Table 2
Sequences of PCR primers used to amplify each of genes in RT-PCR.

Gene	Primer	Sequence (5′→3′)
ALP	Forward	GCCCTCTCCAAGACATATA
	Reverse	CCATGATCACGTCGATATCC
Osteocalcin	Forward	CAAGTCCCACACAGCAGCTT
	Reverse	AAAGCCGAGCTGCCAGAGTT
Collagen type 1 a1	Forward	GCAATCGGGATCAGTACGAA
	Reverse	CTTTCACGCCTTTGAAGCCA
Runx2	Forward	GCTTGATGACTCTAAACCTA
	Reverse	AAAAAGGGCCCAGTTCTGAA
Osterix	Forward	GAAGAAGCTCACTATGGCTC
	Reverse	GAAAAGCCAGTTGCAGACGA
GAPDH	Forward	TGAACGGGAAGCTCACTGG
	Reverse	TCCACCACCCTGTTGCTGTA

in 293 cells (Riken Cell Bank). MC3T3-E1 cells were infected and 2 days later, the medium was replaced with differentiation medium.

Statistical analysis

All data are expressed as means ± SD and a minimum of three independent experiments were performed for each assay. A two-sided unpaired Student's *t*-test, or analysis of variance (ANOVA) for multiple comparisons, was used for statistical analysis. A statistical difference between experimental groups was considered to be significant when the p value was <0.05.

Results

Osteoblastic differentiation of MC3T3-E1 cells is promoted by the PKCα/PKCβI inhibitor Gö6976

Prior to determination of the effects of PKC isoforms on osteoblastic differentiation, we first evaluated the endogenous expression of the PKC isoforms PKCα and PKCβ in MC3T3-E1 cells by western blotting. The expression of PKCα was identified in MC3T3-E1 cells. On the other hand, the expression of PKCβ, which indicates both PKCβI and PKCβII, was almost unidentified in MC3T3-E1 cells (Fig. 1A). We next investigated the effects of the expressed PKCs on osteoblastic differentiation by assay of the effect of incubation of MC3T3-E1 cells with various concentrations of the PKCα/PKCβI inhibitor Gö6976 (0–1.0 μM) for 72 h on ALP staining. In MC3T3-E1 cells, treatment with Gö6976 strongly induced ALP staining in a dose-dependent manner and also enhanced ALP activity (Fig. 1B). Furthermore, Alizarin Red S staining indicated that Gö6976 clearly promoted calcification of the extracellular matrix (ECM) in MC3T3-E1 cells. The degree of this ECM calcification was quantified by measurement of the absorbance of the Alizarin Red S solution (Fig. 1C). Quantitative real-time PCR assay showed acceleration of the mRNA expression of osteoblastic differentiation markers, including ALP, OCN, and Col1a1, and of the transcription factor Runx2, by Gö6976 in a dose-dependent manner (Fig. 1D). These findings indicate that Gö6976 promoted osteoblastic differentiation in MC3T3-E1 cells suggesting that the PKCα and/or PKCβI isoforms might have a suppressive effect on osteoblastic differentiation in MC3T3-E1 cells.

Treatment with the PKCβ inhibitor does not promote osteoblastic differentiation in MC3T3-E1 cells

To investigate which PKC isoform modulates osteoblastic differentiation, we examined the contribution of PKCβ to differentiation using a specific PKCβ inhibitor, which inhibits both PKCβI and PKCβII. Treatment of MC3T3-E1 cells with this PKCβ inhibitor had no influence on ALP activity (Fig. 2A). Moreover, neither calcification of the ECM (Fig. 2B), nor the expression of mRNA related to osteoblastic differentiation (Fig. 2C), changed in the presence of different concentrations of the PKCβ inhibitor. The inhibitor also induced no change in osteoblast-cell proliferation (data not shown). These data indicated that PKCβ, whether it is the PKCβI or PKCβII isoform, did not affect osteoblastic differentiation or cell proliferation. We therefore assumed that inhibition of PKCα by Gö6976 promoted osteoblastic differentiation in MC3T3-E1 cells.

Knockdown of PKCα promotes osteoblastic differentiation

To further confirm the effects of PKCα inhibition on osteoblastic differentiation in MC3T3-E1 cells, we investigated changes in cell differentiation following knockdown of PKCα using an RNA interference method. Fig. 3A shows the low cellular expression level of PKCα, 48 h after transfection of two different anti-PKCα siRNAs (Fig. 3A). Knockdown of PKCα using either siPKCα-1 or siPKCα-2 caused the up-regulation of ALP activity and the acceleration of ECM calcification in MC3T3-E1 cells compared to cells transfected with control siRNA (Figs. 3B and C). Furthermore, quantitative real-time PCR analysis revealed that the gene expression of ALP and OCN was dramatically increased by knockdown of PKCα but not by treatment with control siRNA. Among the other genes tested, the expression of Col1a1 showed some tendency to increase following knockdown of PKCα. Furthermore, knockdown of PKCα increased the mRNA expression of both of the transcription factors Runx2 and Osterix (Figs. 3D, E). These results indicated that PKCα may suppress osteoblastic differentiation.

Activation of PKC by TPA attenuates osteoblastic differentiation in MC3T3-E1 cells

We next investigated the influence of PKC activation by TPA on osteoblastic differentiation. Treatment with TPA (0–10 nM), which activates not only PKCα but also other conventional PKC and novel PKC isoforms, caused a decrease in ALP activity in a dose-dependent manner (Fig. 4A). Activation of PKC by TPA did not stimulate calcification of the ECM in MC3T3-E1 cells (Fig. 4B). In addition, RT-PCR analysis and quantitative real-time PCR showed that the expression of osteoblastic differentiation markers such as ALP and OCN were clearly decreased following TPA treatment in a dose-dependent manner (Figs. 4C, D).

Adenoviral overexpression of PKCα suppresses osteoblastic differentiation in MC3T3-E1 cells

To further confirm the functional role of PKCα in osteoblasts, we performed adenoviral-mediated gene transfer of wild-type PKCα (Ad-PKCα) and PKCβII (Ad-PKCβII) into MC3T3-E1 cells. Following gene transfer, we then confirmed a high expression level of the Ad-PKCα and Ad-PKCβII proteins by western blotting (Fig. 5A). We next measured the proliferation of MC3T3-E1 cells infected with each of the adenovirus vectors Ad-PKCα, Ad-PKCβII or Ad-βgal (control). Compared with cells transfected with Ad-βgal, the proliferation of MC3T3-E1 cells infected with Ad-PKCα was significantly increased on Days 4 and 5 after transfection, while the proliferation of cells transfected with Ad-PKCβII was similar to that of Ad-βgal cells (Fig. 5B). The observed acceleration of the proliferation of Ad-PKCα-transfected MC3T3-E1 cells is consistent with a previous report that PKCα has a stimulatory effect on human osteoblastic proliferation [19]. In addition, the overexpression of PKCα, but not that of PKCβII, suppressed ALP activity compared to overexpression of Ad-βgal (Fig. 5C). Quantitative real-time PCR analysis showed that overexpression of PKCα also suppressed the mRNA expression of ALP, Col1a1, Runx2, and Osterix compared with Ad-βgal (Fig. 5D).

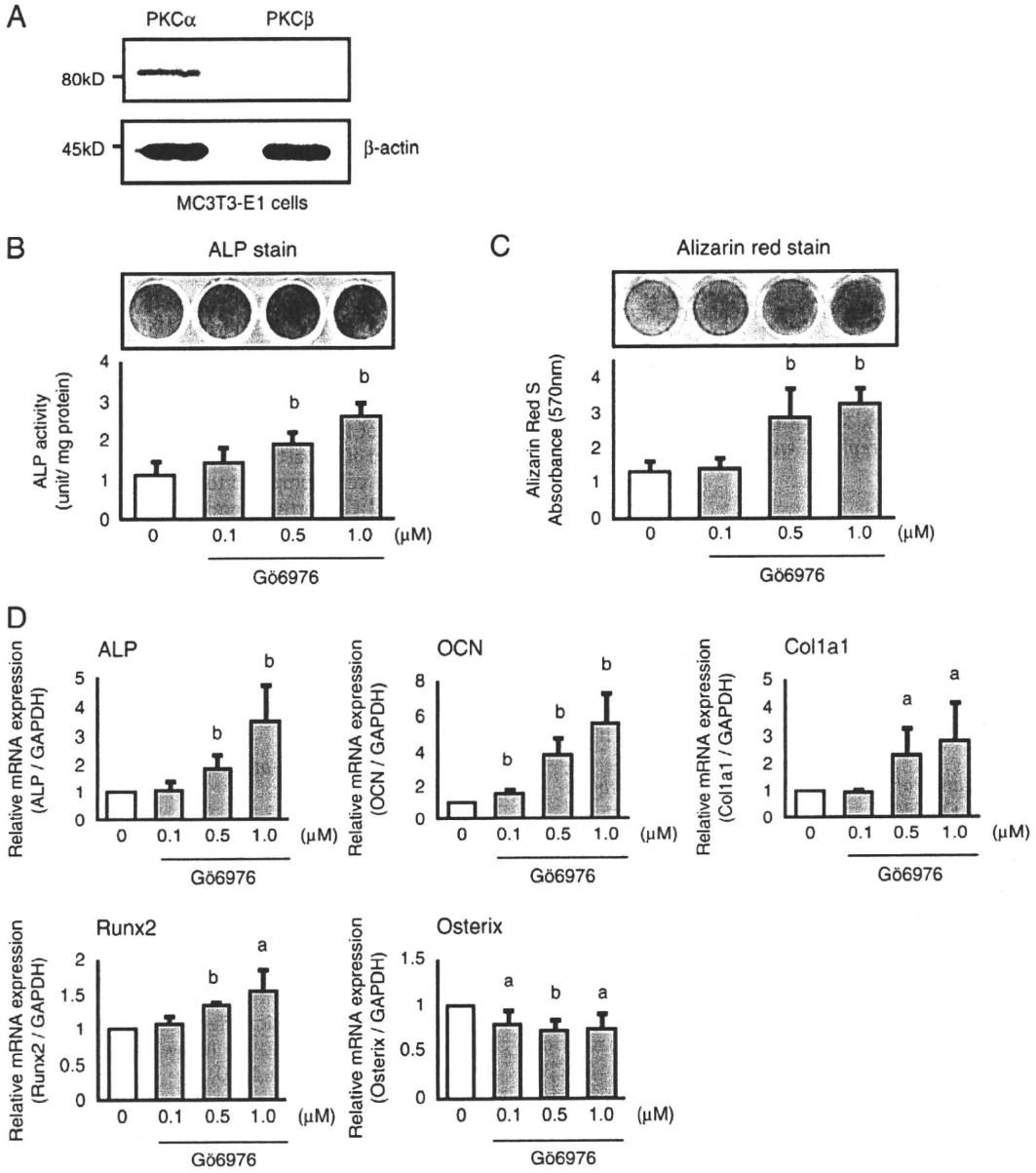

Fig. 1. Osteoblastic differentiation of MC3T3-E1 cells promoted by the PKCα/PKCβI inhibitor Gö6976. (A) endogenous expression of the PKCα, PKCβ proteins in MC3T3-E1 cells by western blotting. β-Actin was used as the internal control. (B) ALP staining and activity of MC3T3-E1 cells treated with Gö6976 which inhibits PKCα and PKCβI. MC3T3-E1 cells (2.0×10^4 cells/cm^2) were cultured in growth medium for 24 h, and then replaced with Gö6976 in differentiation medium for 3 days. (C) MC3T3-E1 cells stained with Alizarin red solution and quantified Ca content in the matrix of the cells. MC3T3-E1 cells were cultured with Gö6976 in differentiation medium for 28 days. Fresh medium was changed twice per week. (D) total RNA isolated from MC3T3-E1 cells treated with Gö6976 for 3 days. mRNA expression of the osteoblast-related genes: *ALP, OCN, Col1α1*; the transcription factor Runx2, and the gene *Osterix* was determined using quantitative real-time PCR analysis and UPL probes. The expression of each gene was normalized to GAPDH expression. (B, C, and D) data are means ± SD of three independent experiments performed in duplicate (a: $p<0.05$, b: $p<0.01$ compared with Gö6976-untreated control).

