and activates the *atrial natriuretic peptide* (*ANP*) promoter by forming complex with CSX/NKX2-5. Cal traffics out of the nucleus by nuclear export signal (NES)–dependent mechanisms and traffics into the nucleus in response to an increase of intracellular calcium (Ca^{2+}) concentration. Nuclear expression of Cal promotes cardiac differentiation of P19CL6 cells in vitro. Characterization of complex formation between CSX/NKX2-5 and Cal will provide a unique framework whereby gene expression during cardiogenesis is fine-tuned by the primarily cytoplasmic LIM proteins that were supposed to be involved in cytoskeletal organization.

Results

Molecular cloning and characterization of Cal

To identify proteins that interact with CSX/NKX2-5, we screened a human heart library by the yeast two-hybrid system using the full length of *CSX/NKX2-5* as a bait, and isolated a gene out of 25 positive clones, which we named *Cal*. Using the human Cal cDNA, we isolated the mouse full-length *Cal* cDNA, which encodes a protein of 375 aa (Fig. 1 A) with three tandemly arrayed LIM domains in the COOH terminus. It contains a region abundant in proline residues in the NH_2 terminus. In addition, there is a leucine-rich motif that matches the consensus sequence for NES. These salient structural features are shared among Zyxin family of LIM domain–containing proteins consisting of *Zyxin* (Beckerle, 1997), *lipoma preferred partner* (*LPP*) (Petit et al., 1996), *Ajuba* (Goyal et al., 1999), and *thyroid receptor interacting protein 6 (trip6;* Yi and Beckerle, 1998). Northern blot analysis revealed that there were two transcripts of different sizes, 3.2 and 6.0 kb, and that Cal was highly expressed in a variety of tissues (Fig. 1 B). Most abundant expression was observed in the heart and relatively abundant expression was observed in the lung, intestine, and uterus, whereas little transcript was detected in the brain and liver. RNA in situ hybridization studies revealed that *Cal* was ex-

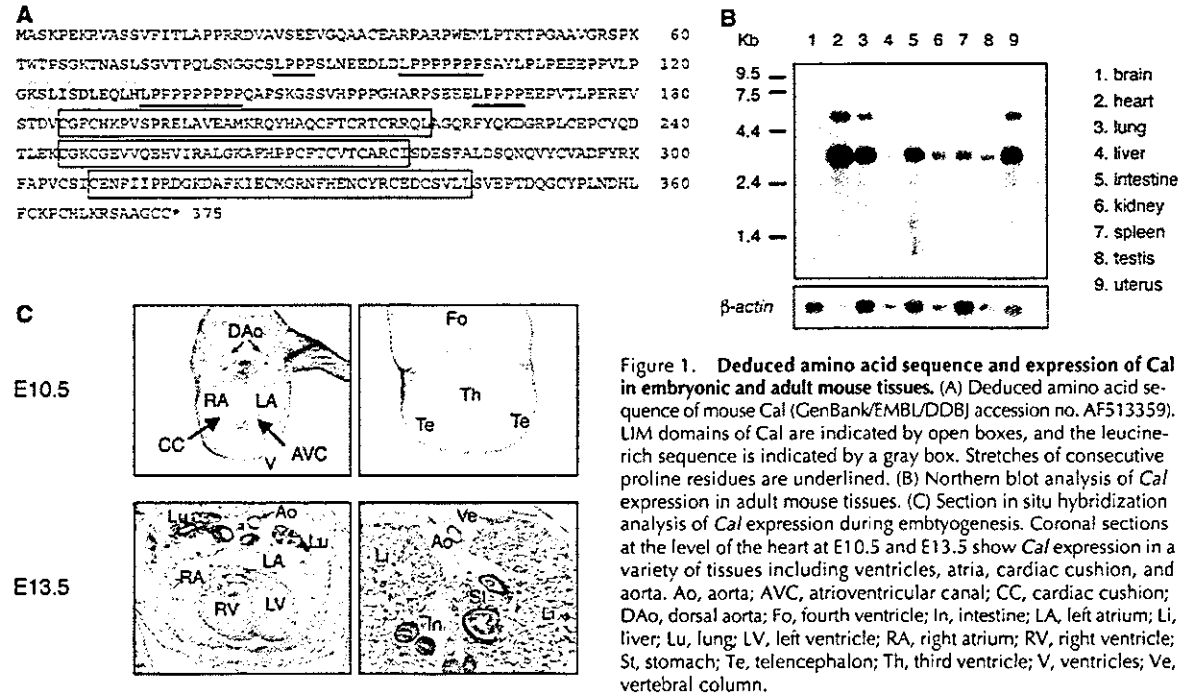

Figure 1. **Deduced amino acid sequence and expression of Cal in embryonic and adult mouse tissues.** (A) Deduced amino acid sequence of mouse Cal (GenBank/EMBL/DDBJ accession no. AF513359). LIM domains of Cal are indicated by open boxes, and the leucine-rich sequence is indicated by a gray box. Stretches of consecutive proline residues are underlined. (B) Northern blot analysis of *Cal* expression in adult mouse tissues. (C) Section in situ hybridization analysis of *Cal* expression during embtyogenesis. Coronal sections at the level of the heart at E10.5 and E13.5 show *Cal* expression in a variety of tissues including ventricles, atria, cardiac cushion, and aorta. Ao, aorta; AVC, atrioventricular canal; CC, cardiac cushion; DAo, dorsal aorta; Fo, fourth ventricle; In, intestine; LA, left atrium; Li, liver; Lu, lung; LV, left ventricle; RA, right atrium; RV, right ventricle; St, stomach; Te, telencephalon; Th, third ventricle; V, ventricles; Ve, vertebral column.

pressed in a wide variety of cell-lineages including the heart, lung, and intestine during mouse embryogenesis (Fig. 1 C). Lesser transcript was observed in the liver, and no transcript was observed in the vertebral column and encephalon.

Cal forms a complex with CSX/NKX2-5

To examine whether CSX/NKX2-5 and Cal directly interact with each other in vivo, we cotransfected COS7 cells with HA-tagged CSX/NKX2-5 and FLAG-tagged Cal. Cell lysates were subjected to immunoprecipitation using anti-FLAG antibody, and coprecipitating CSX/NKX2-5 was detected by immunoblotting with anti-HA antibody (Fig. 2 A). This result suggests that CSX/NKX2-5 and Cal associate with each other in mammalian cells as well as yeast cells.

Next, to confirm the direct interaction between CSX/NKX2-5 and Cal, and if so, to determine the domain responsible for the association, GST pull-down assays were performed with GST-Cal fusion protein and in vitro–translated CSX/NKX2-5. GST-Cal immobilized on glutathione-Sepharose beads retained in vitro–translated CSX/NKX2-5, indicating the direct interaction between CSX/NKX2-5 and Cal (Fig. 2 B). A CSX/NKX2-5 mutant lacking the homeodomain did not associate with Cal, but the homeodomain of CSX/NKX2-5 was enough for association (Fig. 2 B). These results suggest that the homeodomain of CSX/NKX2-5 is necessary and sufficient for the interaction with Cal. We also examined the binding of GST-CSX/NKX2-5 and in vitro–translated Cal and its mutants. A Cal mutant lacking all three LIM domains did not associate with CSX/NKX2-5, but Cal mutants containing at least two LIM domains did associate with CSX/NKX2-5 (Fig. 2 C). These results suggest that the LIM domains of Cal are responsible for interaction with CSX/NKX2-5.

CSX/NKX2-5 and Cal synergistically transactivate the ANP promoter

To examine the effect of Cal on transcriptional activity of CSX/NKX2-5, we performed a series of reporter assays using the luciferase reporter linked to the *ANP* promoter. When the luciferase construct containing the *ANP* promoter was cotransfected with CSX/NKX2-5 expression vector, significant fold induction of the promoter activity was observed as reported previously (Shiojima et al., 1999). Although overexpression of Cal had no effect on the *ANP* promoter, cotransfection of Cal with CSX/NKX2-5 induced much stronger transactivation than CSX/NKX2-5 alone, suggesting that CSX/NKX2-5 and Cal synergistically transactivate the *ANP* promoter (Fig. 3 A). CSX/NKX2-5 and Cal also synergistically transactivated the luciferase construct containing multimerized CSX/NKX2-5–binding sites (Fig. 3 A).

Next, we examined whether the interaction between CSX/NKX2-5 and Cal was required for the synergistic

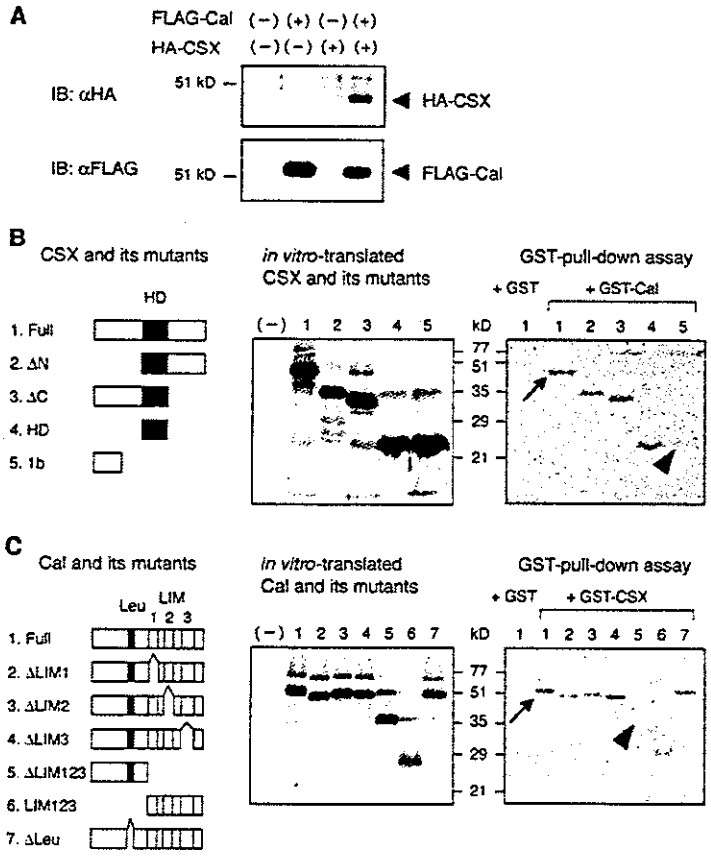

Figure 2. **Complex formation between CSX/NKX2-5 and Cal.** (A) Coimmunoprecipitation of CSX/NKX2-5 and Cal in transfected COS7 cells. Immunoprecipitates with anti-FLAG antibody were separated by SDS-PAGE and immunoblotted with anti-HA antibody (top). The same blot was reprobed with anti-FLAG antibody to confirm the presence of FLAG-tagged Cal (bottom). (B) GST pull-down assay for mapping of a region in CSX/NKX2-5 required for binding to Cal. In vitro–translated CSX/NKX2-5 and its mutants labeled with ^{35}S were incubated with GST-Cal immobilized on glutathione-Sepharose beads, and bound proteins were separated by SDS-PAGE and visualized by autoradiography. The arrow indicates the CSX/NKX2-5 protein bound to GST-Cal. A CSX/NKX2-5 mutant lacking the homeodomain did not associate with Cal (arrowhead), whereas a CSX/NKX2-5 mutant containing only the homeodomain did associate. HD, homeodomain. (C) GST pull-down assay for mapping of a region in Cal required for binding to CSX/NKX2-5. In vitro–translated Cal and its mutants labeled with ^{35}S were incubated with GST-CSX/NKX2-5. The arrow indicates the Cal protein bound to GST-CSX/NKX2-5. A Cal mutant lacking all the LIM domains did not associate with CSX/NKX2-5 (arrowhead), whereas a Cal mutant containing only the LIM domains did associate.