Discussion

In this study, we showed that PKCα has a suppressive effect on osteoblastic differentiation in MC3T3-E1 cells. Since the PKCα/PKCβI inhibitor Gö6976 accelerated ALP activity, and the PKCβ inhibitor had no influence on ALP activity, we concluded that PKCα is the PKC isoform that functions as a suppressor of osteoblastic differentiation. In addition, we confirmed which isoforms of PKC have specific effects on osteoblastic differentiation in ST2 cells, mouse bone marrow stromal cells. Although ST2 cells are more primitive than MC3T3-E1 cells, they are known to differentiate into osteoblast-like cells in differentiation medium in a similar manner to MC3T3-E1 cells [20]. Treatment of ST2 cells with Gö6976 increased ALP activity, with maximum activity observed at a concentration of 0.5 μM rather than at 1.0 μM, which was the concentration which gave maximum activation in MC3T3-E1 cells. Treatment of ST2 cells with the PKCβ inhibitor or TPA in did not alter ALP activity (data not shown). However, inhibition of PKCα also promoted osteoblastic differentiation in ST2 cells. Taken together, these results suggest that PKCα has a suppressive effect on osteoblastic differentiation that is not cell-type dependent. Thus, we focused on the role of PKCα in osteoblastic differentiation in MC3T3-E1 cells. Knockdown of PKCα promoted osteoblastic differentiation. In addition, calcification of ECM in MC3T3-E1 cells was also accelerated at 28 days after PKCα siRNA

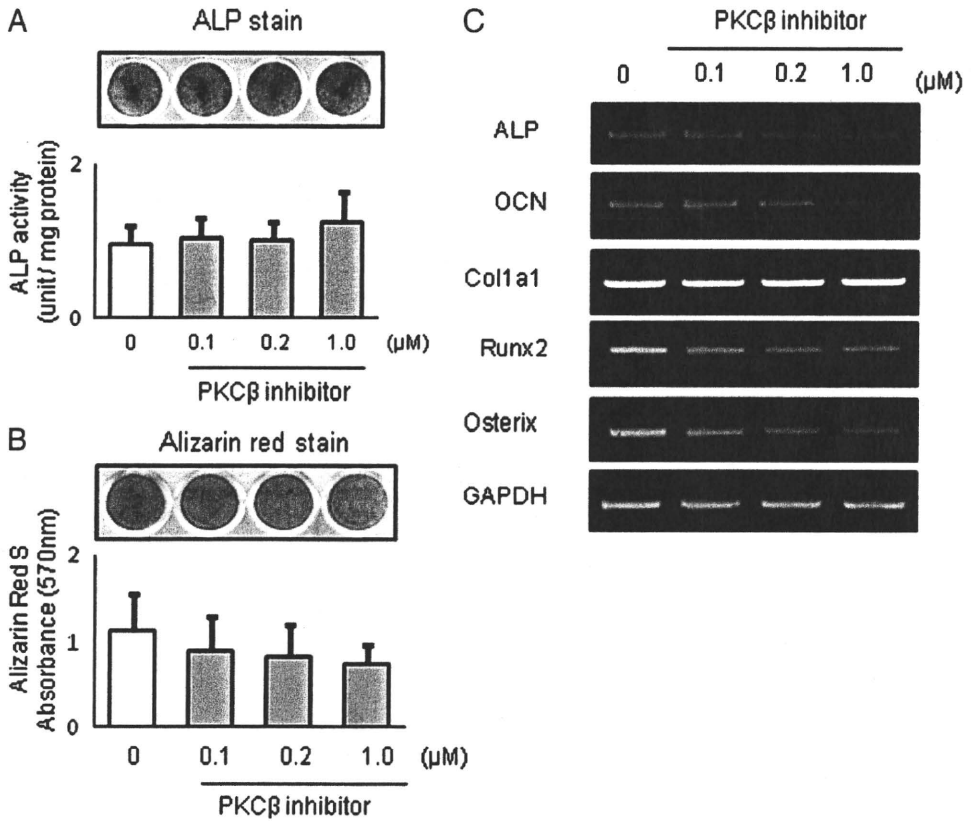

Fig. 2. Effect of PKCβ inhibitor on osteoblastic differentiation in MC3T3-E1 cells. (A) ALP staining and activity of MC3T3-E1 cells. The cells were cultured for 24 h, and then incubated for 3 days with PKCβ inhibitor in differentiation medium. (B) MC3T3-E1 cells stained with Alizarin red solution and quantified Ca content in the matrix of the cells. MC3T3-E1 cells were cultured with PKCβ inhibitor in differentiation medium for 28 days. Fresh medium was changed twice per week. (C) RT-PCR analysis of total RNA isolated from MC3T3-E1 cells treated with PKCβ inhibitor. Expression of osteoblastic related genes: ALP, OCN, Col1α1, Runx2, and Osterix. (A and B) data are means ± SD of three independent experiments performed in duplicate (a: $p<0.05$, b: $p<0.01$ compared with PKCβ inhibitor-untreated control).

transfection (Fig. 3C). In contrast, overexpression of PKCα decreased ALP activity (Fig. 5C) and reduced the expression of the mRNA of osteoblastic markers and transcription factors (Fig. 5D).

PKCα has been implicated in a number of biological functions such as proliferation, differentiation, cell cycle control, apoptosis/cell survival and cell adhesion [21]. In particular, PKCα is known to have an essential role in the proliferation of, not only osteoblasts [19], but also of other normal and tumor cells [22]. In the present study, we further demonstrated that PKCα has a role in the promotion of osteoblastic proliferation (Fig. 5B). Our data are in contrast to two previous reports of the involvement of PKCα in osteoblastic differentiation. Tang et al. [23,24] reported that PKCα is involved in the signal transduction pathway induced by basic fibroblast growth factor (bFGF) during stimulation of fibronectin expression in osteoblasts. The second previous report indicated that fibroblast growth factor receptor 2 (FGFR2) promotes osteogenic differentiation in mesenchymal cells via ERK1/2 and PKCα [25]. In these reports, PKCα was suggested to function in signal transduction pathways that promote osteoblastic differentiation. If PKCα can promote osteoblastic differentiation, inhibition of PKCα by Gö6976 and by PKCα siRNA should decrease osteoblastic differentiation. However, in this study, we showed that inhibition of PKCα promoted osteoblastic differentiation. Since we directly investigated PKCα using an inhibitor of PKCα as well as by knockdown and overexpression of PKCα, our results regarding the role of PKCα in osteoblastic differentiation may be more directly relevant to the cellular role of PKCα. Interestingly, Ogata et al. [26] reported that the G protein, $G\alpha_q$, activated PKC, and subsequently osteoblastic differention was suppressed. Although the isoform of PKC that was involved in the suppression of osteoblastic differentiation was not mentioned in that study, our data suggest the possibility that the results of Ogata might be due to a specific suppressive effect of the PKCα isoform.

Regarding the involvement of other isoforms of PKC in osteoblastic differentiation, there have been some reports that PKCδ activation promotes bone formation [27,28]. We found that treatment of MC3T3-E1 cells with Gö6983, which is an inhibitor of PKCα, β, γ, δ, and ζ, also enhanced ALP activity in a dose-dependent manner (data not shown). To completely rule out the possibility that PKCγ, δ, and ζ may also affect osteoblastic differentiation would require evaluation of the individual roles of PKCγ, δ, or ζ in differentiation. However, our data suggest that it is likely that inhibition of PKCα by Gö6983 strongly contributes to the promotion of ALP activity. Furthermore, PKCα may have a stronger influence on osteoblastic differentiation than PKCδ. Based on the IC_{50} values (half maximal inhibitory concentration) obtained using Gö6983, Gö6983 inhibits PKCα and PKCδ to the same extent [11]. Nevertheless, inhibition of PKCα rather than PKCδ might induce an increase in ALP activity in MC3T3-E1 cells. These results suggest that of the eleven isoforms of PKC, PKCα might have the most important for osteoblastic differentiation. We additionally confirmed that PKCβ, whether it is PKCβI or PKCβII, had little effects on osteoblastic differentiation or cell proliferation. This lack of effect of PKCβ may be related to a lack of expression of PKCβ in osteoblasts, as PKCβ expression has been suggested to be limited to specific tissues such as pancreatic islet cells,monocytes and brain [29]. We suggest that cellular function of PKCα on osteoblasts is not replaced with that of PKCβ, most similar isoform of PKCα.

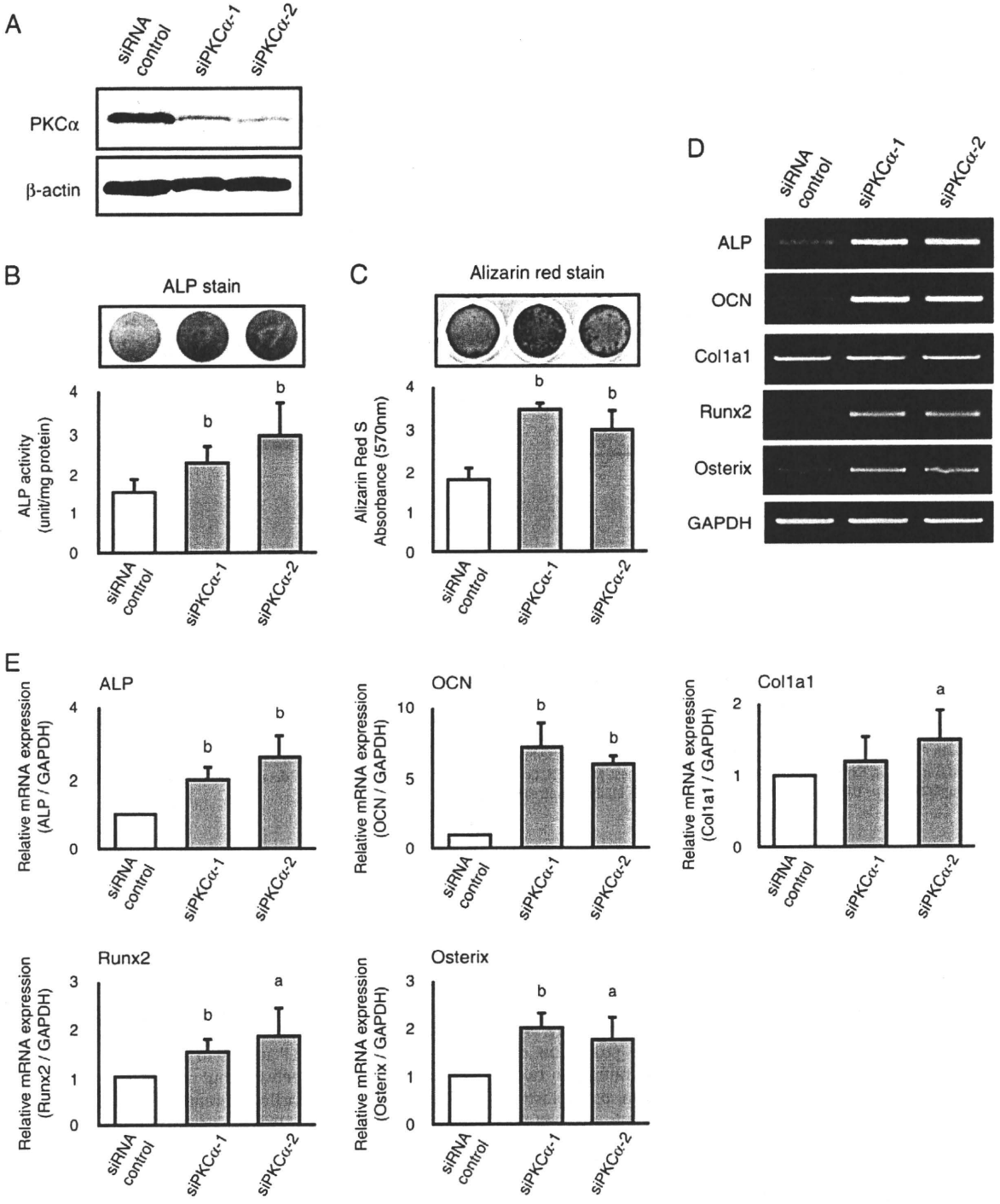

Fig. 3. Knockdown of PKCα stimulates osteoblastic differentiation. (A) Western blotting analysis of PKCα knockdown in MC3T3-E1 cells by transfection with control or PKCα (sites 1 and 2) siRNA. The cells transfected with siRNA were cultured for 48 h. Western blotting was performed using cell lysates as described in Materials and methods. (B) ALP staining and activity of MC3T3-E1 cells transfected with siRNA. The cells transfected with siRNA were incubated for 48 h, following which the medium was changed to differentiation medium. The cells were then incubated for 3 days to evaluate the osteoblastic differentiation. (C) Alizarin red staining and quantified Ca content. MC3T3-E1 cells transfected with control and PKCα siRNA were cultured and incubated in growth medium for 2 days, and then replaced in differentiation medium for 28 days. Fresh medium was changed twice per week. (D and E) expression of osteoblastic-related genes in MC3T3-E1 cells transfected with control and PKCα siRNA was assessed by RT-PCR and quantitative real-time PCR. Total RNA was extracted from MC3T3-E1 cells. The expression of each gene was normalized against GAPDH expression. (B, C, and E) Data are means ± SD of three independent experiments performed in duplicate (a: $p<0.05$, b: $p<0.01$ compared with siRNA control).

Signaling pathways activated downstream of PKCα have been reported to involve the p44/42 MAPK, which is activated by PKCα in various types of cells [19,30–33]. We therefore investigated whether p44/42 MAPK activation is regulated by inhibition of PKCα using the PKC inhibitor or by knockdown of PKCα using RNA interference, or by overexpression of PKCα using Ad-PKCα in MC3T3-E1 cells. However,

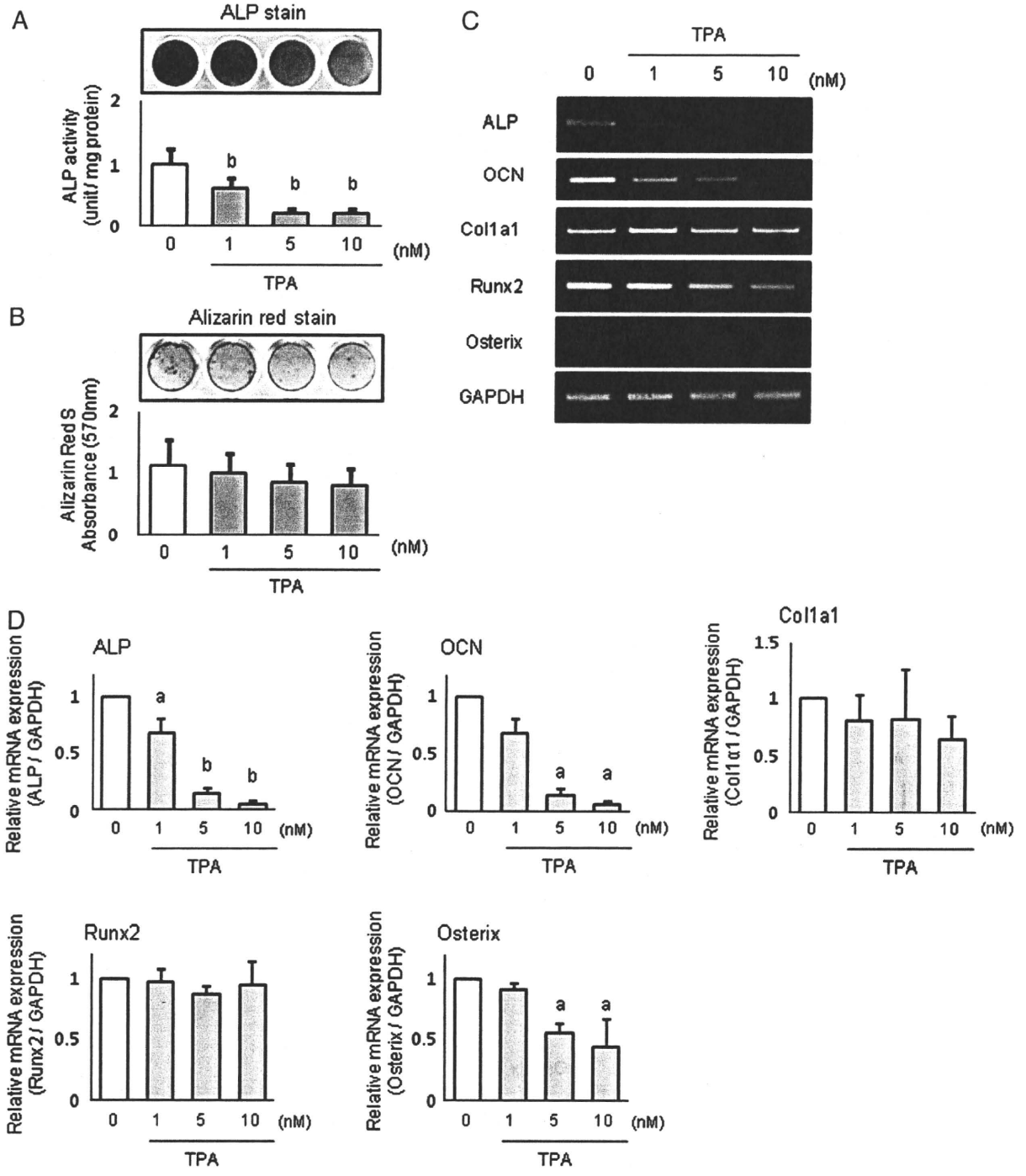

Fig. 4. Effect of TPA on osteoblastic differentiation in MC3T3-E1 cells. (A) ALP staining and activity of MC3T3-E1 cells. The cells were cultured for 24 h, and then incubated for 3 days after treatment with TPA in differentiation medium. (B) MC3T3-E1 cells stained with Alizarin red solution and quantified Ca content in the matrix of the cells. MC3T3-E1 cells were cultured with TPA in differentiation medium for 28 days. Fresh medium was changed twice per week. (C) RT-PCR analysis of total RNA isolated from MC3T3-E1 cells treated with TPA. Expression of osteoblastic-related genes: ALP, OCN, Col1α1, Runx2, and Osterix. (D) total RNA isolated from MC3T3-E1 cells treated with TPA for 3 days. mRNA expression of the osteoblast-related genes: *ALP, OCN, Col1α1*; the transcription factor Runx2, and the gene *Osterix* was determined using quantitative real-time PCR analysis and UPL probes. The expression of each gene was normalized to GAPDH expression. (A, B and D) data are means ± SD of three independent experiments performed in duplicate (a: $p<0.05$, b: $p<0.01$ compared with TPA-untreated control).

significant alteration of the phosphorylation of p44/42 MAPK, as assessed by western blotting, was not correlated with PKCα (data not shown). Interestingly, it is reported that p44/42 MAPK was activated by insulin sitimulation in vastus lateralis skeletal muscles even in a PKCα knockout mouse [34]. Since PKCα plays multiple roles in signal transduction and it does not directly activate p44/42 MAPK [35,36], it is possible that activation of downstream signal pathways other than modulation of p44/42 MAPK by inhibition of PKCα might lead to osteoblastic differentiation. Further study is required to elucidate the signal pathway downstream of PKCα during osteoblastic differentiation.

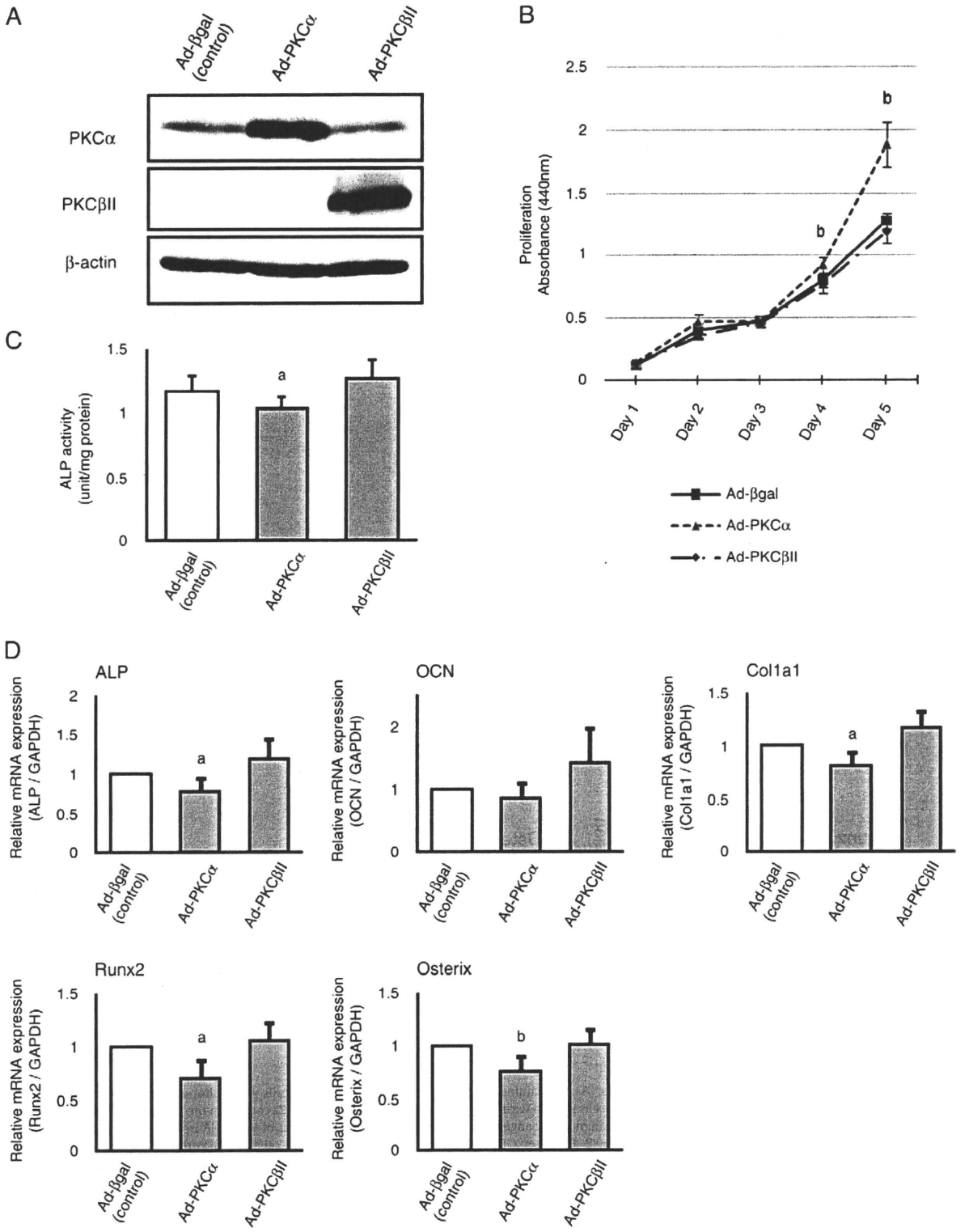

Fig. 5. Effects of PKCα overexpression on MC3T3-E1 cells. (A) Western blotting analysis of PKCα and PKCβII overexpression. Total cell lysates were extracted from MC3T3-E1 cells infected with adenovirus-encoding wild-type of PKCα, PKCβII. (B) proliferation of MC3T3-E1 cells infected with adenovirus encoding an empty vector, (Ad-βgal, control), wild-type PKCα (Ad-PKCα), or PKCβII (Ad-PKCβII). Infected MC3T3-E1 cells were incubated for 2 days following which the medium was changed to differentiation medium and the cells were incubated for a further 3 days. Cell proliferation was assayed at daily intervals over these 5 days of incubation. (C) ALP activity of MC3T3-E1 cells with PKCα overexpression. ALP activity was determined and normalized to the protein content. (D) expression of osteoblastic-related gene in MC3T3-E1 cells infected with Ad-βgal (control), Ad-PKCα, and Ad-PKCβII were assessed by real-time PCR analysis. Total RNA was extracted from MC3T3-E1 cells. (B, C, and D) Data are means ± SD of three independent experiments performed in duplicate (a: $p<0.05$, b: $p<0.01$ compared with Ad-βgal).

In conclusion, the present study indicates that PKCα suppresses osteoblastic differentiation but promoted osteoblastic proliferation. On the other hand, PKCβI and PKCβII had little effect on osteoblastic differentiation or proliferation. In addition, we demonstrated that of the eleven known isoforms of PKC, PKCα is the most important for suppression of osteoblastic differentiation. These results imply that the processes of differentiation and cell proliferation may be different cellular activity, and that PKCα has a pivotal role as a switch between these essential cellular functions.

Acknowledgments

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Appendix A. Supplementary data

Supplementary data to this article can be found online at doi:10.1016/j.bone.2010.09.238.