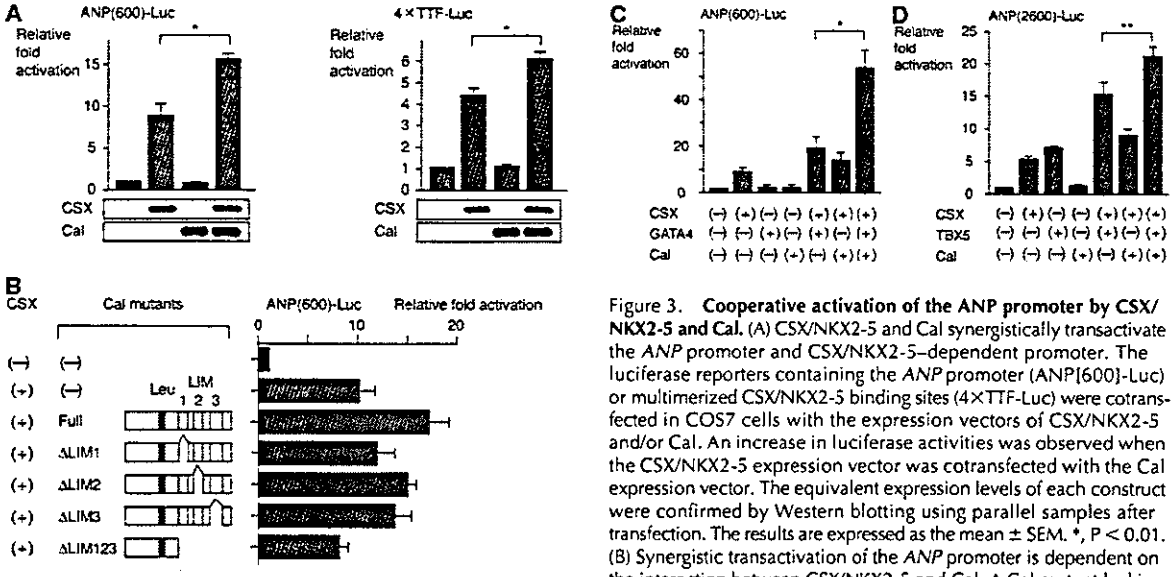

Figure 3. **Cooperative activation of the ANP promoter by CSX/NKX2-5 and Cal.** (A) CSX/NKX2-5 and Cal synergistically transactivate the *ANP* promoter and CSX/NKX2-5–dependent promoter. The luciferase reporters containing the *ANP* promoter (ANP[600]-Luc) or multimerized CSX/NKX2-5 binding sites (4×TTF-Luc) were cotransfected in COS7 cells with the expression vectors of CSX/NKX2-5 and/or Cal. An increase in luciferase activities was observed when the CSX/NKX2-5 expression vector was cotransfected with the Cal expression vector. The equivalent expression levels of each construct were confirmed by Western blotting using parallel samples after transfection. The results are expressed as the mean ± SEM. *, $P < 0.01$. (B) Synergistic transactivation of the *ANP* promoter is dependent on the interaction between CSX/NKX2-5 and Cal. A Cal mutant lacking all three LIM domains, the docking module for binding to CSX/NKX2-5, exhibited no significant cooperation on CSX/NKX2-5–induced promoter activation. The results are expressed as the mean ± SEM. (C) Cal augments synergistic transactivation between CSX/NKX2-5 and GATA-4. COS7 cells were cotransfected with the luciferase reporter containing the *ANP* promoter (ANP[600]-Luc) and the expression vectors of CSX/NKX2-5 and/or GATA-4 and/or Cal. Cotransfection with CSX/NKX2-5 and GATA-4 exhibited synergistic transactivation, that was further enhanced by additional expression of Cal. The results are expressed as the mean ± SEM. *, $P < 0.01$. (D) Cal augments synergistic transactivation between CSX/NKX2-5 and Tbx-5. Cotransfection with CSX/NKX2-5 and Tbx-5 exhibited synergistic transactivation of the *ANP* promoter (ANP[2600]-Luc), that was further augmented by additional expression of Cal. The results are expressed as the mean ± SEM. **, $P < 0.05$.

transactivation of the *ANP* promoter. Although Cal mutants lacking one LIM domain, which retain the ability to bind to CSX/NKX2-5, showed synergistic activation with CSX/NKX2-5 on the *ANP* promoter, the Cal mutant lacking the three LIM domains, which does not bind to CSX/NKX2-5, exhibited no significant cooperation on CSX/NKX2-5–induced promoter activation (Fig. 3 B). These results suggest that the synergistic transactivation was dependent on the mutual binding between CSX/NKX2-5 and Cal.

It has been reported that CSX/NKX2-5 and a zinc-finger transcription factor, GATA-4, display synergistic transcriptional activation of the *ANP* promoter (Durocher et al., 1997; Lee et al., 1998; Shiojima et al., 1999). As shown in Fig. 3 C, Cal augmented this synergistic promoter activation between CSX/NKX2-5 and GATA4. We and others reported recently that CSX/NKX2-5 and a T-box transcription factor, Tbx-5, showed synergistic transcriptional activation of the *ANP* promoter (Bruneau et al., 2001; Hiroi et al., 2001). Cal also augmented this synergistic promoter activation between CSX/NKX2-5 and Tbx-5 (Fig. 3 D).

Cal is a transactivator

To understand how Cal exhibits synergistic transcriptional activation with CSX/NKX2-5, we examined the transcriptional activity of Cal. The expression vector containing Cal fused to GAL4 DNA-binding domain was cotransfected in COS7 cells with the luciferase reporter containing the multimerized GAL4-binding sites. As shown Fig. 4, full length of Cal fused to the DNA-binding domain of GAL4 transactivated a GAL4-dependent reporter ~13.0-fold compared with DNA-binding domain of GAL4 alone. Cal mutants lacking all three LIM domains, LIM2 or LIM3 domains showed no transcriptional activity, whereas the Cal mutant containing only LIM2 and LIM3 domains showed stronger activity than the full length of Cal. Deletion of LIM1 domain showed even stronger activity, suggesting that Cal itself has the transcription-promoting activity and that its transactivation domain is localized

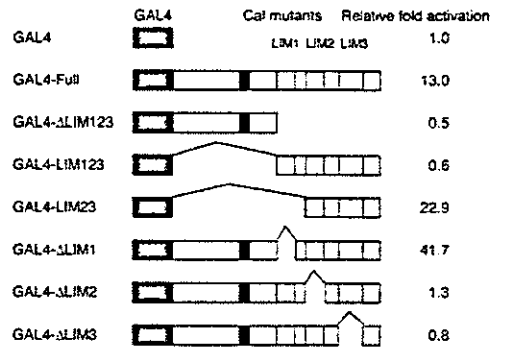

Figure 4. **Transcriptional activity of Cal.** Expression vectors encoding the GAL4 DNA binding domain fused to the indicated regions of Cal were transiently transfected into COS7 cells with the pG5luc-luciferase reporter, which contained five GAL4 binding sites. Cal fused to the DNA binding domain of GAL4 significantly transactivated a GAL4-dependent reporter, indicating that Cal possesses transcriptional activity. Cal mutants lacking LIM2 or LIM3 showed no transcriptional activity, whereas Cal mutants containing LIM2 and LIM3 showed stronger activity.