References

[1] Nishizuka Y. The role of protein kinase C in cell surface signal transduction and tumour promotion. Nature 1984;308:693–8.
[2] Nishizuka Y. Turnover of inositol phospholipids and signal transduction. Science 1984;225:1365–70.
[3] Keenan C, Kelleher D. Protein kinase C and the cytoskeleton. Cell Signal 1998;10:225–32.
[4] Lampasso JD, Chen W, Marzec N. The expression profile of PKC isoforms during MC3T3-E1 differentiation. Int J Mol Med 2006;17:1125–31.
[5] Takai Y, Kishimoto A, Inoue M, Nishizuka Y. Studies on a cyclic nucleotide-independent protein kinase and its proenzyme in mammalian tissues: purification and characterization of an active enzyme from bovine cerebellum. J Biol Chem 1977;252:7603–9.
[6] Inoue M, Kishimoto A, Takai Y, Nishizuka Y. Studies on a cyclic nucleotide-independent protein kinase and its proenzyme in mammalian tissues: proenzyme and its activation by calcium-dependent protease from rat brain. J Biol Chem 1977;252:7610–6.
[7] Nishizuka Y. Protein kinase C and lipid signaling for sustained cellular response. FASEB J 1995;9:484–96.
[8] Newton AC. Protein kinase C: Structure, function and regulation. J Biol Chem 1995;270:28495–8.
[9] Boneh A. A model for PKC involvement in the pathogenesis of inborn errors of metabolism. Trends Mol Med 2002;8:524–31.
[10] Martiny-Baron G, Kazanietz MG, Mischak H, Blumberg PM, Kochs G, Hug H, et al. Selective inhibition of protein kinase C isozymes by the indolocarbazole Gö6976. J Biol Chem 1993;268:9194–7.
[11] Gschwendt M, Dieterich S, Rennecke J, Kittstein W, Mueller HJ, Johannes FJ. Inhibition of protein kinase C μ by various inhibitors: differentiation from protein kinase c isoenzymes. FEBS Lett 1996;392:77–80.
[12] Carter CA. Protein kinase C as a drug target: implications for drug or diet prevention and treatment of cancer. Curr Drug Targets 2000;1:163–83.
[13] Teicher BA. Protein kinase C as a theraupic target. Clin Cancer Res 2006;12:5336–45.
[14] Ishii H, Jirousek MR, Koya D, Takagi C, Xia P, Clermont A, et al. Amelioration of vascular dysfunctions in diabetic rats by an oral PKC beta inhibitor. Science 1996;272:728–31.
[15] Tuttle KR, Anderson PW. A novel potential therapy for diabetic nephropathy and vascular complications: protein kinase C beta inhibition. Am J Kidney Dis 2003;42:456–65.
[16] Zini N, Bavelloni A, Lisignoli G, Ghisu S, Valmori A, Martelli AM, et al. PKCζ-expression is lower in osteoblasts from arthritic patients: IL1-β and TNF-α induce a similar decrease in non-arthritic human osteoblasts. J Cell Biolchem 2008;103:547–55.
[17] Cheung WMW, Ng WW, Kung AWC. Dimethyl sulfoxide as an inducer of differentiation in preosteoblast MC3T3-E1 cells. FEBS Lett 2006;580:121–6.
[18] Ohba M, Ishino K, Kashiwagi M, Kawabe S, Chiba K, Huh NH, et al. Induction of differentiation in normal human keratinocytes by adenovirus-mediated introduction of the η and δ isoforms of protein kinase C. Mol Cell Biol 1998;18:5199–207.
[19] Lampasso JD, Marzec N, Margarone J, Dziak R. Role of protein kinase Cα in primary human osteoblastic proliferation. J Bone Miner Res 2002;17:1968–76.
[20] Otsuka E, Yamaguchi A, Hirose S, Hagiwara H. Characterization of osteoblastic differentiation of stromal cell line ST2 that is induced by ascorbic acid. Am J Physiol Cell Physiol 1999;277:132–8.
[21] Michie AM, Nakagawa R. The link between PKCα regulation and cellular transformation. Immunol Lett 2005;96:155–62.
[22] Griner EM, Kazanietz MG. Protein kinase C and other diacylglycerol effectors in cancer. Nat Rev Cancer 2007;7:281–94.
[23] Tang CH, Yang RS, Huang TH, Liu SH, Fu WM. Enhancement of fibronectin fibrillogenesis and bone formation by basic fibroblast growth factor via protein kinase C-dependent pathway in rat osteoblasts. Mol Pharmacol 2004;66:440–9.
[24] Tang CH, Yang RS, Chen YF, Fu WM. Basic fibroblast growth factor stimulates fibronectin expression through phospholipase Cγ, protein kinase Cα, c-Src, NF-κB, and p300 pathway in osteoblasts. J Cell Physiol 2007;211:45–55.
[25] Miraoui H, Oudina K, Petite H, Tanimoto Y, Moriyama K, Marie PJ. Fibroblast growth factor receptor 2 promotes osteogenic differentiation in mesenchymal cells via ERK1/2 and protein kinase C signaling. J Biol Chem 2009;284:4897–904.
[26] Ogata N, Kawaguchi H, Chung UI, Roth SI, Segre G. Continuous activation of $G\alpha_q$ in osteoblasts results in osteopenia through impaired osteoblast differentiation. J Biol Chem 2007;282:35757–64.
[27] Tu X, Joeng KS, Nakayama KI, Nakayama K, Rajagopal J, Carroll TJ, et al. Noncanonical Wnt signaling through G protein-linked PKCδ activation promotes bone formation. Dev Cell 2007;12:113–27.
[28] Kim HJ, Kim JH, Bae SC, Choi JY, Kim HJ, Ryoo HM. The protein kinase C pathway plays a central role in the fibroblast growth factor-stimulated expression and transactivation activity of Runx2. J Biol Chem 2003;278:319–26.
[29] Way KJ, Chou E, King GL. Identification of PKC-isoform-specific biological actions using pharmacological approaches. Trends Pharmacol Sci 2000;21:181–7.
[30] Ansari HR, Teng B, Nadeem A, Roush KP, Martin KH, Schnermann J, et al. A_1 adenosine receptor-mediated PKC and p42/44 MAPK signaling in mouse coronary artery smooth muscle cells. Am J Physiol Heart Circ Physiol 2009;297:1032–9.
[31] Cheng JJ, Wung BS, Chao YJ, Wang DL. Sequential activation of protein kinase C (PKC)-α and PKC-ε sustained Raf/ERK1/2 activation in endothelial cells under mechanical strain. J Biol Chem 2001;276:31368–75.
[32] Braz JC, Bueno OF, De Windt LJ, Molkentin JD. PKCα regulates the hypertrophic growth of cardiomyocytes through extracellular signal-regulated kinase1/2 (ERK1/2). J Cell Biol 2002;156:905–19.
[33] Mauro A, Ciccarelli C, Cesaris PD, Scoglio A, Bouche M, Molinaro M, et al. PKCα-mediated ERK, JNK and p38 activation regulates the myogenic program in human rhabdomyosarcoma cells. J Cell Sci 2002;115:3587–99.
[34] Letiges M, Plomann M, Standaert ML, Bandyopadhyay G, Sajan MP, Kanoh Y, et al. Knockout of PKCα enhances insulin signaling through PI3K. Mol Endcrinol 2002;16:847–58.
[35] Schönwasser DC, Marais RM, Marshall CJ, Parker PJ. Activation of the mitogen-activated protein kinase/extracellular signal-regulated kinase pathway by conventional, novel, and atypical protein kinase C isotypes. Mol Cell Biol 1998;18:790–8.
[36] Johnson GL, Lapadat R. Mitogen-activated protein kinase pathways mediated by ERK, JNK, and p38 protein kinases. Science 2002;298:1911–2.

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Isolation and Expression Profiling of Genes Upregulated in Bone Marrow-Derived Mononuclear Cells of Rheumatoid Arthritis Patients

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Abstract

We have comprehensively identified the genes whose expressions are augmented in bone marrow-derived mononuclear cells (BMMC) from patients with Rheumatoid Arthritis (RA) as compared with BMMCs from Osteoarthritis (OA) patients, and named them *AURA* after *au*gmented in *RA*. Both stepwise subtractive hybridization and microarray analyses were used to identify *AURA* genes, which were confirmed by northern blot analysis and/or reverse transcription polymerase chain reaction (RT–PCR). We also assessed their expression levels in individual patients by quantitative real-time RT–PCR. Of 103 *AURA* genes we have identified, the mRNA levels of the following 10 genes, which are somehow related to immune responses, were increased in many of the RA patients: *AREG* (=*AURA9*), FK506-binding protein 5 (FKBP5 = *AURA45*), C-type lectin superfamily member 9 (*CLECSF9* = *AURA24*), tyrosylprotein sulfotransferase 1 (*TPST1* = *AURA52*), lymphocyte G0/G1 switch gene (*G0S2* = *AURA8*), chemokine receptor 4 (CXCR4 = *AURA86*), nuclear factor-kappa B (NF-κB = *AURA25*) and two genes of unknown function (FLJ11106 = *AURA1*, BC022398 = *AURA2* and XM_058513 = *AURA17*). Since *AREG* was most significantly increased in many of the RA patients, we subjected it to further analysis and found that AREG-epidermal growth factor receptor signaling is highly activated in synovial cells isolated from RA patients, but not in OA synoviocytes. We propose that the expression profiling of these *AURA* genes may improve our understanding of the pathogenesis of RA.

Key words: stepwise subtraction; microarray; RA; OA; amphiregulin; synoviolin

1. Introduction

Rheumatoid arthritis (RA) is a systemic autoimmune disease characterized by arthritis that predominantly results in chronic inflammation of systemic joints associated with the overgrowth of synovial cells. This induces progressive cartilage and bone destruction in the joint and subsequent disability. Since RA pathogenesis is likely to involve genetic elements, a number of groups have subjected samples from healthy and affected individuals to DNA microarray analyses for a broad-scale comparison. These studies have provided

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significant insights into RA pathogenesis.[1,2] The first samples tested were synovial specimens,[3–8] and peripheral blood mononuclear cells (PBMC),[9] from RA and osteoarthritis (OA) patients, and cluster analysis of the resulting microarray gene-expression data revealed some candidate genes that may play a specific role in RA pathogenesis.

In other studies searching for key factors in RA pathogenesis, immunoscreening by using an antirheumatoid synovial cell antibody identified synoviolin/Hrd1 to be a highly expressed enzyme (E3 ubiquitin ligase) in the rheumatoid synovium.[10] Synoviolin appears to be a pathogenic factor for RA because mice overexpressing this enzyme developed spontaneous arthropathy, while heterozygous knockdown results in increased synovial cell apoptosis and resistance to collagen-induced arthritis.[11] It was proposed that the excess elimination of unfolded proteins due to synoviolin overexpression triggers synovial cell overgrowth.[12] Thus, synoviolin may play a pivotal role in the pathogenesis of arthropathy due to its functions in the quality control of proteins through the endoplasmic reticulum (ER)-associated degradation (ERAD) system; its elevated expression may therefore have an anti-apoptotic effect that causes synovial hyperplasia.

Bone marrow-derived mononuclear cells (BMMC) are another target for analyses aiming to identify the key genes that participate in RA pathogenesis because accumulating evidence suggests that BMMC cell abnormalities may contribute to the pathogenesis of RA and experimental arthritis models.[13–17] Moreover, RA patients suffer from defective central and peripheral B-cell tolerance checkpoints,[18] the first of which occurs in the bone marrow between the early immature and immature B-cell stages (the second counter selection step of autoantibody-expressing B cells takes place in the periphery, when the new emigrant becomes a mature naive B cell).[18,19] In addition, inflammatory changes similar to those found in RA synovium seem to occur in the subchondral bone marrow of the involved RA joint,[20] and synovial inflammatory tissue can reach the adjacent bone marrow by fully breaking the cortical barrier.[21] Thus, BMMC cells are an interesting subject for studies seeking to identify specific genes involved in RA pathogenesis.

To identify the genes whose expressions are dramatically induced or reduced in the pooled BMMC mRNAs of 50 RA patients as compared with 50 OA patients, we here subjected these pooled mRNAs to stepwise subtraction, which is a unique technique that we have developed previously.[22] This method permitted the comprehensive identification of those genes that are specifically up- or down-regulated during RA pathogenesis. In addition, we also used microarray analysis, since DNA microarray analyses on the BMMC of RA patients have not been described previously. As a control, we also subjected the BMMC RNA from OA patients to stepwise subtraction and microarray analysis to identify the genes that are specifically involved in OA pathogenesis. These analyses together resulted in the isolation of 103 RA-upregulated genes, of which amphiregulin (AREG) was revealed by quantitative real-time RT–PCR (QRT–PCR) to be the most conspicuously induced gene in RA patients. Interestingly, we also show here that AREG operates upstream of synoviolin in isolated synovial cells through an epidermal growth factor receptor (EFGR) signaling pathway. We discuss how AREG upregulation could contribute to RA pathogenesis.

2. Patients, Materials and Methods

2.1. Human subjects and ethical considerations

All RA patients satisfied the 1987 revised diagnostic criteria of the American College of Rheumatology (ACR: formerly the American Rheumatism Association).[23] All OA patients fulfilled the ACR criteria for hip or knee OA.[24] The RA and OA patient groups were largely matched in terms of their average age and sex (Supplementary Figure S1A and B). This study was reviewed and approved by the Internal Review Board of the Research Institute for Microbial Diseases, Osaka University. Accordingly, a written informed consent was obtained from each participant before obtaining human tissues.

2.2. Cell proliferation assay

The synovial cells from each patient were seeded onto uncoated 35 mm tissue culture plates at 1×10^5 cells/well and cultured in 5% FBS/DMEM. After 12 h, the cells were incubated in fresh 5% FBS/DMEM with (100 ng/ml) or without AREG (Sigma-Aldrich, A 7080). Four photos were taken from fixed areas in four quadrants near the central area of each plate at the 0, 1, 3 and 4 day time points. The cells at each time point were counted from these four photos and expressed as mean ± standard error (SE).

2.3. Statistical analysis

Significant differences were determined using the Spearman's rank correlation (Supplemenatry Figure S4) or the Mann–Whitney *U*-test (Figs 2, 4 and Supplementary Figure S3). The data are expressed as means ± SE. $P < 0.05$ or $P < 0.01$ was considered to be statistically significant.