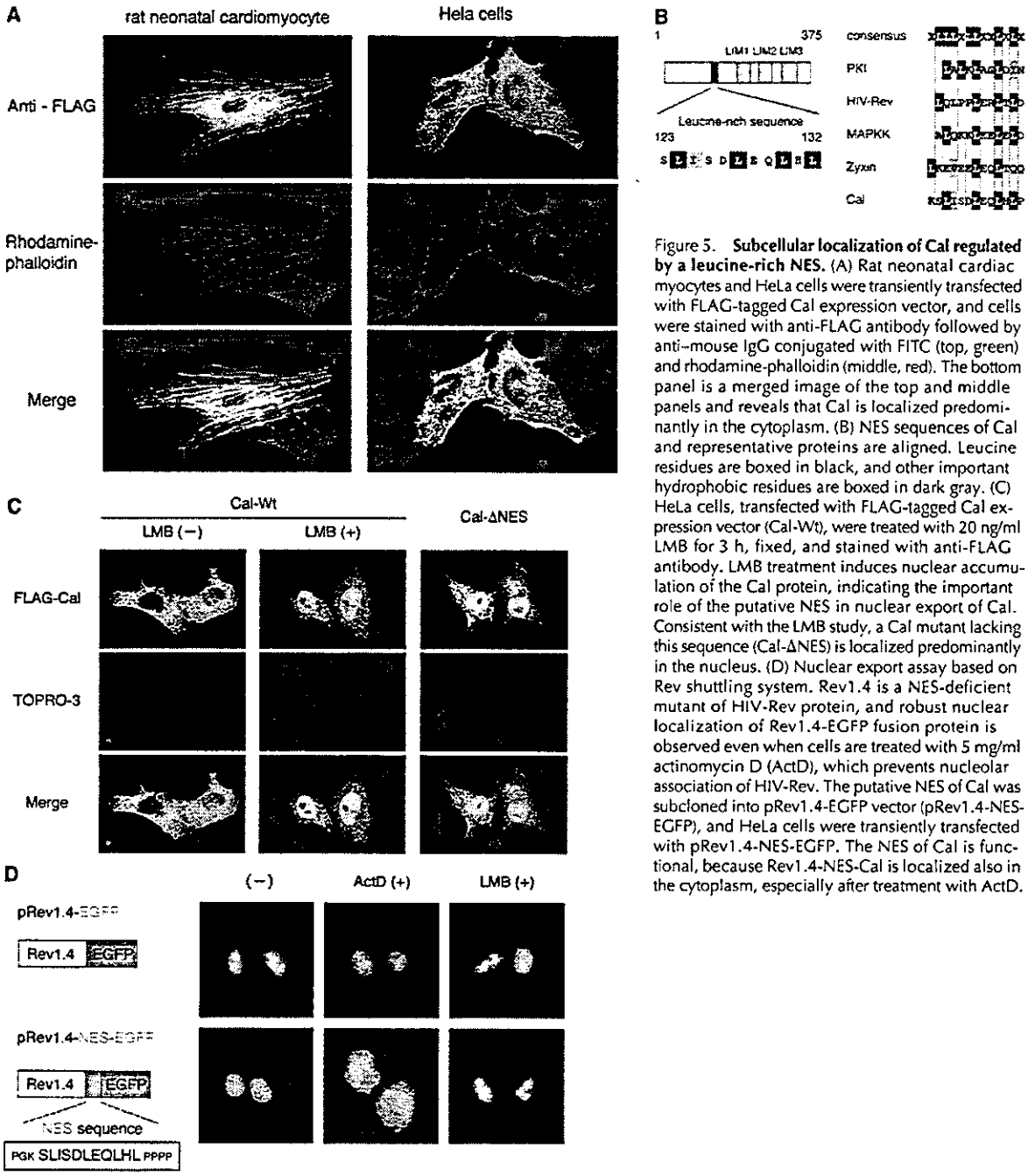

Figure 5. **Subcellular localization of Cal regulated by a leucine-rich NES.** (A) Rat neonatal cardiac myocytes and HeLa cells were transiently transfected with FLAG-tagged Cal expression vector, and cells were stained with anti-FLAG antibody followed by anti-mouse IgG conjugated with FITC (top, green) and rhodamine-phalloidin (middle, red). The bottom panel is a merged image of the top and middle panels and reveals that Cal is localized predominantly in the cytoplasm. (B) NES sequences of Cal and representative proteins are aligned. Leucine residues are boxed in black, and other important hydrophobic residues are boxed in dark gray. (C) HeLa cells, transfected with FLAG-tagged Cal expression vector (Cal-Wt), were treated with 20 ng/ml LMB for 3 h, fixed, and stained with anti-FLAG antibody. LMB treatment induces nuclear accumulation of the Cal protein, indicating the important role of the putative NES in nuclear export of Cal. Consistent with the LMB study, a Cal mutant lacking this sequence (Cal-ΔNES) is localized predominantly in the nucleus. (D) Nuclear export assay based on Rev shuttling system. Rev1.4 is a NES-deficient mutant of HIV-Rev protein, and robust nuclear localization of Rev1.4-EGFP fusion protein is observed even when cells are treated with 5 mg/ml actinomycin D (ActD), which prevents nucleolar association of HIV-Rev. The putative NES of Cal was subcloned into pRev1.4-EGFP vector (pRev1.4-NES-EGFP), and HeLa cells were transiently transfected with pRev1.4-NES-EGFP. The NES of Cal is functional, because Rev1.4-NES-Cal is localized also in the cytoplasm, especially after treatment with ActD.

within the LIM2 and LIM3 domains, whereas LIM1 may function as a repressor domain.

Cal is predominantly localized in the cytoplasm and shuttles between the cytoplasm and the nucleus

We examined the subcellular localization of Cal protein in cultured cells. Cultured cardiac myocytes of neonatal rats were transiently transfected with FLAG-tagged Cal expression vector, and immunofluorescence analysis was performed using anti-FLAG antibody. Cal protein was predominantly localized in the cytoplasm of cardiac myocytes at steady state (Fig. 5 A). Similar pattern of immunofluorescence was obtained in other cell lines such as HeLa (Fig. 5 A), COS7, and NIH3T3 cells (not depicted).

Within the amino acid sequence of Cal, there was a leucine-rich sequence that matched the consensus sequence of NES (Fig. 5 B). During a nuclear export cycle, an exportin molecule CRM1 recognizes the NES and forms a complex

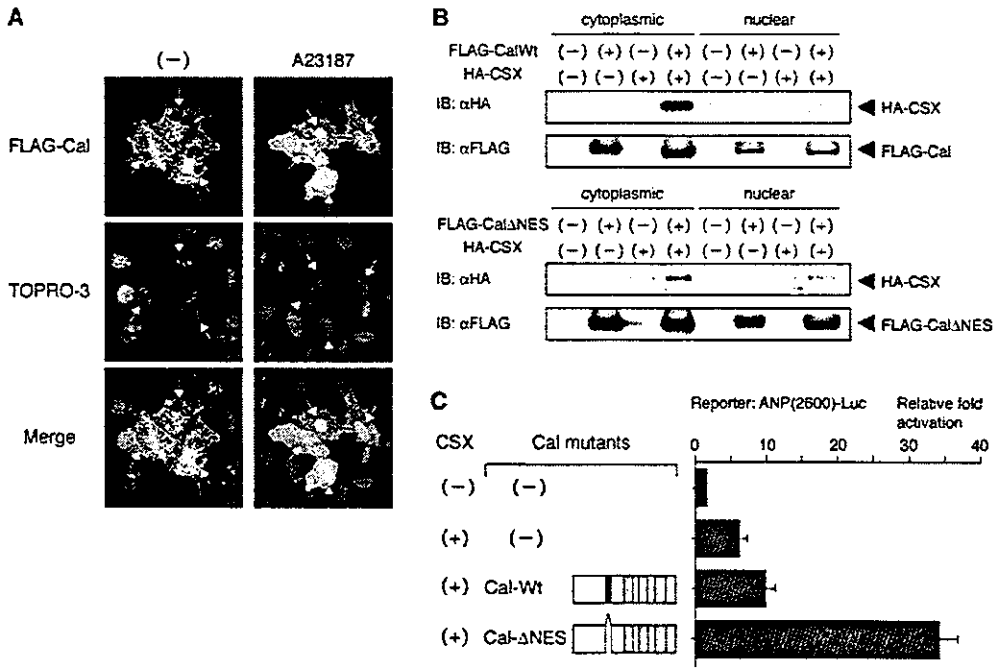

Figure 6. **Nuclear transport of Cal in response to calcium ionophore and implications of nuclear accumulation of Cal in transcriptional cooperativity with CSX/NKX2-5.** (A) HeLa cells, transfected with FLAG-tagged Cal expression vector, were treated with vehicle or calcium ionophore A23187 (2 μM) for 15 min, fixed, and stained with anti-FLAG antibody. Nuclear accumulation of Cal is observed in significant portions of transfected cells after treatment with A23187. The arrows indicate the nuclei of the transfected cells. (B) Coimmunoprecipitation of CSX/NKX2-5 and Cal (Cal-Wt) or nuclear form of Cal (Cal-ΔNES) in preparations of cytoplasmic or nuclear fractions of transfected COS7 cells. Cal-ΔNES showed significantly stronger interaction with CSX/NKX2-5 in the nucleus than Cal-Wt. (C) The luciferase reporter containing the *ANP* promoter was cotransfected in COS7 cells with the expression vectors of CSX/NKX2-5 and Cal-Wt or Cal-ΔNES. Cal-ΔNES showed much stronger synergistic activation with CSX/NKX2-5 than Cal-Wt. The results are expressed as the mean ± SEM.

with RanGTP, and mediates transport to the cytoplasm (Fornerod et al., 1997; Mattaj and Englmeier, 1998; Ohno et al., 1998; Kuersten et al., 2001). NES-dependent nuclear export is inhibited by leptomycin B (LMB) that interferes with the binding of CRM1 to NES (Kudo et al., 1998). Inhibition of CRM1-dependent nuclear export using LMB resulted in rapid nuclear accumulation of Cal protein in HeLa cells (Fig. 5 C). Although immunofluorescence studies indicated that the main compartment where Cal is localized at steady state was the cytoplasm, the accumulation of CAL after treatment with LMB suggested that Cal can shuttle between the cytoplasm and the nucleus.

To confirm that the putative NES contributes to nuclear export of Cal, we deleted the NES sequence (residues 123–132) in the FLAG-tagged Cal expression vector (Cal-ΔNES) and examined the subcellular localization of Cal-ΔNES mutant. Cal-ΔNES was predominantly localized in the nucleus (Fig. 5 C), suggesting that this sequence mediates the CRM1-dependent nuclear export of Cal. To test this sequence of Cal functions as an NES, we introduced this sequence into the export-deficient form of Rev-EGFP, and tested its nuclear export activity in HeLa cells. The putative NES of Cal displayed the export activity, especially in the presence of actinomycin D, which prevents nucleolar association of Rev protein (Fig. 5 D). These results indicate that this 123-132–amino acid sequence of Cal really functions as an NES.

Cal shuttles into the nucleus in response to Ca^{2+} signal

We explored a specific signal capable of targeting Cal protein to the nucleus. When intracellular Ca^{2+} levels were increased by Ca^{2+} ionophore A23187, Cal protein was transported to the nucleus (Fig. 6 A). Nuclear accumulation of Cal was detected at 10 min after addition of A23187. No other cellular signals possessed ability to transport Cal into the nucleus. For example, treatment with cytochalasin D, an actin filament disrupting reagent, tetradecanoylphorbol 13-acetate, PKC activator, forskolin, an adenylate cyclase activator, anisomycin, Jun-NH_2–terminal kinase agonist, okadaic acid, a serine/threonine phosphatase inhibitor did not induce nuclear translocation of Cal protein.

Next, we examined whether nucleocytoplasmic shuttling of Cal protein had important implications for modifying the transcriptional activity of CSX/NKX2-5. As indicated by coimmunoprecipitation experiments by using cytoplasmic and nuclear fractions of transfected cells, interaction between CSX/NKX2-5 and wild-type of Cal (Cal-Wt) was detectable predominantly in the cytoplasm and slightly in the nucleus (Fig. 6 B). When Cal-ΔNES, which lacks the NES and is predominantly localized in the nucleus, was cotransfected, the level of coprecipitating CSX/NKX2-5 in the nuclear fraction increased significantly (Fig. 6 B). Furthermore, Cal-ΔNES showed much stronger synergistic transactivation of the *ANP* promoter than Cal-Wt, when cotransfected with CSX/

NKX2-5 (Fig. 6 C). These results suggest that nuclear translocation of Cal enhances CSX/NKX2-5–induced promoter activation by promoting mutual interaction in the nucleus.

Nuclear accumulation of Cal induces cardiac differentiation of P19CL6 cells

To determine whether synergistic transactivation by Cal has a significant effect on cardiomyocyte differentiation, we isolated P19CL6 clones, which stably overexpress wild-type Cal (P19CL6-CAL-Wt) or Cal mutant lacking the NES (P19CL6-Cal-ΔNES). When cultured in the medium containing 1% DMSO, P19CL6 cells differentiated into cardiomyocytes, which exhibit spontaneous beating and express cardiac-specific genes (Monzen et al., 1999). The expression of cardiac-specific genes was examined in P19CL6 cells, P19CL6-Cal-Wt, and P19CL6-Cal-ΔNES during differentiation (Fig. 7 A). Northern blot analysis revealed that expression levels of a cardiac transcription factor *GATA-4* and *sarcoplasmic reticulum Ca^{2+}-ATPase 2* (*SERCA2*) as well as *connexin 43* and *calreticulin*, known as downstream targets for CSX/NKX2-5, were increased in P19CL6-Cal-ΔNES cells. RT-PCR analysis revealed that expression of *ANP* gene was also up-regulated in P19CL6-Cal-ΔNES cells, which was consistent with the results that Cal augmented *ANP* promoter activation induced by CSX/NKX2-5. Immunocytochemical analysis revealed that in P19CL6-Cal-ΔNES, a larger number of cells were stained positive with anticardiac troponin T antibody than the parental P19CL6 cells (Fig. 7 B), suggesting that nuclear accumulation of Cal strongly promotes cardiac differentiation.

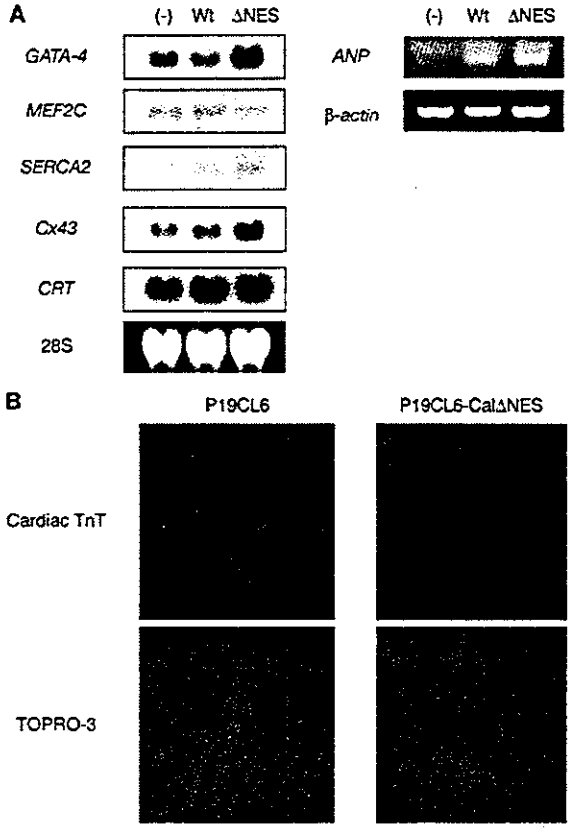

Figure 7. **Promotion of cardiac differentiation in P19CL6 cells by nuclear accumulation of Cal.** (A) Expression of cardiac genes was examined on differentiation day nine of P19CL6 cells, P19CL6 cells stably expressing Cal-Wt and Cal-ΔNES. Northern blot analysis was performed with *GATA-4, MEF2C, SERCA2, Connexin43* (*Cx43*), and *calreticulin* (*CRT*) cDNAs and RT-PCR was performed using specific primers for *ANP*. Notably, expression levels of target genes for CSX/NKX2-5 such as *Cx43, CRT,* and *ANP* were increased in P19CL6-Cal-ΔNES. (B) Cardiac differentiation in P19CL6 cells on differentiation day 14 was determined by immunofluorescence with anticardiac troponin T (TnT) antibody. Much larger number of cells were stained positive for cardiac TnT in P19CL6-Cal-ΔNES.

Discussion

Cal is a novel LIM domain–containing protein

We identified a novel protein Cal, which associates with the cardiac homeobox transcription factor CSX/NKX2-5. *Cal* is a member of Zyxin family, that commonly have a proline-rich region at the NH_2 terminus, a leucine-rich sequence, and three tandem LIM domains located at the COOH terminus. The proline-rich regions of Zyxin serve as interface to bind to SH3 domain of Vav (Hobert et al., 1996) and EVH1 domain of Ena/VASP family proteins (Renfranz and Beckerle, 2002) that are implicated in control of actin organization (Gertler et al., 1996). LPP also contains proline-rich motifs that are required for the interaction with the EVH1 domain (Prehoda et al., 1999). This proline-rich region of LPP directly interacts with VASP in vitro, and LPP is colocalized with VASP in the focal adhesion. The proline-rich regions of Ajuba interact with Grb2 (Goyal et al., 1999). Expression of Ajuba enhances MAPK activity in fibroblasts and promotes meiotic maturation of *Xenopus* oocytes through activation of MAPK in Grb2- and Ras-dependent manner (Goyal et al., 1999). The NH_2-terminal portion of *Cal* also contains stretches of proline-rich sequences. Especially, two proline-rich sequences (LPPPPPPP 98-105 and LPPPPPPPPP 133-142) of Cal lead us to speculate that Cal might associate with profilin and be involved in the organization of cytoskeletal actin in the cytoplasm because the sequence of consecutive prolines flanked by leucine has been thought to be a ligand motif for profilin (Mahoney et al., 1997). Identification of proteins binding to the proline-rich region of Cal would provide further insights into its cellular function.

Cal interacts with CSX/NKX-2.5 both in vitro and in vivo

GST pull-down assays and coimmunoprecipitation experiments indicated the association of Cal with CSX/NKX2-5 both in vitro and in vivo. Analyses using mutants of both proteins revealed that the mutual binding was mediated through the homeodomain of CSX/NKX2-5 and the LIM domains of Cal. Besides binding to DNA, the homeodomain of CSX/NKX2-5 acts as a module for the interaction with its binding partner such as GATA-4 (Durocher et al., 1997; Lee et al., 1998; Shiojima et al., 1999), SRF (Chen and Schwartz, 1996), and Tbx-5 (Hiroi et al., 2001). The LIM domains of Cal have a cysteine-histidine rich, double zinc-finger motif that functions as a protein–protein in-

teraction module (Dawid et al., 1998; Bach, 2000). The LIM domains of Zyxin interact with members of CRP family (Sadler et al., 1992) and serine/threonine kinase h-warts/LATS1 (Hirota et al., 2000). During mitosis, phosphorylation of Zyxin by Cdc2 promotes the binding between Zyxin and h-warts/LATS1, and the complex is targeted to the mitotic apparatus. The possibility that interaction between CSX/NKX2-5 and Cal is modulated by specific protein modification remains to be determined.

Abundant expression of *Cal* was detected in the heart during embryogenesis and maintained in the atrial and ventricular chambers through the adulthood. *Cal* was also expressed in a variety of tissues such as the aorta, lung, and intestine, but little expression was detected in the brain and liver. Although the functional roles of Cal in tissues other than the heart remain unknown at present, Cal may associate with other NK homeobox transcription factors, because the amino acid sequences of homeodomains, which are responsible for binding to Cal, are highly conserved among this class of homeoproteins. Interestingly, Ajuba has been reported to associate with thyroid transcription factor-1/Nkx2-1, a member of NK homeobox transcription factors, in mammalian cells, although the physiological function of their interaction remains unknown (Missero et al., 2001). It is possible that there are more combinatorial patterns of physical interaction between Zyxin family LIM proteins and NK homeoproteins.

Cal shuttles between the cytoplasm and the nucleus

The leucine-rich sequence of Cal is thought to function as an NES, based on the following results: (a) the leucine-rich sequence of Cal matches the consensus of the NES; (b) predominant nuclear distribution was observed when treated with LMB, that is a specific inhibitor of CRM1-dependent nuclear export (Kudo et al., 1998); (c) the Cal mutant lacking the leucine-rich sequence was localized predominantly in the nucleus; and (d) fusion of leucine-rich sequence of Cal to Rev1.4-EGFP transported the Rev1.4-EGFP from the nucleus to the cytoplasm (Henderson, 2000). Functional leucine-rich NESs have been identified in other Zyxin family members such as *Zyxin* (Nix and Beckerle, 1997), *trip6* (Wang and Gilmore, 2001), *LPP* (Petit et al., 2000), and *Ajuba* (Kanungo et al., 2000). Although the role of Zyxin family members in the nucleus has not been fully defined, the interaction between Zyxin and h-wartz/LATS1 on the mitotic apparatus implicates the specific role of Zyxin in the regulation of cell cycle (Hirota et al., 2000).

Cal augments CSX/NKX2-5–induced promoter activation

The interaction between CSX/NKX2-5 and Cal implicates a certain role of transcriptional regulation of cardiac-specific genes. CSX/NKX2-5 and Cal synergistically activated both the *ANP* promoter and the artificial promoter containing multimerized CSX/NKX2-5–binding sites. Furthermore, Cal enhanced cooperative promoter activation of *ANP* gene between CSX/NKX2-5 and GATA-4 or Tbx-5. These results suggest that transcriptional regulation by cardiac transcription factors may be fulfilled harmoniously by multiprotein complex.

The GAL4-based reporter assay revealed that Cal itself possesses transcriptional activity. LIM2 and LIM3 domains were endowed with the capacity to activate transcription, whereas the LIM1 domain suppressed the transcriptional activity. On the other hand, the ΔLIM1 mutant failed to augment CSX/NKX2-5–induced transactivation of the *ANP* reporter (Fig. 3 B). GST pull-down assays revealed that the LIM domains are required for binding to CSX/NKX2-5 and that deletion of LIM1 reduced the mutual binding (Fig. 2 C), suggesting that deletion of LIM1 may also decrease the binding affinity for CSX/NKX2-5. In addition, there is a possibility that the LIM1 interferes the GAL4-DNA binding but not inhibits the transcription. It has been reported that Trip6 and LPP have transcriptional activity, and the transactivation domains were attributed to the LIM domains and a region containing the NES of *trip6* (Wang and Gilmore, 2001) and to the LIM domains and the proline-rich region of *LPP* (Kanungo et al., 2000). Based on the fact that transactivation domains reside in modules for protein–protein interaction, it is likely that the interaction with components of transcriptional initiation complex is involved in transcriptional activation.