3. RESULTS

3.1. Identification of RA- or OA-specific genes by stepwise subtraction and DNA microarray analysis

To isolate the putative RA-specific genes that are upregulated in BMMC of RA patients relative to those

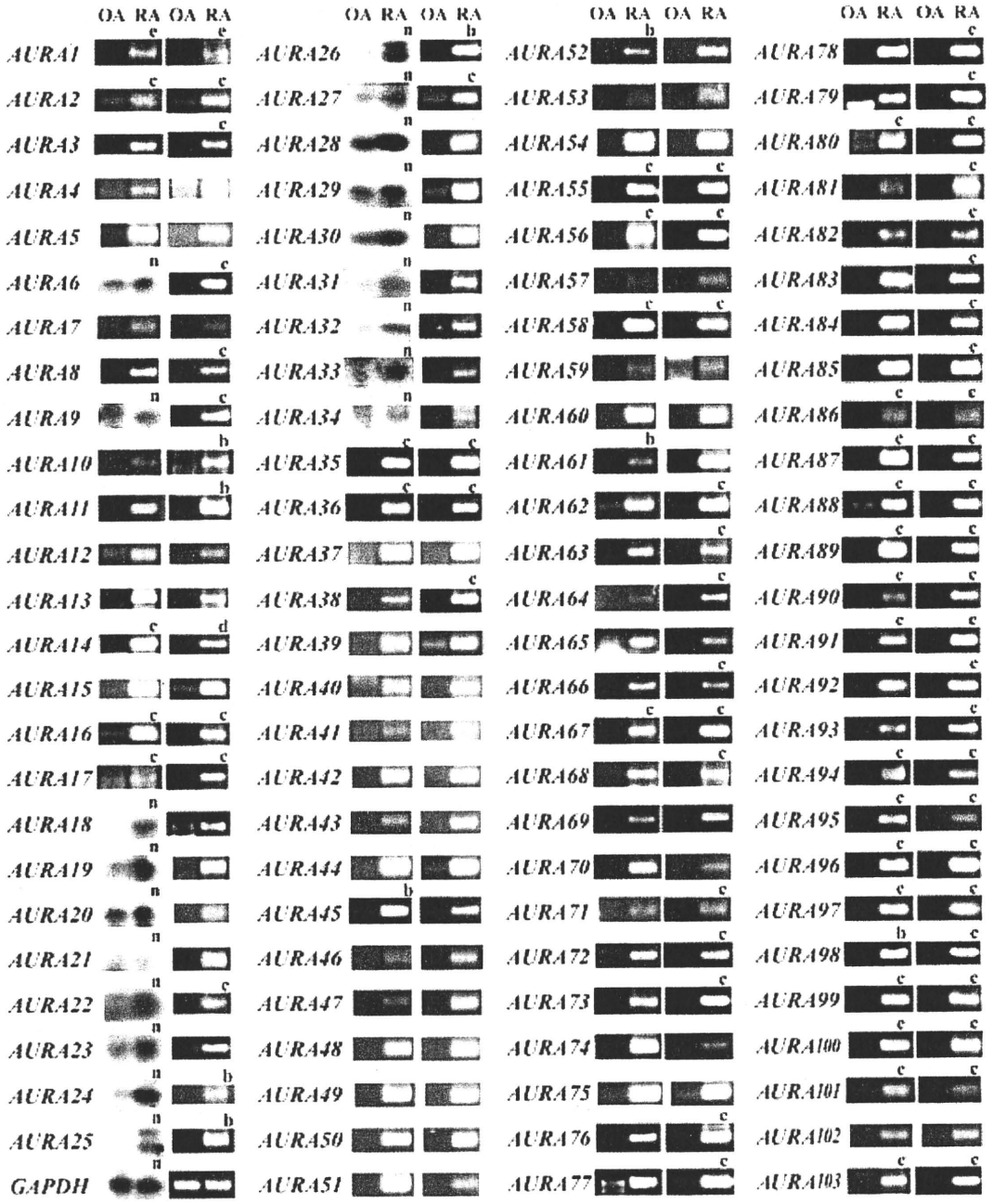


Figure 1. Northern blot or RT-PCR analysis of individual *AURA* cDNA clones to compare the expression levels of the genes in the BMMC of 50 RA patients and 50 OA patients (see Table 1 for their gene names). A northern blot or RT-PCR for *GAPDH* is also shown as a loading control. Left row: expression levels as detected by RT-PCR or northern blot analysis (denoted as n above each picture). Right row: confirmation of the expression level of each gene as determined by RT-PCR. The annealing temperature and amplification cycles for RT-PCR were always 50°C and 40 cycles, respectively, with the exception of the reactions denoted by a (50°C and 35 cycles, respectively), b (50°C and 30 cycles, respectively), c (55°C and 35 cycles, respectively), d (55°C and 40 cycles, respectively), and e (60°C and 40 cycles, respectively).

that are upregulated in OA patients, we first used our stepwise subtractive hybridization method. Briefly, we prepared a cDNA library from the pooled mRNA from the BMMC of 50 RA patients (Supplementary Figure S1A) by the linker-primer method using a pAP3neo vector.[25] Stepwise subtractive hybridization was then performed with the biotinylated pooled mRNA from the BMMC of 50 OA patients (Supplementary Figure S1A) to select candidate genes that may show upregulation in RA BMMC only as described previously.[22] To examine if the candidate genes are actually upregulated in RA but not OA BMMC, we performed northern blot analysis and/or RT-PCR using the pooled mRNA from the BMMC of 50 RA and 50 OA patients (Fig. 1). To reduce

the possibility of missing important RA-specific pathogenic genes by this method, we also performed a genome-wide complementary DNA microarray analysis using the Agilent Hu44K array with the same pooled RNA samples obtained from the BMMC of RA and OA patients that were described above. When we tested top 70 genes from the microarray list of RA-upregulated genes by northern blot analysis and/or RT–PCR as described above, we found that only 20 genes really displayed RA-upregulated expressions. Thus, we identified 103 RA-upregulated genes (Fig. 1) and named them *AURA* (*augmented in RA*). As shown in Table 1, 15 *AURA* genes (*AURA1*~*AURA7* and *AURA10*~*AURA17*) are uncharacterized novel genes.

We also performed similar experiments to obtain candidate OA-upregulated genes by generating a cDNA library from the pooled mRNA from the BMMC of 50 OA patients (Supplementary Figure S1A) and then using biotinylated pooled mRNA from the BMMC of 50 RA patients for subtraction (Supplementary Figure S1A). DNA microarray analysis also yielded a number of candidate OA-specific genes, as described above. However, when we checked whether these candidate genes are truly specifically up-regulated in OA BMMCs by northern blot analysis and/or RT–PCR, we could confirm this for only two genes (Supplementary Figure S2). These two OA-upregulated genes encode nuclear receptor coactivator 1 and a hypothetical protein (FLJ20581). This result suggests that the gain of function due to the enhanced expression of the RA-upregulated candidate genes is important in the pathogenesis of RA. Thus, we subsequently concentrated our study on the RA-upregulated genes.

3.2. *Expression profiles of RA-upregulated genes in individual RA or OA patients*

To determine whether the upregulation of the 103 RA-specific candidate genes is widespread in many RA patients or occurs in only a few patients, we performed QRT–PCR using individually prepared RNA samples from the BMMC or PBMC of RA patients. Of the 103 candidate genes, 5 genes whose functions are unknown and 12 genes that may be related to growth regulation or immune response were analyzed by QRT–PCR. OA patients were also examined as negative controls. In every QRT–PCR, a standard RNA from the PBMC of a healthy volunteer (male, age 52) was used (denoted as normal with a relative intensity of 1.0). This allowed us to compare the expression profiles of the genes tested in this study. In addition, since we used this control, we could also compare the expression profiles of the genes in this study with those of other genes tested in our previous reports on other autoimmune diseases.[26]

Of the 17 tested *AURA* genes (denoted x in Table 1), AREG (*AURA9*) was the most conspicuously upregulated in the BMMC of many of the RA patients, while in contrast OA BMMCs invariably expressed this gene at very low levels (Fig. 2A). Similarly, the PBMC of many RA patients strongly expressed AREG, while only very low expression was detected in the PBMC of the OA patients (Fig. 2A). AREG is one of the EGF-like growth factors that stimulate cell growth by activating the EGF receptor (EGFR) signaling of the target cells in an autocrine/juxtacrine fashion.[27]

AURA1 was the next most conspicuously upregulated gene in the BMMC of many RA patients, while the BMMC of all OA patients showed only very low expression of this gene (Fig. 2B). However, unlike *AREG*, the PBMC of RA patients showed negligible enhancement in the expression of *AURA1*. *AURA1* encodes an uncharacterized protein containing a thioesterase domain (Fig. 2B inset) that may cleave thioester bonds of an unknown target.

The gene encoding FK506 (tacrolimus)-binding protein 5 (FKBP5 = *AURA45*) also showed enhanced expression in nearly half of the RA patient BMMC samples, while no such increase was observed in the OA patient BMMC samples or in the PBMC of the RA patients (Fig. 2C). FKBP5 is a cellular receptor for FK506 and has an immunosuppressive effect on activated T cells because it inhibits the protein phosphatase calcineurin.[28]

Nearly half of the RA patient BMMC samples showed 5- to 50-fold greater expression of *CLECSF9* (=*AURA24*), *TPST1* (=*AURA52*) and *AURA2* than the normal control PBMC sample (Fig. 2D–F). No such increase was observed in the BMMC of OA patients or in the PBMC of the RA patients. *CLECSF9* encodes a macrophage-inducible C-type lectin (Mincle) that harbors a calcium-dependent carbohydrate-recognition domain. *TPST1* is one of the two Golgi tyrosylprotein sulfotransferases (*TPST1* and *TPST2*) that mediate the post-translational modification tyrosine O-sulfation.

G0S2 (=*AURA8*), chemokine receptor 4 (CXCR4 = *AURA86*), nuclear factor-kappa B (NF-κB = *AURA25*) and *AURA17* showed augmented expression in both the BMMC and PBMC of some of the RA patients when compared to the expression in the BMMC and PBMC of the OA patients, although the differences between the RA and OA samples are not as significant as for the previously discussed genes (Supplementary Figure S3A–D). G0S2 is one of the G0/G1 switch (G0S) genes that are differentially expressed in lymphocytes during their lectin-induced switch from the G0 to the G1 phases of the cell cycle.[29] CXCR4, the receptor for a chemokine called stromal cell-derived factor-1 (SDF-1/CXCL12), is important in the migration, homing and survival of hematopoietic stem cells. SDF-1, which is secreted by ischemic myocardium, is involved in the homeostatic and inflammatory traffic of leukocytes, and is highly expressed in the synovial tissues of RA patients.[30] NF-κB

Table 1. List of *AURA* genes

AURA no.	Accession no.	Sequence description	SS/DM	QRT-PCR
AURA1	AK001968	Unknown cDNA (FLJ11106)	b	r
AURA2	BC022398	Unknown cDNA	b	r
AURA3	BC031341	Unknown cDNA (hypothetical protein MGC45871)		
AURA4	NM_052862.2	Unknown cDNA (hypothetical protein MGC21854)		
AURA5	AK097275.1	Unknown cDNA (FLJ39956) L-PLASTIN-like		
AURA6	BC019355	Unknown cDNA (ring finger protein 149: IMAGE:3956746)		
AURA7	AF078845.1	Unknown cDNA (16.7Kd protein)		
AURA8	M69199	Putative lymphocyte G0/G1 switch gene (G0S2)=Aile1	b	r
AURA9	AH002608	Amphiregulin	b	r
AURA10	AK026118	Unknown cDNA (Ch20-ORF43)		r
AURA11	AK094006	Unknown cDNA		
AURA12	AK095896.1	Unknown cDNA (FLJ38577)		
AURA13	BC014435	Unknown cDNA (IMAGE:4855747)		r
AURA14	ZF161365	Unknown cDNA (HSPC102)	m	
AURA15	FLJ23431	Unknown cDNA (FLJ23431) MHC class I -like		
AURA16	BC066334	Unknown cDNA (FLJ37760)		
AURA17	XM_058513	Unknown cDNA (DKFZp434H2111)	m	r
AURA18	BC016660	Heat shock 70 kDa protein 8		
AURA19	BC022347	Lactotransferrin		
AURA20	NM_001800.2	Cyclin-dependent kinase inhibitor 2D (p19) (CDKN2D)		
AURA21	X55668.1	Proteinase 3		
AURA22	BC013946	Kruppel-like factor 13		
AURA23	BC022463	Dual specificity phosphatase 1 (DUSP1)		r
AURA24	AY358499	C-type lectin, superfamily member 9 (CLECSF9)	b	r
AURA25	AY033600	NF-kB alpha	b	r
AURA26	AF194172	Androgen-regulated protein 6 (AIG6)	m	
AURA27	NM_021810	Cadherin-like 26 (CDH26)		
AURA28	X52053.1	HP-1 (corticostatin/defensin family)		r
AURA29	BC018857.2	Translation elongation factor 1 gamma		
AURA30	BC053585.1	Colony stimulating factor 3 receptor (granulocyte)		
AURA31	AY124010	Interleukin 1 receptor, type II (IL1R2)	m	
AURA32	BC020635	Ficolin 1 (FCN1: collagen/fibrinogen domain-containing)		
AURA33	BC106068	Microtubule-associated protein, RP/EB family, member 1		
AURA34	AF443591	Death effector domain-containing DNA binding protein2		
AURA35	BC032491	Ubiquitin-conjugating enzyme E2L 6 (UBE2L6)		
AURA36	BC004967	Ubiquitin associated domain containing 1 (UBADC1)		
AURA37	NM_006313.1	Ubiquitin specific protease 15 (USP15)		
AURA38	BC011358	ADP-ribosylation factor 1		
AURA39	AY366510.1	Pre-mRNA 3'end processing factor FIP1		
AURA40	NM_175039.1	Sialyltransferase 7D (SIAT7D). transcript variant 2		
AURA41	BC030230.2	Aminolevulinate, delta- synthase 2		
AURA42	NM_014390.1	Staphylococcal nuclease domain containing 1 (SND1)		
AURA43	NM_015999.2	Adiponectin receptor 1 (ADIPOR1)		
AURA44	BC033877.1	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV)		r
AURA45	NM_004117	FK506 binding protein 5 (FKBP5)	b	r
AURA46	NM_000211.1	Integrin beta 2 (antigen CD18 (p95)		
AURA47	BC015641.2	Enolase 1 (alpha)		

Table 1. continued.