Cooperative transactivation of the *ANP* promoter by CSX/NKX2-5 and Cal was enhanced when Cal protein was targeted into the nucleus by deleting its NES. We found that treatment with Ca^{2+} ionophore A23187 induced nuclear transport of Cal. Pathophysiological significance of Ca^{2+} signaling in cardiac development has not been fully defined. However, Ca^{2+} signals are induced by various conditions including G-protein–coupled receptors (Clapham, 1995) and receptor tyrosine kinases (Schlessinger, 2000). It is possible to assume that Cal might modulate the transcriptional activity of CSX/NKX2-5 in response to Ca^{2+} signals triggered by G-protein–coupled receptors or receptor tyrosine kinases during cardiogenesis. Exploration of physiological ligands that activate Ca^{2+} signals and subsequent nuclear import of Cal will undermine the molecular framework of cardiac development.

Ca^{2+} signaling plays an important role in generation of cardiac hypertrophy (Frey et al., 2000). Nuclear import of NF-AT transcription factors is induced by Ca^{2+}-activated phosphatase calcineurin and that transgenic mice expressing nuclear form of NF-AT3 in the heart exhibited cardiac hypertrophy (Molkentin et al., 1998). CSX/NKX2-5 is expressed in the adult heart (Komuro and Izumo, 1993), and it has been proposed that CSX/NKX2-5 is involved in generation of cardiac hypertrophy (Akazawa and Komuro, 2003) on the basis of in vivo findings that expression levels of CSX/NKX2-5 were increased in response to hypertrophic stimuli including pressure overload (Thompson et al., 1998) and phenylephrine or isoproterenol (Saadane et al., 1999). Therefore, Cal may be another Ca^{2+}-sensitive effector that translocates into the nucleus like NF-AT transcription factors and it is possible to speculate that Cal may play a certain role in generation of cardiac hypertrophy by modulating transcriptional activity of CSX/NKX2-5.

Cal may function as a signal mediator that links cytoplasmic signals and gene expression

Cal was localized in the cytoplasm at steady state and translocated into the nucleus in response to calcium, and Cal functioned as a transcriptional activator in the nucleus by cooper-

ating with the cardiac transcription factor CSX/NKX2-5. These results indicate a novel function of LIM proteins that link cytoplasmic signals and nuclear gene expression.

Recently, some proteins associated with cell junctions have been reported to be involved in transcriptional regulation. A membrane-associated guanylate kinase, CASK/LIN-2, interacts with a T-box transcription factor, Tbr-1, and stimulates the transcriptional activity of Tbr-1 in the nucleus of mammalian cells (Hsueh et al., 2000). Jun activation domain-binding protein 1, colocalizing with integrin LFA-1, translocates into the nucleus in response to LFA-1 stimulation and acts as a coactivator for AP-1 complex (Bianchi et al., 2000). β-Catenin, linking cadherins to actin cytoskeleton at adherens junctions, interacts with T cell factor to form a transcriptional activator complex in response to Wnt signaling (Barth et al., 1997). Although CRP3/MLP binds to Zyxin and α actinin in the cytoplasm (Louis et al., 1997), forced expression of CRP3/MLP in the nucleus by fusing it to nuclear localization signal led to a cooperative enhancement of the transcriptional activity of MyoD (Kong et al., 1997). Trip6 also acts as a coactivator for v-Rel transcription factor (Zhao et al., 1999). However, it remains unclear how subcellular localization of CRP3/MLP and trip6 is regulated. We first clarify the molecular mechanism of how the cytoplasmic LIM protein is translocated into the nucleus and functions as a transcriptional activator.

Cal promotes cardiac differentiation in P19CL6 cells

Mouse P19CL6 cells, derived from P19 embryonal carcinoma cells, are used as a good in vitro system for molecular analysis of cardiac differentiation. In the presence of 1% DMSO, mouse P19CL6 cell efficiently differentiate into spontaneously beating cardiac myocytes that exhibit the biological features recapturing embryonic cardiogenesis in vivo (Monzen et al., 1999, 2001). P19CL6 cells that overexpress nuclear form of Cal (P19CL6-Cal-ΔNES) differentiated into cardiac myocytes more efficiently than the parental P19CL6 cells. In P19CL6-Cal-ΔNES cells, expression levels of *SERCA2*, *calreticulin*, *connexin43*, *ANP*, and *cardiac troponin T* were up-regulated, which convey properties characteristic of cardiomyocytes. Expression levels of cardiac transcription factor *MEF2C* did not change, whereas expression levels of *GATA-4* were increased. Although there has been no evidence indicating that *GATA-4* is a downstream target for CSX/NKX2-5, it is possible that expression of *GATA-4* is up-regulated through undefined functions of Cal. Up-regulation of *GATA-4* might have an influence on myocardial cell differentiation in P19CL6-Cal-ΔNES. These results leave an open question whether the nuclear target for Cal is solely CSX/NKX2-5. However, based on the up-regulated expression of the target genes for CSX/NKX2-5, it is reasonable to assume that cooperation of CSX/NKX2-5 and Cal promoted cardiac differentiation in P19CL6 cells. Our present studies elucidate a novel role of LIM proteins in cardiac development as a transcriptional activator, and suggest that fine-tuned gene expression during cardiogenesis is orchestrated by multiprotein complex including LIM proteins as well as transcription factors.

Materials and methods

Molecular cloning of Cal

We performed a yeast two-hybrid screening using the MATCHMAKER Two-Hybrid System (CLONTECH Laboratories, Inc.) as described previously (Hiroi et al., 2001). The plasmid pGBT9-CSX, which encodes the GAL4 DNA-binding domain fused to the human CSX/NKX2-5, was used as a bait in screening of a human heart MATCHMAKER cDNA Library (CLONTECH Laboratories, Inc.). One clone containing a fragment of CAL cDNA was scored positive, and the full-length mouse Cal cDNA was obtained by screening a mouse heart cDNA library (Stratagene).

Northern blot, RT-PCR, and in situ hybridization analysis

For Northern blot analysis, total RNA was hybridized with cDNA corresponding to 3′-UTR of *Cal*. Probes for *GATA-4*, *MEF2C*, *connexin 43*, and *SERCA2* were described previously (Hiroi et al., 2001). A probe for *calreticulin* was a gift from M. Michalak (University of Alberta, Alberta, Canada). RT-PCR analysis for *ANP* expression was performed as described previously (Hiroi et al., 2001). Digoxygenin labeled riboprobes were synthesized by using the 1.5-kb *Cal* cDNA, and RNA in situ hybridization was performed as described previously (Akazawa et al., 2000).

Plasmids construction

The following plasmids were described previously: the expression vectors of CSX/NKX2-5 (pEFSA-HA-CSX), GATA-4 (pSSRa-hGATA4), and Tbx-5 (pcDNA3-Tbx5); the luciferase reporters containing the *ANP* promoter (ANP[600]-Luc and ANP[2600]-Luc); and multimerized CSX-binding sites (4×TTF-Luc; Shiojima et al., 1999; Hiroi et al., 2001). FLAG-tagged Cal was subcloned into pCAGGS vector (pCAGGS-FLAG-Cal; Niwa et al., 1991; Aoki et al., 2000). pCAGGS vector was provided by J. Miyazaki (Osaka University Graduate School of Medicine, Suita, Japan) and T. Kobayashi and O. Hino (The Cancer Institute, Japanese Foundation for Cancer Research, Tokyo, Japan). Cal derivatives were subcloned into pcDNA3.1 (Invitrogen) and pBIND (Promega) for in vitro transcription and translation and expression of GAL4-fusion protein, respectively. For deletion analyses, the following Cal derivatives were subcloned into the corresponding vectors: Cal-ΔLIM1 (1-184, 221-375), Cal-ΔLIM2 (1-244, 279-375), Cal-ΔLIM3 (1-307, 345-375), Cal-ΔLIM123 (1-184), Cal-LIM123 (185-375), Cal-LIM23 (245-375), and Cal-ΔNES (1-121, 135-375).

Cell culture, transfection, and reporter gene assay

Primary cultures of cardiac myocytes were prepared from ventricles of 1-d-old Wistar rats as described previously (Kudoh et al., 1997). Transient transfections were performed by standard calcium phosphate methods. For reporter gene assays, pRL-SV40 (Promega) was cotransfected as an internal control. Luciferase activities were measured as described previously (Shiojima et al., 1999). P19CL6 cells were cultured as described previously (Monzen et al., 1999). To isolate the permanent cell lines, P19CL6 cells were transfected with pcDNA3.1-Cal and pcDNA3.1-Cal-ΔNES by the lipofection method (TfxTM reagents; Promega). Stable transformants were selected with 400 μg/ml of neomycin (G418; Sigma-Aldrich).

Coimmunoprecipitation experiment

We performed a coimmunoprecipitation experiment as described previously (Shiojima et al., 1999). COS-7 cells were transiently transfected with expression plasmids of pEFSA-HA-CSX and pCAGGS-FLAG-Cal or pCAGGS-FLAG-CalΔNES. For preparation of the cytoplasmic fraction, transfected cells were lysed in digitonin buffer (20 mM Hepes/KOH, pH 7.5, 150 mM NaCl, 1 mM EDTA, and 50 μg/ml digitonin) on ice for 10 min. The lysates were centrifuged at 1,000 *g* and the supernatant was collected as the cytoplasmic fraction. The pellets were resuspended Triton buffer (20 mM Hepes/KOH, pH 7.5, 150 mM NaCl, 1 mM EDTA, and 10 mg/ml Triton X-100) and the lysates were used as the nuclear fraction. Protein samples were subjected to immunoprecipitation with the anti-FLAG mAb M2 (KODAK), fractionated by 10% SDS-PAGE, and immunoblotted with the rabbit polyclonal anti-HA antibody (Santa Cruz Biotechnology, Inc.). HRP-conjugated anti-rabbit IgG antibody was used as the secondary antibody and immune complex was detected by the ECL detection kit (Amersham Biosciences).

GST pull-down assay

We performed GST pull-down assays as described previously (Shiojima et al., 1999). GST fusion protein of CSX/NKX2-5 has been described previously. cDNA fragment corresponding to the full length of Cal was subcloned in frame into the EcoRI site of pGEX-3X (Amersham Biosciences). CSX/NKX2-5 derivatives (Shiojima et al., 1999) and Cal derivatives, subcloned

into pcDNA3.1 vector (Invitrogen), were labeled with [^{35}S]methionine by the TNT Quick Coupled Transcription/Translation Systems (Promega). GST and GST fusion proteins immobilized on glutathione-Sepharose 4B beads were mixed with in vitro–translated proteins. Bound proteins were fractionated by SDS-PAGE and visualized by autoradiography.

Immunostaining

Rat neonatal cardiac myocytes or HeLa cells were transfected with the expression vector of Cal and Cal mutants. Cells were stained with the anti-FLAG mAb M2 (KODAK), and visualized with FITC-labeled anti–mouse IgG (CAPPEL). Calcium ionophore A23187 was purchased from Sigma-Aldrich. Differentiated P19CL6 cells were stained with anticardiac troponin T mAb (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH) and visualized with Cy3-labeled anti–mouse IgG (CHEMICON International, Inc.). The cells were double stained using rhodamine-phalloidin (Molecular Probes) or TO-PRO-3 (Molecular Probes).

Nuclear export assays

Nuclear export assays were performed as described previously (Henderson, 2000). pRev(1.4)-NES-EGFP plasmid was constructed by subcloning the NES of Cal between BamHI and AgeI sites of pRev(1.4)-EGFP plasmid (provided by B.R. Henderson, Westmead Institute for Cancer Research, Sydney, Australia). The NES of Cal was amplified by PCR using specific primers (5′-AGGGAAGCCCCCACCCCCGCCTC-3′, and 5′-GGTGGGGGCTTCCCTG-GTAAGACA-3′). Actinomycin D (Sigma-Aldrich) was added at 5 mg/ml to prevent nucleolar association of Rev protein. LMB was provided by M. Yoshida (The University of Tokyo, Tokyo, Japan).

Acquisition and processing of images

For light microscopic analysis (Fig. 1 C), images were acquired by a stereomicroscope (MZ12; objective lens, Plan 1.0×; Leica) and captured by DC100 program (Leica), or by a light microscope (Axioskop 2 plus; objective lens, Plan-Neofluar 2.5×/0.075; Carl Zeiss MicroImaging, Inc.) and captured by Axio Cam CCD camera and Axio Vision 3.0 imaging system (Carl Zeiss MicroImaging, Inc.). For immunofluorescence microscopic analysis, images were acquired by a laser-scanning microscope (model Eclipse E600; Nikon) using Plan-Fluor 10×/0.30 (Fig. 7 B), Plan-Fluor 40×/0.75 (Fig. 6 A), and Plan-Apo 60×A/1.40 oil (Fig. 5). Radiance 2000 confocal scanning system (Bio-Rad Laboratories) was used.

Accession no.

The deduced amino acid sequence of mouse Cal was deposited in GenBank/EMBL/DDBJ accession no. AF513359.

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Review Article

Vascular cell senescence and vascular aging☆

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Abstract

Vascular cells have a finite lifespan when cultured in vitro and eventually enter an irreversible growth arrest called "cellular senescence". A number of genetic animal models carrying targeted disruption of the genes that confer the protection against senescence in vitro have been reported to exhibit the phenotypes of premature aging. Similar mutations have been found in the patients with premature aging syndromes. Many of the changes in senescent vascular cell behavior are consistent with the changes seen in age-related vascular diseases. We have demonstrated the presence of senescent vascular cells in human atherosclerotic lesions but not in non-atherosclerotic lesions. Moreover, these cells express increased levels of pro-inflammatory molecules and decreased levels of endothelial nitric oxide synthase, suggesting that cellular senescence in vivo contributes to the pathogenesis of human atherosclerosis. One widely discussed hypothesis of senescence is the telomere hypothesis. An increasing body of evidence has established the critical role of the telomere in vascular cell senescence. Another line of evidence suggests that telomere-independent mechanisms are also involved in vascular cell senescence. Activation of Ras, an important signaling molecule involved in atherogenic stimuli, induces vascular cell senescence and thereby promotes vascular inflammation in vitro and in vivo. It is possible that mitogenic-signaling pathways induce telomere-dependent and telomere-independent senescence, which results in vascular dysfunction. Further understanding of the mechanism underlying cellular senescence will provide insights into the potential of antisenescence therapy for vascular aging.

Keywords: Senescence; Aging; Atherosclerosis; Telomere; Ras; Akt; Inflammation; Cyclin-dependent kinase inhibitor

1. Introduction

Cellular senescence is the limited ability of primary human cells to divide when cultured in vitro and is accompanied by a specific set of phenotypic changes in morphology, gene expression and function. These changes in phenotype have been implicated in human aging [1]. This hypothesis, the hypothesis of cellular aging, was first described by Hayflick [2] and supported by evidence that cellular senescence and the division potential of human primary cultures are dependent on donor age [3] and that the growth potential of cultures correlates well with mean maximum lifespan of the species from which the cultures are derived [4]. Human primary cultures derived from the patients with premature aging syndromes, such as Werner syndrome and Bloom syndrome, are known to have shorter lifespan than the cultures from age-matched healthy populations [5], thus supporting the hypothesis of aging. However, until recently, little attention has been paid on the potential impact of vascular cell senescence in vivo on age-related vascular disorders.

In the past decades, significant progress has been made in our understanding of the mechanisms underlying cellular senescence. One widely discussed hypothesis is the telomere hypothesis of senescence [6]. A growing body of evidence has demonstrated a critical role of telomere and telomerase in regulating not only cellular lifespan but also organismal aging. However, recent findings suggest that cellular senescence can also be induced by DNA damage, cellular stress or oncogenic activation, which is independent of replicative age [7]. For example, the constitutive activation of mitogenic stimuli by expression of oncogenic Ras induces senescent phenotypes [8–10]. Thus, it is possible that atherogenic stimuli increase cell turnover at the sites of atherosclerosis, thereby promoting telomere shortening, whereas it also re-

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sults in activation of proliferative signals that potentially induce senescence independent of telomere shortening.

In this review, we will describe recently accumulating evidence that supports the hypothesis of cellular aging in the vasculature and discuss the potential of antisenescence therapy for age-related human vascular disorders.

2. Occurrence of vascular cell senescence in vivo

Vascular cells have a finite lifespan in vitro and eventually enter an irreversible growth arrest called cellular senescence. Flattened and enlarged cell morphology is known to be one of the characteristics of cellular senescence [11]. Expression of negative regulators for the cell cycle machinery, such as p53 and p16, is increased with cell division and thereby promotes growth arrest [12]. Primary cultured cells undergoing cellular senescence in vitro express the increased activity of β-galactosidase (β-gal) when assayed at pH 6, which is distinguishable from endogenous lysosomal β-gal activity that can be detected at pH 4. This activity, senescence-associated β-gal (SA β-gal) activity, has been shown to correlate with cellular aging and thus is regarded as a biomarker for cellular senescence [13]. The in vitro growth properties of vascular cells derived from human atherosclerotic plaque are impaired, and they develop senescence earlier than those from normal lesions [14,15]. The histology of the lesions of human atherosclerosis has been extensively studied, and these studies have demonstrated that there are endothelial cells (ECs) and vascular smooth muscle cells (VSMCs) that exhibit the morphological features of cellular senescence [16,17]. These suggest the occurrence of cellular senescence in vivo. Recently, this notion has been confirmed by cytochemical analysis in vivo using SA β-gal activity. Fenton et al. [18] have successfully detected SA β-gal-positive vascular cells in rabbit carotid arteries subjected to vascular injury. With repeated denudation, the accumulation of SA β-gal-positive cells was markedly enhanced. The authors have recently demonstrated SA β-gal-positive vascular cells in human atherosclerotic plaque of the coronary arteries obtained from the patients who had ischemic heart disease [19]. SA β-gal-positive cells were predominately localized on the luminal surface of atherosclerotic plaque and identified as ECs, but no positive cells were observed in the internal mammary arteries from the same patients where atherosclerotic changes were minimally observed. In advanced plaque, however, SA β-gal-positive VSMCs were detected in the intima but not in the media [20], which may represent extensive replication in the lesions, as observed in the arteries subjected to double-denudation (Fig. 1). SA β-gal-positive cells exhibit increased expression of p53 and p16, alternative markers for cellular senescence, in human atheroma, suggesting the further evidence of in vivo senescence. These cells also show impaired function, such as the decreased expression of endothelial nitric oxide synthase (eNOS) and the increased expression of pro-inflammatory molecules

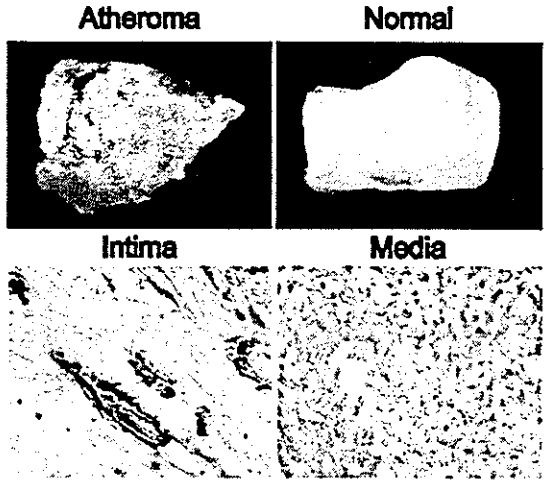

Fig. 1. Senescent vascular cells in human atheroma. Photographs of the luminal surface of human atheroma (atheroma, left) and non-atherosclerotic normal artery (normal, right) stained with SA β-gal staining. SA β-gal activity was observed in human atheroma but not in normal arteries (upper panel). A double staining for SA β-gal and α-smooth muscle actin of the sections of atheroma identified SA β-gal-positive cells as VSMCs in the intima but not in the media (lower panel).

[20]. Thus, cellular senescence in vivo may contribute to the pathogenesis of vascular aging.