AURA no.	Accession no.	Sequence description	SS/DM	QRT-PCR
AURA48	BC028299.1	Non-POU domain containing. octamer-binding.		
AURA49	BC000734.2	Eukaryotic translation initiation factor 3. subunit 648 kDa		
AURA50	NM_012198.2	Grancalcin. EF-hand calcium binding protein (GCA)		
AURA51	BC026690.2	CD97 antigen. transcript variant 2.		
AURA52	CR542060	Tyrosylprotein sulfotransferase 1 (TPST1)	m	r
AURA53	NM_005875.1	Translation factor sui1 homolog (GC20)		
AURA54	NM_004048.2	Beta-2-microglobulin (B2M)		
AURA55	BC017934	NudC domain containing 2 (NUDCD2)		
AURA56	NM_000569	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	b	
AURA57	BC018649.2	Polymerase (RNA) II (DNA directed)		
AURA58	BC013293	Synuclein, alpha (a molecular chaperone)		
AURA59	NM_033405.2	PRIC285		
AURA60	J02694.1	Myeloperoxidase		
AURA61	BC020219	Zinc finger protein 143 (clone pHZ-1)	m	
AURA62	BC071590	Nijmegen breakage syndrome 1 (nibrin)		
AURA63	BC003186	DNA replication complex GINS protein PSF2		r
AURA64	NM_006060	Zinc finger protein, subfamily 1A, 1 (ZNFN1A1)		
AURA65	BC015859	T-cell activation GTPase activating protein		
AURA66	Z50749	Sds22 (protein phosphatase regulatory subunit)-like		r
AURA67	AF411850	C-type lectin-like receptor CLEC-6	m	
AURA68	BC064831	HMT1 hnRNP methyltransferase-like 3		
AURA69	BC022797	Mof4 family associated protein 1		
AURA70	BC032437	Heterogeneous nuclear ribonucleoprotein A3		
AURA71	M87790	Anti-hepatitis A immunoglobulin lambda chain variable region		
AURA72	K01763	Haptoglobin alpha(1S)-beta precursor		
AURA73	BC016800	Aldolase A, fructose-bisphosphate, transcript variant		
AURA74	BC001391	Actin-like 6A, transcript variant 1		
AURA75	NM_003512.3	H2 histone, family 2AC (H2AC)		
AURA76	BC017558	H3 histone, family 3B (H3.3B)		
AURA77	BC032748	Myosin regulatory light chain MRCL3		
AURA78	S60099	APPH = amyloid precursor protein homolog		
AURA79	BC067100	Fas (TNFRSF6) associated factor 1		
AURA80	NM_000896	Cytochrome P450, family 4, subfamily F (CYP4F3)	b	
AURA81	BC010577	Granulin (an association partner of cyclin T1)		
AURA82	AF054186	p18		
AURA83	BC028626	Trinucleotide repeat containing 6B		
AURA84	L43631	Scaffold attachment factor B (SAF-B)		
AURA85	M11124	MHC HLA DQ alpha-chain mRNA from DRw9 cell line		
AURA86	AF025375	Chemokine (C-X-C motif) receptor 4 (CXCR4)	b	r
AURA87	BC000163	Vimentin (VIM)		
AURA88	BC071860	Lactate dehydrogenase B (LDHB)		
AURA89	BC100032	Ribosomal protein S13 (RPS13)		
AURA90	BC011852	Glutamine synthetase (GLUL)		
AURA91	NM_000045	Arginase, liver (ARG1)		
AURA92	BC006510	Cyclin B1		
AURA93	BC007063	Peroxiredoxin 1		
AURA94	NM_005746	Pre-B-cell colony enhancing factor 1 (PBEF1)	m	

Table 1. continued.

AURA no.	Accession no.	Sequence description	SS/DM	QRT-PCR
AURA95	BC018711	RNA-binding region (RNP1. RRM) containing 1		
AURA96	NM_001126	Adenylosuccinate synthase (ADSS)		
AURA97	BC008929	rab2 mRNA. YPT1-related and member of ras family		
AURA98	NM_004226	Serine/threonine kinase 17b (apoptosis-inducing) (STK17B)	m	
AURA99	BC096336	Insulin-degrading enzyme		
AURA100	AF501883	G protein Beta polypeptide 2 (GNB2)		
AURA101	BC007237	Myeloid/lymphoid or mixed-lineage leukemia		
AURA102	BC034149.1	Ribosomal protein S3		
AURA103	NM_020980	Aquaporin 9 (AQP9)	m	

Of 103 *AURA* genes, 83, 10 or 10 genes were identified by stepwise subtraction (SS) alone (no mark), by DNA microarray (DM) alone (denoted by m) or by both techniques (denoted by b), respectively. The *AURA* genes that were subjected to QRT-PCR analysis are denoted by r.
PRIC285: peroxisomal proliferator-activated receptor A interacting complex 285.

is a transcription factor that resides in the cytoplasm of every cell and translocates to the nucleus when activated by a wide variety of agents, including cytokines.[31] *AURA17* is an uncharacterized novel gene that encodes a large protein with 8 leucine rich repeats, Mitochondrial Rho (Miro) motif and protein tyrosine kinase domain (Supplementary Figure S3D inset).

We also tested seven other genes in RA and OA BMMC and PBMC samples by QRT-PCR, but none showed a widespread and conspicuous increase in expression in the RA BMMC samples (data not shown). Consequently, these genes appear to play a less significant role in RA pathogenesis. Since these experiments and those described above consumed almost all BMMC and PBMC samples from the RA and OA patients, the remaining *AURA* genes will have to be tested in the future with another RA patient set.

3.3. *Expression pattern of AURA genes in PBMC*

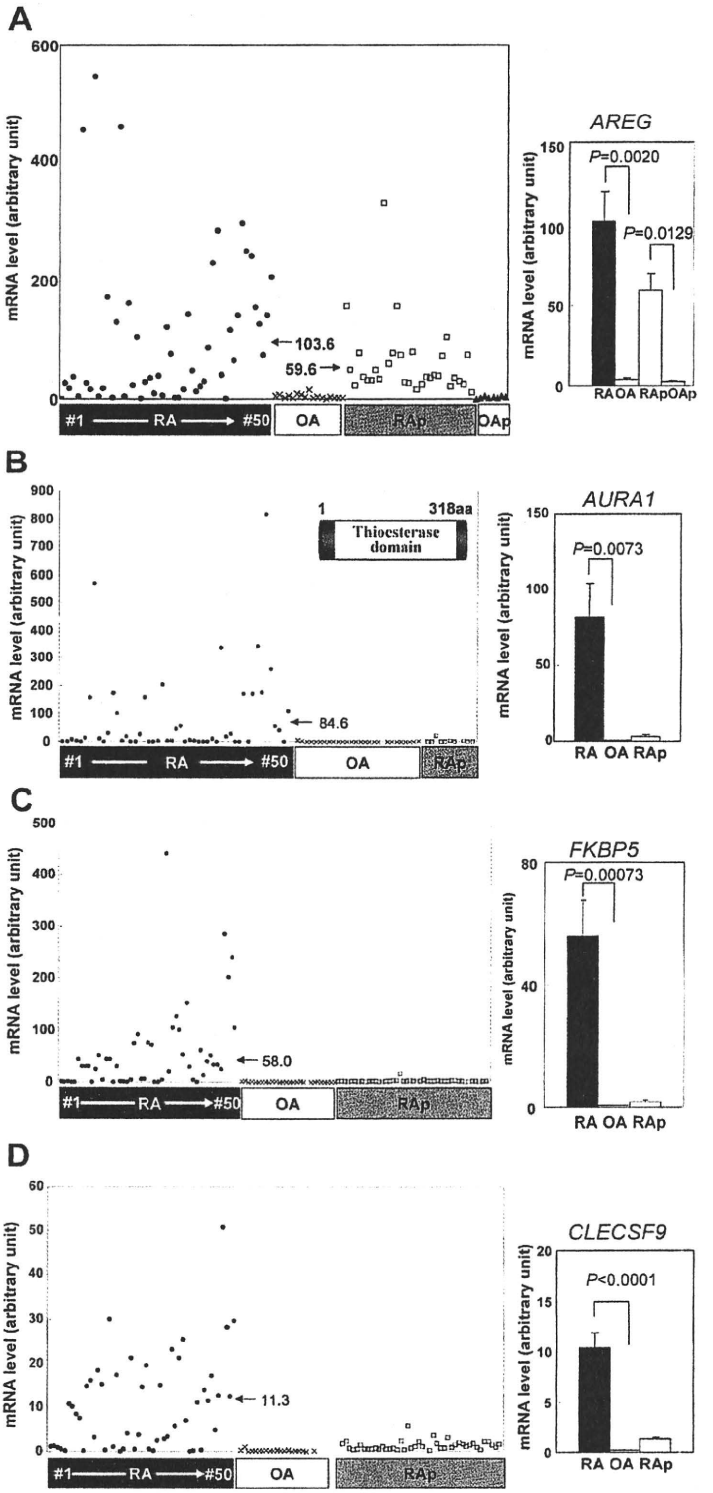
To determine whether the *AURA* genes are expressed in particular human blood cells, we performed RT-PCR on multiple tissue cDNA panels (MTC) from Clontech (Palo Alto, CA). As shown in Fig. 3, RT-PCR detected *AREG* mRNA in both monocytes (lane 4) and T and B cells (lanes 2–4), in particular in activated $CD4^+$ T cells (lane 8). *AURA1* is detected predominantly in resting $CD4^+$ (T helper/inducer; lane 3) and activated $CD4^+$ T (lane 8) cells. *CLECSF9* is expressed in most cell types except for activated $CD19^+$ T cells (lane 6), while *G0S2* is found primarily in monocytes (lanes a and 4). *FKBP5*, *TPST1*, *CXCR4*, *AURA2* and *NFκB* are ubiquitously expressed in most cell types. Thus, the analysis of the functions these *AURA* genes, apart from *AURA1* and *G0S2*, play in specific blood cells will not be easy because they are already expressed in normal blood. However, the function of *AURA1* can be studied by using $CD4^+$ T cells of RA and OA patients. In this study, however, we could not perform this analysis because of the low amounts of BMMC that we could obtain from the RA patients.

3.4. *AREG stimulates the growth of synovial cells*

Since AREG appears to be the most conspicuously unpregulated gene in many RA patients, we subjected it to further analysis. We first examined its ability to stimulate the growth of isolated synovial cells because AREG is one of the ligands of EGFR and is known to induce cell growth. Thus, we isolated synovial cells from synovial tissues that were obtained from five RA and three OA patients during joint reconstructive surgery. In the absence of AREG in the culture medium, the synovial cells from both the RA and OA patients grew at a similar rate (Fig. 4A and B). However, when AREG was present, the synovial cells from RA patients appeared to grow slightly faster than the synovial cells from OA patients, which is statistically significant ($P < 0.05$) (Fig. 4A).

To examine if this phenomenon is reflected in the signal transduction machinery of synovial cells, we investigated the activation of the EGFR signaling pathway in the AREG-treated and untreated RA synoviocytes. We first examined the phosphorylation of the extracellular signal-regulated kinases (ERK1/2) at Thr202 and Tyr204 by western blot analysis. ERK1/2 phosphorylation indicates the activation of the EGFR signaling pathway.[32] As shown in Fig. 5A, the phosphorylated ERK1/2 bands in the RA synoviocytes showed an increase in intensity when the cells had been treated with AREG; this effect peaked 8–12 h after AREG treatment but continued for 2–3 days. In contrast, the ERK1/2 protein levels remained largely unaffected by AREG treatment.