3. Role of cellular senescence in vascular pathophysiology

Age-associated changes in the blood vessels include a decrease in compliance and an increase in inflammatory response that promote atherogenesis [21]. It has also been reported that angiogenesis is impaired with advanced age [22,23], whereas aging decreases the antithrombogenic property of the endothelium [24]. A number of studies have reported that many of the changes in senescent vascular cell behavior are consistent with known changes seen in age-related vascular diseases, suggesting a critical role of cellular senescence in vascular pathophysiology. The production of nitric oxide (NO) and the eNOS activity are reduced in senescent human ECs [25]. Induction of NO production by shear stress is also decreased in senescent ECs [26]. A decline in the eNOS activity of senescent ECs is attributable to a decrease in expression of eNOS protein as well as in eNOS phosphorylation mediated by Akt [27]. The levels of prostacyclin production are significantly decreased with in vitro aging of ECs [28], whereas senescent ECs upregulate plasminogen activator inhibitor-1 [29]. All these alterations are likely involved in the impairment of endothelium-dependent vasodilation but also increased sensitivity of thrombogenesis in human atherosclerosis. The interaction between monocytes and ECs is enhanced by EC senescence [30], thereby promoting atherogenesis. This appears to be mediated by upregulation of adhesion molecules and pro-inflammatory

cytokines as well as a decrease in the production of NO in senescent ECs [19,26]. It is reported that the ability to form capillary structures in vitro is reduced in senescent ECs [31]. Bone marrow-derived circulating endothelial progenitor cells (EPCs) are known to participate in postnatal neovascularization and vascular repair [32,33]. The in vitro growth property and function of bone marrow-derived EPCs are impaired in the patients with coronary artery disease and negatively correlate with risk factors including age [34,35]. Thus, aging may promote senescence of EPCs as well as ECs, resulting in decreases in angiogenesis and vascular healing.

4. Telomere-dependent vascular cell senescence

Telomeres are non-nucleosomal DNA–protein complexes at the end of chromosomes that serve as protective caps and are substrates for specialized replication mechanisms. As a consequence of semi-conservative DNA replication, the extreme termini of chromosomes are not duplicated completely, resulting in successive shortening of telomeres with each cell division. Critically short telomere was thought to trigger the onset of cellular senescence, but recent studies suggest that the single-strand telomeric overhang and associated proteins are key components for signals of senescence [36,37]. Telomerase is a ribonucleoprotein that adds telomeres onto chromosome ends with its RNA moiety as a template. Forced expression of the catalytic component of telomerase TERT in telomerase-negative human fibroblasts results in the stabilization of telomere length and extension of cell lifespan [38]. This observation has established the importance of telomere shortening in human cellular senescence. It has been also reported that there is another mechanism of telomere maintenance without telomerase activity, called telomerase-independent alternative lengthening of telomeres (ALT) [39]. In the field of vascular biology, it has been shown that telomere shortening with cell divisions occurs in human-cultured ECs and VSMCs, and that introduction of TERT extends cell lifespan of human ECs and VSMCs, suggesting a critical role of telomere shortening in vascular cell senescence as well [31,40,41]. It is likely that shortened telomeres are in some way sensed in a cell, and that a pathway is activated that results in exit from cell cycle (Fig. 2). The p53, p21 and p16 proteins and their downstream effectors are important for cellular senescence, and thus are likely to be a part of the telomere-response pathway. However, less is known about what links telomeres and these factors. Until present, several telomeric-binding proteins have been identified that contribute to the integrity of telomere functions and are potentially involved in the telomere-response pathway [42]. These include protection of telomeres-1 (Pot-1) [43], Ku [44], telomeric repeat-binding factor 1 and 2 (TRF1 and TRF2, respectively) [45]. Pot-1 is identified as a telomeric protein that binds to a tip of telomere and is thought to constitute the telomere shortening signal [46]. The protein

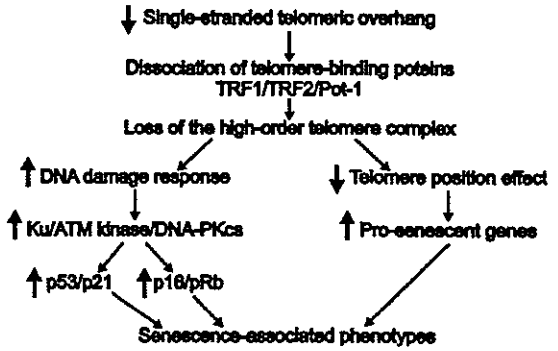

Fig. 2. Putative telomere-responsible pathways. As cells age, single-stranded telomeric overhangs are eroded, resulting in the dissociation of telomeric proteins. Loss of the high-order telomere complex is recognized as DNA breaks, thereby activating the molecules involving DNA repair that also play a critical role for telomere maintenance. These signals of DNA damage response are conducted to the cell cycle machinery. Telomere dysfunction also results in a release of telomere position effects that have the impact on expression of the genes at subtelomeric regions.

Ku, originally defined by its role in the repair of chromosomal DNA breaks, is found at telomeres and is necessary for normal telomere maintenance and functions. Genetic ablation studies demonstrated an essential role of Ku in mediating the telomere-response pathway [47]. Likewise, the catalytic subunit of the DNA-dependent protein kinase complex [48] and ATM kinase [49], both of which function in the double-strand break repair, have been implicated in the signal pathway of telomere shortening. Recently, it has been proposed that telomeres form large duplex loops, and telomeric proteins, TRF1 and TRF2, are essential for their formation [50,51]. Particularly, inhibition of TRF2 function is reported to cause cellular senescence in a p53/p16-dependent manner [19,52]. Thus, it is supposed that, as a result of telomere shortening, the efficacy of forming a high-order telomeric complex is impaired, leading to a release of various telomeric proteins from telomeres that elicit signals for cellular senescence (Fig. 2). Cytologically, telomeric regions are heterochromatic, implying that local DNA folding is increased. Positioning a gene in a telomeric heterochromatic region can impose telomere position effect on that gene. Telomere position effect, which has been characterized in the yeast and recently in human cells, is known to induce the reversible silencing of the gene [53]. Consequently, the modification of gene expression by telomere position effect may also contribute to the signaling pathway for cellular senescence.

5. Telomere shortening and vascular dysfunction

There is evidence indicating that telomere shortening occurs in human vasculature, which may be related to age-associated vascular diseases [54]. In most of the previous reports mentioned, changes in cell phenotypes associated with senescence were studied in vascular cell populations

undergoing replicative senescence, thus suggesting telomere-dependent vascular dysfunction. However, it remains unclear whether phenotypic changes in senescent vascular cells result from telomere dysfunction. Inhibition of TRF2 has been shown to induce either cellular senescence or apoptosis in various cells by destroying telomere loop structure [51,55]. The authors have demonstrated that the introduction of a dominant-negative form of TRF2 into human ECs induces a growth arrest with phenotypic characteristics of cellular senescence [19]. Telomere dysfunction significantly increases expression of pro-inflammatory molecules and reduces the activity of eNOS, suggesting a causal link between telomere and vascular dysfunction associated with senescence.

Telomerase-deficient mice have been developed and found to reveal a normal phenotype at the first generation presumably because of mice having much longer telomeres [56,57]. Telomeres are shortened with successive generations, and they become infertile at the sixth generation due to the impairment of reproductive system. Some aspects of the late generation mice mimic age-associated phenotypes. They exhibit shortened lifespan and a reduced capacity to respond to stress, such as wound healing and hematopoietic ablation [58]. The ability of neovascularization is reduced in the late generation of telomerase-deficient mice [59]. Decreased vessel formation may be attributable to the impaired function and replicative capacity of ECs induced by telomere shortening. Recently, the heart in late generation of telomerase-deficient mice has been shown to mimic the end-stage-dilated cardiac myopathy in humans [60].

6. Telomerase

Since early studies reported that telomerase activity was detected in cancer cells but not normal somatic cells, the idea emerged that telomerase activity might be essential for tumor growth [61]. Multiple tumor-suppressor pathways are likely to repress telomerase expression in normal somatic cells [62]. Increasing evidence has suggested that telomerase activity regulates cell proliferation in normal somatic cells by telomere lengthening or upregulating growth-controlling genes in a telomere length-independent manner [57,63]. Human ECs and VSMCs express telomerase activity, which is drastically activated by mitogenic stimuli via a protein kinase C-dependent pathway [64] but the activity declined with in vitro aging due to a decrease in expression of TERT, leading to telomere shortening and cellular senescence [41,65]. Introduction of TERT prevents endothelial dysfunction associated with senescence, such as a decrease in eNOS activity and an increase in monocyte binding to ECs [19,26]. Immortalized human ECs (TERT-ECs) have been established by introduction of TERT [31]. TERT-ECs appear to retain EC characteristics including various cell surface markers. When examined in Matrigel, they form capillary-like structures in response to extracellular matrix signals as efficiently as early passage of ECs, whereas senescent or transformed ECs do not. In addition, TERT-ECs are more resistant to apoptotic induction than pre-senescent ECs. They maintain a normal growth control and exhibit no transformed phenotype. These telomerized human ECs are functional in vivo as demonstrated by the Matrigel implantation mouse model [66]. In this model, whereas primary human EC-derived vessel density decreased with time after implantation, telomerized ECs maintained durable vessels, indicating that telomerase activity is important for the maintenance of a microvascular phenotype.

7. Telomere-independent vascular cell senescence

Signals other than extended proliferation have been shown to result in cells developing a phenotype indistinguishable from that of senescent cells at the end of their replicative lifespan. For example, the constitutive activation of mitogenic stimuli by expression of oncogenic Ras or E2F induce a senescent phenotype [8,67]. Cellular senescence triggered by mitogenic stimuli is independent of replicative age, and these signals act before the replicative limits of cells. Hence, it is apparently telomere independent and thus termed as premature senescence. The constitutive activation of Ras provokes premature senescence in vascular cells, which is associated with accumulation of the proteins p53 as well as p16 [20]. Activation of extracellular signal-regulated kinase (ERK) appears to be critical for Ras-induced senescence since inhibition of ERK restores cell growth arrest elicited by Ras activation [20], whereas introduction of an active form of ERK results in premature senescence involving p53 and p16 [9]. p38 mitogen-activated protein kinase (MAPK) is also implicated in Ras-induced senescence. p38 MAPK is activated in a ERK-dependent fashion, thus indicating that Ras promotes premature senescence by sequentially activating the ERK and p38 MAPK pathway [68].