To compare the activation of EGFR signaling between RA and OA patients, we examined the activation of the EGFR signaling pathway in the synoviocytes from the five RA and three OA patients (Fig. 5B). We thus assessed the phosphorylated ERK1/2 expression levels by western blot analysis and expressed the results quantitatively by measuring the intensity of the lower phosphorylated band by densitometry and comparing it with the ERK1/2 band intensity (Fig. 5C). We found that the synoviocytes from the RA and OA patients expressed equivalent levels of EGFR and ERK1/2 proteins, regardless of AREG treatment. In contrast,



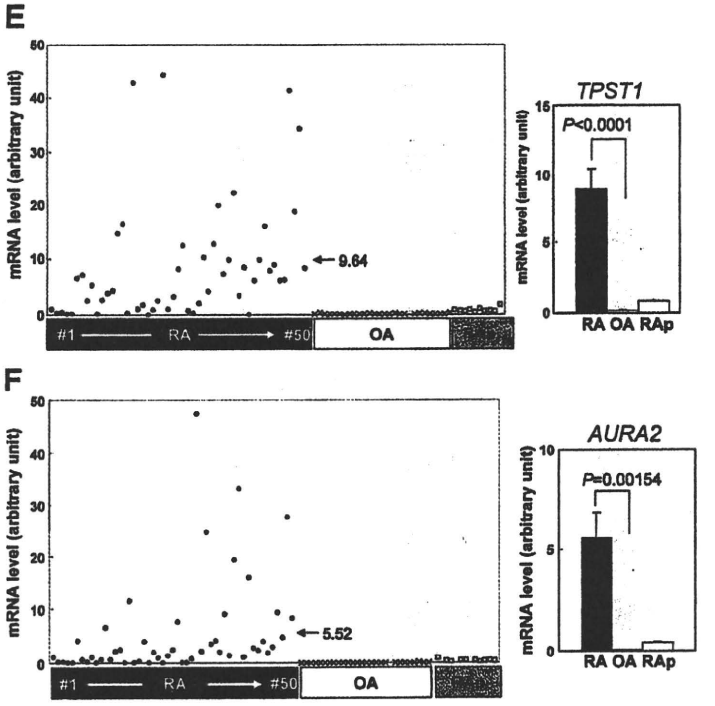


Figure 2. Expression levels of *AURA* genes in individual RA and OA patients. QRT-PCR analyses show that the mRNA levels of (A) *AREG*, (B) *AURA1*, (C) *FKBP5*, (D) *CLECSF9*, (E) *TPST1* and (F) *AURA2* are conspicuously upregulated in RA patient BMMC (and sometimes PBMC), while the BMMC and PBMC of OA patients show negligible upregulation. Expression levels in the BMMC for 50 RA patients (from #1 to 50) are arranged in the denoted order. The inset in (B) shows that the thioesterase domain occupies most of the Aural protein. The mean values of the samples analyzed in triplicate from each individual RA BMMC, RA PBMC, OA BMMC and OA PBMC are indicated by filled circles, open squares, x's, or filled triangles, respectively. The average values for the RA patient group are shown by the horizontal arrows. The bar graphs in the right panels show the average ± SE values of these measurements using the RA or OA BMMC or PBMC. All measurements are statistically significant when RA and OA are compared ($P < 0.01$).

AREG treatment upregulated the phosphorylated ERK1/2 expression levels much more strongly in the synoviocytes from RA2, RA3 and RA4 than in the synoviocytes of any of the OA patients. RA1 is an exception to this pattern as its limited phosphorylated ERK1/2 expression levels were similar to those in OA1–3. The AREG-induced upregulation of ERK1/2 phosphorylation was less apparent in the RA5 synovial cells because ERK1/2 was already activated in the absence of AREG.

Synoviolin plays a role in the synovial hyperplasia of RA by controlling the ERAD system.[10] To determine if the RA synovial cells have an abnormal ERAD system, we measured their levels of the ER stress proteins GRP78/BiP and GRP94, which protect cells from the stress-induced ER dysfunction that could lead to the accumulation of unfolded proteins.[33] We found that while the synovial cells of the RA and OA patients have similar levels of GRP78/BiP (Fig. 5B and D), the RA synoviocytes show enhanced levels of GRP94, irrespective of whether they have been stimulated with AREG. This suggests that at least part of the ER-stress responsive pathway, namely, that mediated by GRP94, is more activated in RA synoviocytes than in OA synoviocytes. Thus, the ERAD pathway does appear to be abnormally upregulated in RA synoviocytes. We confirmed by QRT-PCR that the BMMC and PBMC cells of RA patients RA1–5 show enhanced AREG mRNA levels, unlike the BMMC and PBMC of OA patients OA1–3 (Supplementary Figure S5A). Thus, chronic activation of AREG/EGFR signaling appears to be augmented in RA patients. Since AREG is expressed as transmembrane precursors that are cleaved in the extracellular domain to release soluble growth factor,[34] we speculated that the sera (PB) and bone marrow fluid (BM) of RA1–5 may show enhanced levels of cleaved AREG compared to the equivalent fluids of OA1–3. We tested this by enzyme-linked immunosorbent assay but found only one patient, RA2, showed levels of cleaved AREG that exceeded the detection level of the assay (Supplementary Figure S5B). Thus, it is not clear whether RA patients indeed secrete higher AREG levels than OA patients.

We also examined whether RA synoviocytes expressed higher synoviolin mRNA levels than OA synoviocytes in the presence or absence of AREG. However, we could not detect any significant differences between the RA and OA patients in this regard (Supplementary

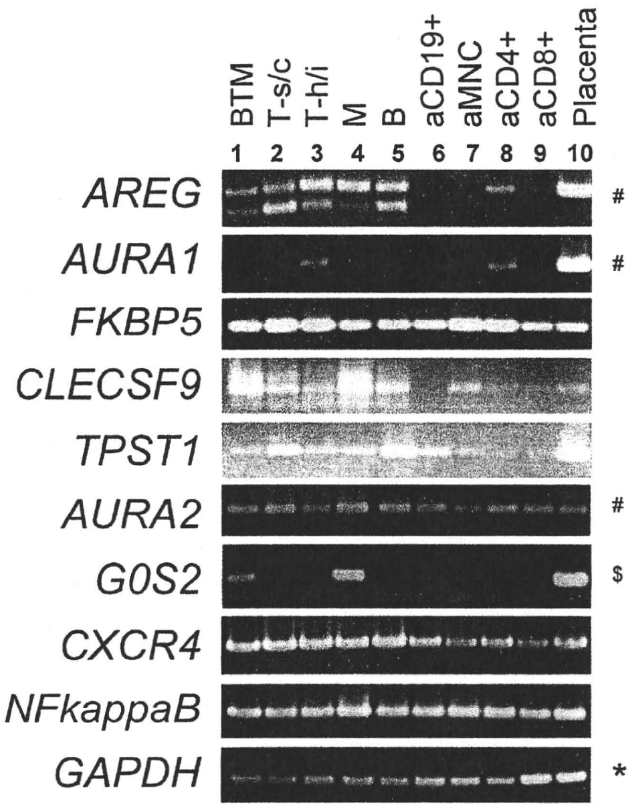


Figure 3. Determination by RT–PCR of the human blood cells that express *AREG*, *AURA1*, *FKBP5*, *CLECSF9*, *TPST1*, *AURA2*, *G0S2*, *CXCR4* and *NFκB*. RT–PCR was performed using the multiple tissue cDNA panel for human blood fractions (MTC, Clontech). *GAPDH* was also amplified as a loading control. PCR amplifications were conducted at 55°C and over 30 cycles except as indicated on the right of the panels: 55°C and 35 cycles (#), 55°C and 27 cycles (*) or 53°C and 25 cycles ($). Lane 1, mononuclear cells (B, T cells and monocytes). Lane 2, resting CD8+ cells (T-suppressor/cytotoxic cells). Lane 3, resting CD4+ cells (T-helper/inducer). Lane 4, resting CD14+ cells (monocytes). Lane 5, resting CD19+ cells (B cells). Lane 6, activated mononuclear cells. Lane 7, activated CD4+ cells. Lane 8, activated CD8+ cells. Lane 9, activated CD19+ cells. Lane 10, human placenta control cDNA served as a DNA size marker.

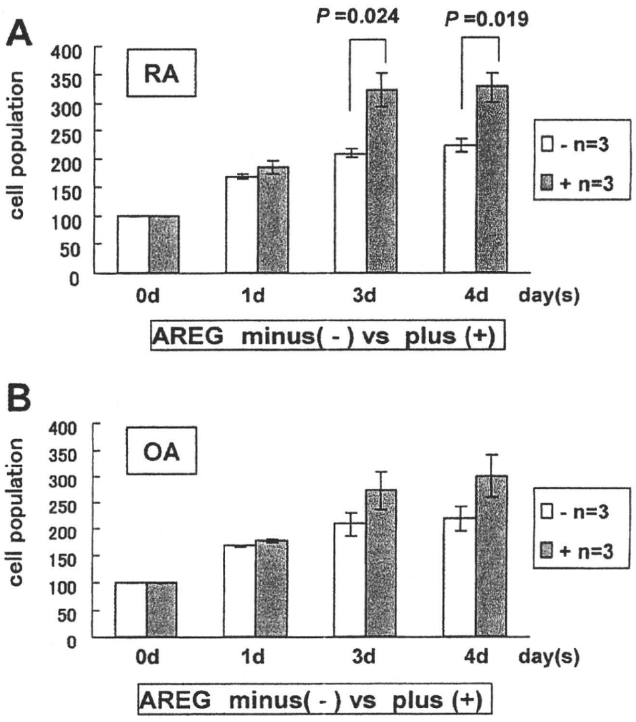


Figure 4. The effect of AREG on the proliferation of synoviocytes from RA and OA patients. The synovial cells from three RA patients (RA1, RA2 and RA3) (A) and three individual OA patients (OA1, OA2 and OA3) were counted on days 0, 1, 3 and 4 after incubation with or without AREG. The cell counts on days 1, 3 and 4 are expressed relative to 0 day. Statistically significant measurements are indicated ($P < 0.05$).

Figure S5C). It is not clear whether the synovial tissues of the patients would, like their cultured derivatives, show a similar lack of synoviolin upregulation.

4. Discussion

In this study, we report our comprehensive isolation of *AURA* genes that show augmented mRNA expression in the BMMC of RA patients as compared to their expression in OA patient BMMC (Fig. 1 and Table 1). Since RA patients suffer from defective central and peripheral B-cell tolerance checkpoints, and often display unusual immunoglobulin light chain repertoires that suggest impaired secondary recombination regulation,[18] we had expected that many immune response genes would be identified as *AURA* genes. Indeed, >10% of the *AURA* genes are directly related to immune responses; moreover, while the other *AURA* genes may seem at first glance to be unrelated to immune responses, many of these can also be linked to immune responses (Table 1). QRT–PCR analysis on individual patient samples revealed that the *AURA* genes discussed below are significantly increased in the BMMC of many of the 50 RA patients we tested (Fig. 2). Thus, the identification of these genes may help us to understand the pathogenesis of RA.

FKBP5, one of the cellular receptors for the immunosuppressant FK506, was expressed at higher mRNA levels in many RA patients than in the OA patients; this was true for the BMMC of the RA patients but not for their PBMC (Fig. 2C). FK506 has been suggested to be an effective drug for reducing the pain associated with RA.[35] This is because it can suppress inflammation by inhibiting the production by synovial cells of prostaglandin E2; it does so by suppressing the IL-1β production by leukocytes.[36] The enhanced FKBP5 expression in RA BMMC is not due to FK506 treatment since at the time of this study, treatment with FK506