8. Cell cycle regulators

It is clear that cellular senescence entails the activation of several tumor-suppressor proteins and inactivation of several oncoproteins, each of which ultimately engages either the p53 or pRb pathway and interacts with each other at multiple levels (Fig. 3). p53 activity and in some cases protein levels are increased in senescent cells. The mechanisms responsible for p53 activation in senescent cells remain elusive, however some molecular details are emerging. One cause of p53 activation may be an increase in expression of p14, a tumor-suppressor protein encoded by the INK4a locus. p14 activates p53 through a mechanism involving sequestration of MDM2, a protein that promotes degradation of p53 [69]. p14 is induced by oncogenic Ras and E2F [70], whereas TBX2, a member of T-box family of transcription factors, suppresses p14 expression [71]. Another cause of p53 activation is the

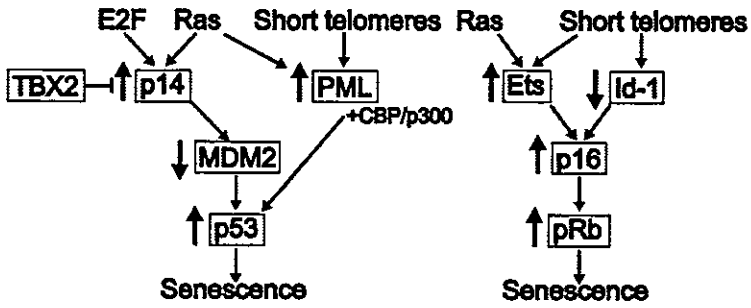

Fig. 3. Control of cellular senescence by the p53/p21 and p16/pRb pathways. Shown are the consequences of senescence-inducing signals on cell cycle regulators in the p53/p21 and p16/pRb pathways. Senescence-inducing signals, such as oncogenic Ras and E2F, increase expression of p14, whereas TBX2 represses p14 promoter activity, thus counteracting with each other. p14 sequesters MDM2, leading to an increase in p53 activity. Signals, such as oncogenic Ras, telomere shortening and possibly other signals increase expression of PML, which interacts with CBP/p300 and stimulates p53 activity. Oncogenic Ras stimulates the activity of Ets that induces p16 transcription by promoting its phosphorylation. Short telomeres lead to an increase in Ets and a decrease in Id, a protein that inhibits Ets activity, resulting in the accumulation of p16. p16 inhibits the cyclin-dependent kinases that phosphorylate pRb, leading to an increase in its active form.

promyelocytic leukemia (PML) tumor suppressor. PML is induced by replicative senescence and Ras activation by unknown mechanisms [72,73]. PML interacts with CBP/p300 acetyltransferase, which acetylates p53, thus stimulating p53 activity. Recently, p53 is found at telomeres and ablation of p53 function restores adverse effects of telomere loss [74], suggesting active roles of p53 in telomere maintenance as well as the telomere-response pathway. pRb exists in hypophosphorylated form that binds to E2F and inhibits cell cycle progression in senescent cells because of high levels of the cyclin-dependent kinase inhibitors, p21 and p16. p21 is transcriptionally induced at least partly by p53, although p53-independent, post-transcriptional mechanisms also contribute to an increase in p21 expression in senescent cells [75]. p16, another tumor-suppressor protein encoded by INK4a locus, increases in part because Ets, a transcription factor that stimulates p16 expression, is induced by senescent signals including telomere shortening and Ras activation, whereas Id1, a protein that inhibits Ets activity, is decreased in senescent cells [76]. It is demonstrated that ectopic expression of the cyclin-dependent kinase inhibitors, such as p21, p16 and p14, causes premature senescence [77], suggesting pivotal roles in the signaling pathways of senescence.

p53 immunoreactivity is present in vascular cells in areas with chronic inflammation of human atheroma, while a few cells positive for p53 immunoreactivity are found in control arteries [78]. p21 immunoreactivity is also detected in human atheroma but not in normal lesions and is colocalized with p53. Forced expression of cyclin-dependent kinase inhibitors induces premature senescence that is associated with cell dysfunction in cultured vascular cells (Minamino et al. unpublished data). These observations suggest a pathological role of p53 and p21 in atherogenesis. However, their precise roles remain unclear. It is demonstrated that atherosclerosis is aggravated in p53/apolipoprotein E (ApoE) double-knockout mice through an increase in p53-controlled proliferation [79]. In contrast, the study using perivascular collar model in ApoE-knockout mice shows that p53 overexpression results in a marked decrease in the cellular and extracellular contents in the cap lesions, leading to spontaneous plaque rupture [80]. Thus, in the clinical settings, elevated expression of p53 and cyclin-dependent kinase inhibitors may be deleterious in human atherosclerosis.

9. Ras-induced senescence and vascular inflammation

It has been demonstrated that various molecules including growth factors, vasoactive peptides and oxidative stresses, such as ROS and oxidized low-density lipoproteins, are induced during the lesion formation and regulate numerous critical cell functions, thereby contributing to atherogenesis [81]. These stimuli function as mitogens for vascular cells through the signaling cascades that activate Ras [81]. Inhibition of Ras has been reported to prevent intimal formation after vascular injury, suggesting a critical role of Ras activation in VSMC proliferation [82]. In addition to its role in cell proliferation, we have found that constitutive activation of Ras induces vascular cell senescence that is associated with vascular inflammation [20]. Activation of Ras drastically increased expression of pro-inflammatory cytokines partially through ERK activation in cultured vascular cells. Introduction of Ras into balloon-injured arteries enhanced vascular inflammation as well as senescence compared with control-injured arteries (Fig. 4). Moreover, senescent cells express inflammatory molecules in human atherosclerotic plaque, and ERK is activated in these cells, suggesting that telomere-independent mechanisms may also contribute to vascular cell senescence in human atherosclerosis. Consistent with our findings, functional inhibition of Ras has been demonstrated to suppress pro-inflammatory molecules, thereby reducing lesion formation in ApoE-deficient mice [83]. Moreover, angiotensin II, an important atherogenic molecule that activates the Ras-signaling pathway, has been demonstrated to promote vascular cell senescence as well as vascular inflammation [84]. Thus, it is assumed that atherogenic stimuli may

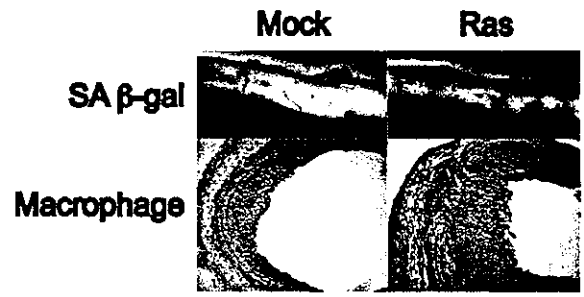

Fig. 4. Activation of Ras induces senescence and inflammation in vivo. The adenoviral vector encoding H-*ras*V12 (Ras) or the empty vector (Mock) was transduced into rat carotid arteries injured by a balloon catheter. It is known that accumulation of macrophages is minimally involved in the lesion formation in this model. Whereas only a little SA β-gal activity was found in mock-infected injured arteries, transduction of adeno-Ras into injured arteries increased SA β-gal activity (upper panel). The area of accumulated macrophages (brown) in the intima was markedly increased in Ras-infected injured arteries compared with mock-infected injured arteries (lower panel), indicating a causal relationship between Ras activation and vascular inflammation. Adapted from Ref. [20] with permission.

initially promote cell proliferation, and when overstimulated to proliferate, mitogenic-signaling pathways may induce telomere-dependent and telomere-independent senescence, which results in vascular dysfunction. Vascular inflammation is known to induce degradation of extracellular matrix by various proteinases, such as collagenases and gelatinases, and by inhibition of matrix production [85]. Therefore, decreased cellularity and enhanced inflammation associated with vascular cell senescence may contribute to plaque vulnerability.

10. Genetic models for aging

Many molecular mechanisms have been suggested to contribute to human aging and age-associated disease. Recent genetic analyses have demonstrated that reduction-of-function mutations of the signaling pathway of insulin/insulin-like growth factor-1 (IGF-1)/phosphatidylinositol-3 kinase (PI3K)/Akt (also known as protein kinase B) extends the longevity of the nematode *Caenorhabditis elegans* [86–92]. The forkhead transcription factor DAF-16, which is phosphorylated and thereby inactivated by Akt, plays an essential role in this longevity pathway [93,94]. More recently, it has been reported that the genes regulating longevity are conserved in organisms ranging from yeast to mice. The mutation of *Sch9*, which is homologous to *Akt*, extends the lifespan of yeast [95] and mutations that decrease the activity of insulin/IGF-1-like pathway increase the longevity of fruit flies [96] and mice [97,98]. These mutations that extend the lifespan are associated with increased resistance to oxidative stress, which is mediated in part by an increase in expression of antioxidant genes [99–101]. In mammalian cells, activation of Akt has been reported to induce cell proliferation and survival toward tumorigenesis [102–104]. The insulin pathway has also been shown to be essential for the maintenance of normal metabolic homeostasis [105]. Restriction of caloric intake extends the longevity of yeast, worms, fruit flies, mice and probably humans and postpones or prevents age-dependent deterioration and chronic diseases [91]. Since calorie restriction associates with the persistent decrease in the insulin signals, one might think that the insulin pathway could be involved in human aging and age-associated diseases, especially in the patients with diabetes.

Mice models that exhibit an early onset of phenotypes associated with aging have been reported. These include mouse mutants carrying targeted disruption of the genes involving DNA damage repair, such as *ku86* [106], *XPD* [107] and *BRCA1* [108]. Activation of p53 [109] as well as telomerase deficiency [58] also cause premature aging, which is characterized by reduced longevity, osteoporosis, organ atrophy and a diminished stress tolerance. All these molecules have been implicated in cellular senescence. More importantly, cellular senescence in vivo has been detected in premature aging mice [108]. Thus, these results provide in vivo evidence that links cellular senescence to organismal aging.

11. Conclusion

Accumulating evidence indicates a critical role of cellular senescence in organismal aging and age-related disease including atherosclerosis. Young adult bone marrow-derived EPCs have been shown to restore aging-impaired angiogenic function [110]. Chronic treatment with EPCs from young non-atherosclerotic ApoE-deficient mice prevents atherosclerosis progression in ApoE-deficient recipients despite persistent hypercholesterolemia [111]. Moreover, introduction of telomerase into EPCs has been reported to extend cell lifespan and to increase the efficacy of vasculogenesis in vivo [112]. These reports indicate that progressive progenitor cell deficits contribute to age-associated vascular dysfunction and suggest the potential utility of cell-based antisenescence therapy as a novel therapeutic strategy for vascular aging. Further understanding of mechanisms underlying cellular senescence will provide new insights into the pathogenesis of age-associated vascular disorders.

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