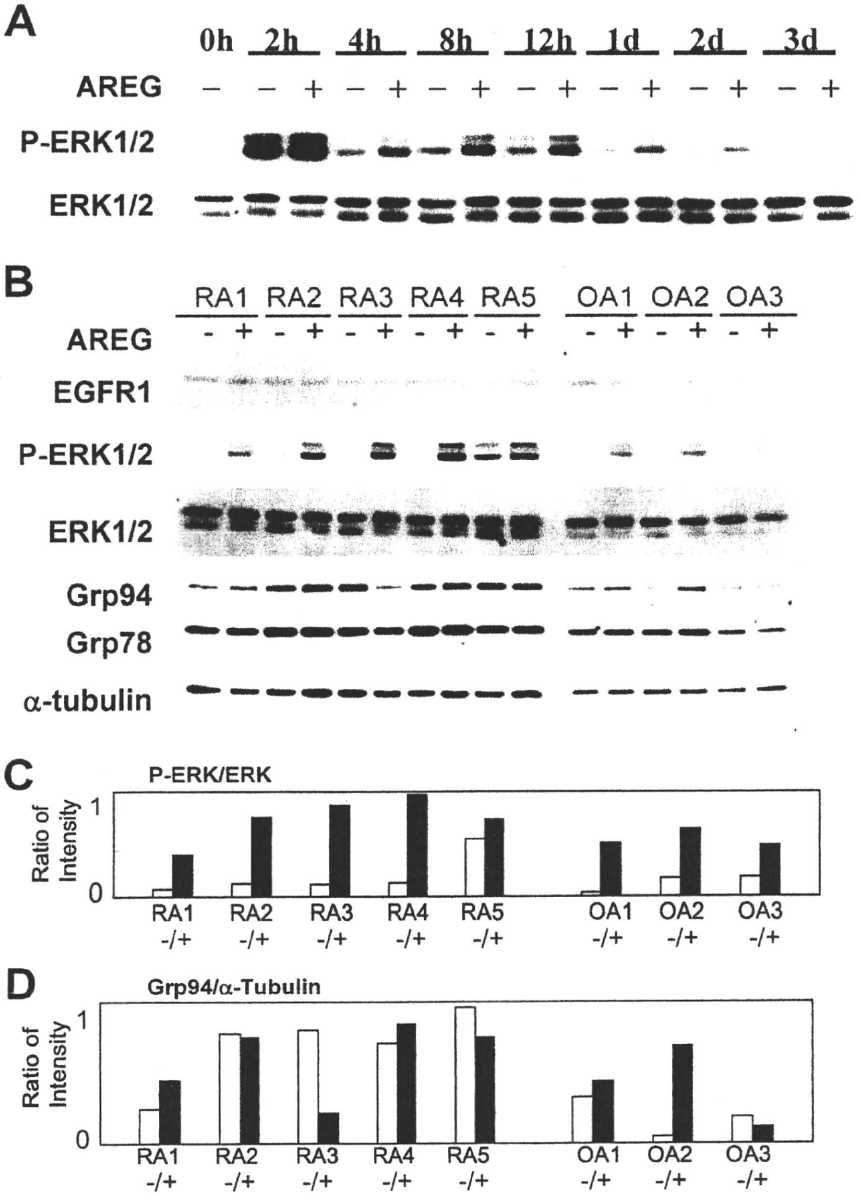


Figure 5. Western blot analysis of RA and OA synovial cells incubated in the presence or absence of AREG. (A) Expression levels of ERK1/2 and its phospho-form (P-ERK1/2) that is phosphorylated at Thr202 and Tyr204. Pooled synovial cells from five RA patients were incubated with (100 ng/ml) or without AREG for varying periods ranging from 0 h to 3 days. (B) Expression levels of EGFR1, ERK1/2, P-ERK1/2, Grp94, Grp78 and synoviolin in synovial cells from individual RA and OA patients that were incubated with or without AREG (100 ng/ml) for 8 h. Alpha-tubulin served as a loading control. (C) Relative optical densities of the western blot bands in (B) to determine P-ERK1/2 expression relative to ERK1/2 expression. (D) Relative optical densities of the western blot bands in (B) to determine Grp94 expression relative to alpha-tubulin expression.

was not permitted in Japan; consequently, none of the patients tested here have ever received FK506. In addition, the enhanced FKBP5 expression by RA BMMC does not correlate with therapeutic treatment using steroids. It remains possible, however, that the increased FKBP5 mRNA levels in the BMMC of RA patients may be due to treatment with other drugs. Alternatively, it may reflect genuine and spontaneous pathological events. Nevertheless, regardless of the cause of its elevated expression, the augmented FKBP expression may strongly inhibit the phosphatase activity of calcineurin, which could increase the dephosphorylation and thus inactivation of various substrates, including the NFAT family proteins and cytokines that are required for the expression of immunoregulatory molecules.

TPST1 mediates tyrosine sulfation within the trans-Golgi system, which affects 1% of all tyrosines in eukaryotic cells. It has been previously suggested that this post-translational modification may play an

important role in the pathogenesis of autoimmune diseases because it regulates mononuclear cell function at various stages of the immune response by enhancing interactions between ligands and receptors.[37] Notably, of the 62 identified target proteins of tyrosine sulfation, nine are cell adhesion molecules and chemokine receptors, which are both central players in leukocyte trafficking. Thus, the augmented expression of *TPST1* in RA patients may elevate the sulfation of crucial tyrosine residues in chemokine receptors that could constitutively increase their binding affinities with their ligands (e.g. the binding of CXCL12–CXCR4).

CLECSF9 belongs to the macrophage-inducible C-type lectin that serves multiple functions by recognizing carbohydrate chains; it plays important roles in macrophage function. Notably, a C-type lectin called DC-specific intercellular adhesion molecule 3-grabbing non-integrin is also highly expressed by macrophages in the synovium of RA patients.[38] However, the HH mRNA expression of macrophage-inducible C-type lectins is strongly induced in response to several inflammatory stimuli. Thus, the augmented expression of *CLECSF9* in the BMMC of RA patients may simply be due to the inflammation in the joint.

Unlike *FKBP5* and *TPST1* genes, the mRNA levels of G0S2, CXCR4 and NF-κB are increased in both the BMMC and PBMC of RA patients (Fig. 2 and Supplementary Figure S3). We previously showed that the PBMC of both systemic lupus erythematosus (SLE) patients and healthy young females express enhanced levels of *G0S2* mRNA.[26] Thus, G0S2 may not actually be involved in the pathogenesis of RA. With regard to the chemokine receptor CXCR4, it was also identified as a inflammation-related gene that is upregulated in synovial cells of patients with pigmented villonodular synovitis (PVNS), which is a joint problem that usually affects the hip or knee and involves the lining of the joint becoming swollen and growing.[8] The enhanced tyrosine sulfation of CXCR4 by augmented TPST1 activity, as described above, may also activate CXCR4, thereby elevating the ability of the CXCR4 ligand to induce the migration of bone marrow cells that could enhance the growth of synovial cells.[39] CXCR4 expression is also upregulated in the spinal cord of animals with experimental autoimmune encephalomyelitis, which is an animal model of autoimmune central nervous system inflammation.[40] With regard to NF-κB, this molecule along with the receptor activator of NF-κB (RANK) and its ligand RANKL have been found to play pivotal roles in the pathophysiological process of RA.[41] Thus, the increased mRNA levels of NF-κB in both the BMMC and PBMC of RA patients may contribute to the bone destruction mediated by activated NF-κB signaling pathway.[42]

AURA1 encodes a novel protein that is similar to thioesterase. Since the thioesterase homologs are widespread, functions of thioesterase vary in the human genome.[43] Thus, the physiological function of *AURA1* remains unknown. A possible role that it could play in RA pathogenesis is suggested by the following observations. First, the stable overexpression of acyl-CoA thioesterase III in human and murine T-cell lines increased both peroxisome numbers and lipid droplet formation, which suggests that it participates in the metabolic regulation of peroxisome proliferation in T cells.[44] Second, altered immune responsiveness is observed in mice deficient in palmitoyl protein thioesterase (PPT1) gene that is mutated in infantile neuronal ceroid lipofuscinosis.[45] Third, $CD4^+$ T cells are the prime mediators of RA in a mouse model SKG strain,[46] and *AURA1* expression is detected predominantly in resting and activated $CD4^+$ T cells (Fig. 3).

AREG is not directly related to immune responses but of all the genes examined, it showed the most conspicuously enhanced expression in both the BMMC and PBMC of many RA patients (Fig. 2A). We also found that the synovial cells of RA patients showed higher sensitivity to AREG, in terms of proliferation, than those of OA patients (Fig. 4). This is not due to augmented expression of EFGR (Fig. 5B, uppermost pane), but due to elevated activation of EGFR signaling pathway because the phosphorylation of ERK1/2 was more enhanced in AREG-treated RA patient synovial cells than that of AREG-treated OA patient synovial cells (Fig. 5). We here present a working hypothesis to explain how augmented AREG expression in BMMC and PBMC of RA patients and subsequent activation of EGFR signaling pathway lead to hyperproliferation of synovial cells in the joints of the RA patients (Fig. 6). Namely, this enhanced phosphorylation of ERK1/2 elevates the expression of many downstream target genes, which may also require the activation of the ERAD system. [12] Given that the Ets-binding site (EBS) of the proximal promoter of the synoviolin gene is responsible for its expression,[47] and that EBS-carrying genes are also activated by signaling events from the ERK pathway,[48] it is possible that the enhanced activation of EGFR signaling induced by AREG may directly activate the expression of synoviolin as well as that of other genes, thereby inducing the hyperproliferation of synovial cells. Thus, it is possible that the ERAD system in RA patients is hyperactivated by synoviolin because of augmented AREG expression in blood cells, possibly in the macrophages that occur in the vicinity of the synovial cells of RA patients, releasing augmented amount of AREG. This hypothesis should be tested more rigourously *in vivo* in the future because the experiments using the isolated synoviocyte cells in tissue culture medium may display distinct response to AREG. Likewise, examination of other EGF family proteins *in vivo* can also be interesting future subjects.

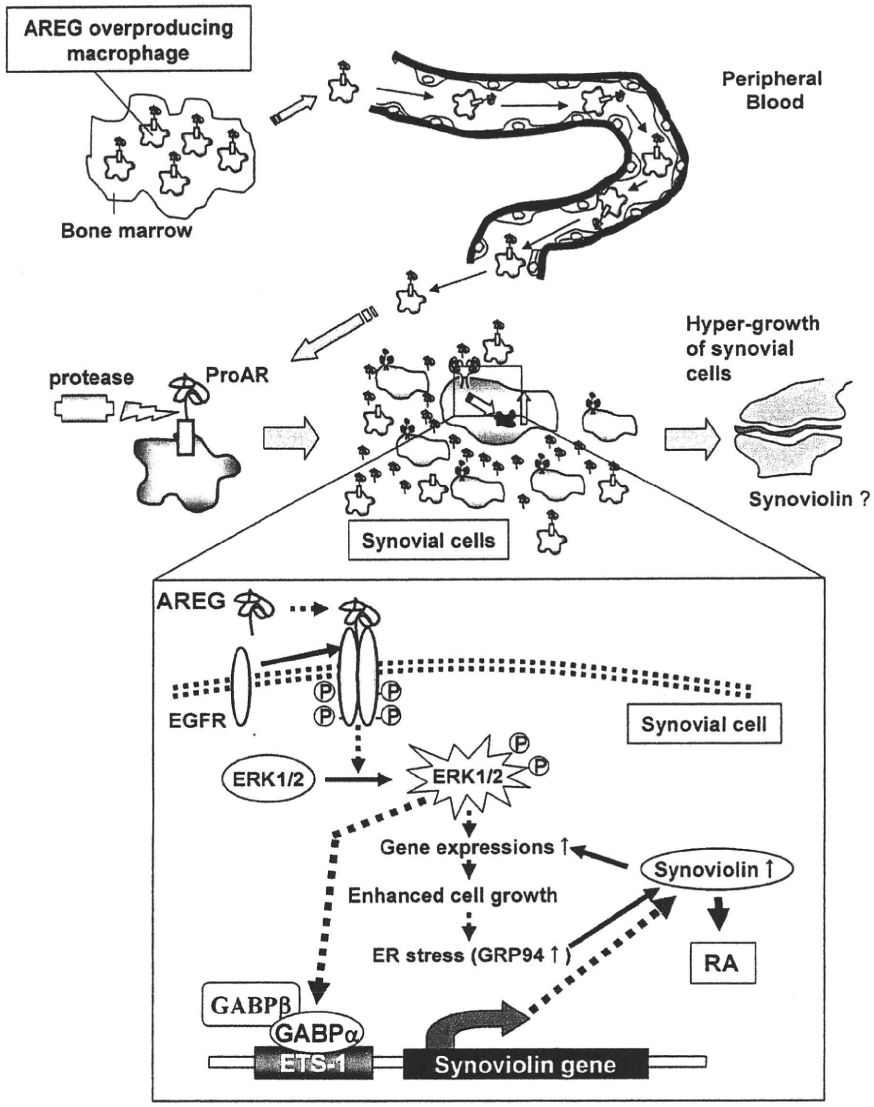


Figure 6. A working hypothesis to explain how augmented level of AREG in BMMC of RA patients may lead to hyperproliferation of synovial cells. Putative macrophages with enhanced expression of AREG precursor (ProAR) may approach to the synovial cells of the joint through blood flow, where they release AREG and activate the EGFR signaling pathway of synovial cells. Since Ets-binding site (ETS-1) of the proximal promoter of the synoviolin gene is one of the downstream targets of ERK pathway, the enhanced activation of EGFR signaling may directly activate the expression of synoviolin gene. The enhanced level of synoviolin activates the ERAD system, which may lead to hyperproliferation of synovial cells.

Overexpression of AREG has been linked to psoriasis in mice and humans.[19,50] Psoriasis is characterized by the hyperproliferation of keratinocytes and the loss of epidermal barrier function that leads to the infiltration of inflammatory cells into the epidermis and dermis.[51] AREG is also upregulated in a synoviocyte cell line derived from an RA patient in which the wild type and a dominant negative form of the orphan nuclear receptor Nurr1 were overexpressed.[52] Interestingly, AREG overexpression in the basal epidermis of transgenic mice induces a phenotype that is associated with synovial membrane inflammation.[19] Moreover, we showed previously that AREG expression is also enhanced in the PBMC of SLE and idiopathic thrombocytopenic purpura patients,[26] which suggests that AREG overexpression may also be associated with other autoimmune diseases. Notably, metalloprotease-mediated AREG shedding and the subsequent activation of EGFR appears to play a critical role in the secretion of IL-8 by the human airway epithelium-like NCI-H292 cells that is induced by tumor necrosis factor-α (TNF-α), a potent multifunctional cytokine that plays a central role in the pathogenesis of many inflammatory diseases like RA.[53] Since TNF-α-induced IL-8 secretion was completely inhibited by the neutralizing antibody against AREG,[53] this antibody could constitute a novel therapeutic tool for RA. Taken