

# Identification of Bach2 as a B-cell-specific partner for small Maf proteins that negatively regulate the immunoglobulin heavy chain gene 3' enhancer

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**Maf family transcription factors are important regulators in various differentiation systems. Putative Maf recognition elements (MAREs) are found in the 3' enhancer region of the immunoglobulin heavy chain (IgH) gene. These elements are bound in B-cell extracts by a heterodimeric protein complex containing both Bach2 and a small Maf protein. Analysis of normal hematopoietic cells revealed that Bach2 is specifically expressed in B cells. Bach2 is abundantly expressed in the early stages of B-cell differentiation and turned off in terminally differentiated cells. Bach2 acts together with MafK as a negative effector of the IgH 3' enhancer and binds to the co-repressor SMRT (silencing mediator of retinoid and thyroid receptor). Hence the Bach2–small-Maf heterodimer may represent the first example of a B-cell lineage, and of a developmental stage-restricted negative effector of the MARE in the IgH 3' enhancer region.**

**Keywords:** B cell/immunoglobulin/Maf/transcription factor

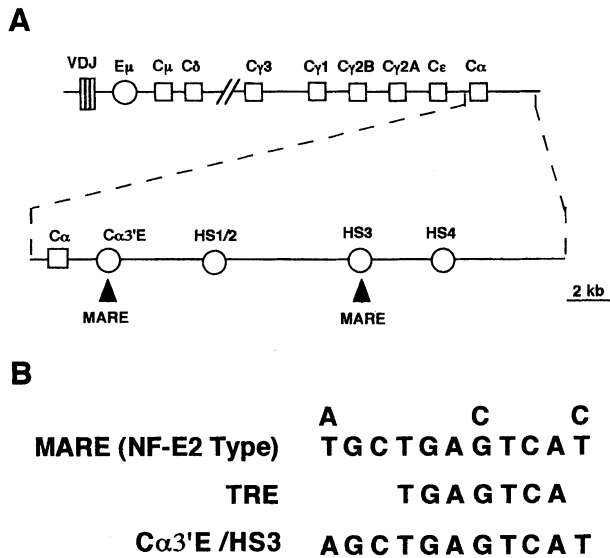
## Introduction

Maf family transcription factors possess a conserved basic-region leucine zipper (bZip) domain which mediates protein–protein interactions and DNA binding (Nishizawa *et al.*, 1989; Kataoka *et al.*, 1993). While c-Maf, MafB and NRL contain putative transcription activation domains (Nishizawa *et al.*, 1989; Swaroop *et al.*, 1992; Kataoka *et al.*, 1994a), MafF, MafK and MafG lack canonical *trans*-activation domains (Andrews *et al.*, 1993b; Fujiwara *et al.*, 1993; Igarashi *et al.*, 1994, 1995b; Kataoka *et al.*, 1995; Blank *et al.*, 1997). MafF, MafG and MafK are essentially composed of bZip domains and are collectively referred to as the small Maf family proteins. Various

dimeric combinations of Maf family proteins bind *in vitro* to a DNA sequence motif called T-MARE (TGCTGA<sup>G/C</sup>TCAGCA) containing a 12-*O*-tetradecanoylphorbol-13-acetate (TPA)-responsive element (TRE), TGA<sup>G/C</sup>TCA (Kataoka *et al.*, 1994a,b, 1995).

Maf family proteins are emerging as important regulators of cell differentiation in various systems (Blank and Andrews, 1997; Motohashi *et al.*, 1997). The hematopoietic cell-specific transcription factor NF-E2 is a heterodimer formed between the erythroid- and megakaryocyte-specific bZip protein, p45 NF-E2 and one of the small Maf family proteins (Andrews *et al.*, 1993a,b; Ney *et al.*, 1993; Igarashi *et al.*, 1994). Resulting heterodimers bind to a NF-E2 consensus site (TGCTGA<sup>G/C</sup>TCA<sup>T/C</sup>), which is related to T-MARE (Andrews *et al.*, 1993a,b; Igarashi *et al.*, 1994). A simple nomenclature of NF-E2 binding sites as Maf recognition elements (MAREs, including T-MARE and its derivatives) was recently suggested (Motohashi *et al.*, 1997). Besides generating NF-E2, the expression patterns of the small Maf proteins suggest that they also function in other cell lineages and tissues (Fujiwara *et al.*, 1993; Igarashi *et al.*, 1995b; Motohashi *et al.*, 1996). Fos and several p45-related bZip factors such as Nrf1 (LCR-F1/TCF-11), Nrf2 (ECH), Bach1 and Bach2 have been shown to form heterodimers with the small Maf proteins and bind to the MARE *in vitro* (Chan *et al.*, 1993; Caterina *et al.*, 1994; Luna *et al.*, 1994; Moi *et al.*, 1994; Itoh *et al.*, 1995; Oyake *et al.*, 1996; Toki *et al.*, 1997; Johnsen *et al.*, 1998). However, the precise role of these potential heterodimeric combinations during development and cell differentiation has remained elusive. Among these bZip proteins, Bach proteins may play mechanistically distinct roles as MARE-binding proteins, since they bear a BTB/POZ domain (Oyake *et al.*, 1996). Several lines of evidence suggest that the BTB domain may be involved in the regulation of chromatin structure (Albagli *et al.*, 1995).

MARE-like elements are found in the regulatory regions of an increasing number of genes (Kataoka *et al.*, 1994b). Of particular interest, we noticed that TREs within the 3' enhancer region of the immunoglobulin heavy chain (IgH) gene (Pettersson *et al.*, 1990; Matthias and Baltimore, 1993; Madisen and Groudine, 1994) resemble MAREs. Since immunoglobulin genes are regulated by B-cell-specific transcription factors (Fitzsimmons and Hagman, 1996; Arulampalam *et al.*, 1997), the presence of MARE-like elements in the IgH enhancer region suggests the presence of B-cell-specific MARE effector proteins. In this study, we examined MARE-binding activity in B cells. The results presented here indicate that Bach2 functions as a B-cell- and developmental-stage-specific partner for a small Maf protein and that the heterodimer interacts with the MAREs. Interestingly, co-expression of Bach2 and MafK repressed activity of the IgH 3' enhancer.



**Fig. 1.** Structure of mouse IgH locus. (A) Schematic representation of mouse IgH gene after recombination of the variable region. Boxes and circles indicate exons and enhancers, respectively. Cα3'E and HS3 contain identical putative MAREs. (B) Comparison of the putative MAREs in the IgH Cα3'E and HS3 with NF-E2-type MARE and TRE.

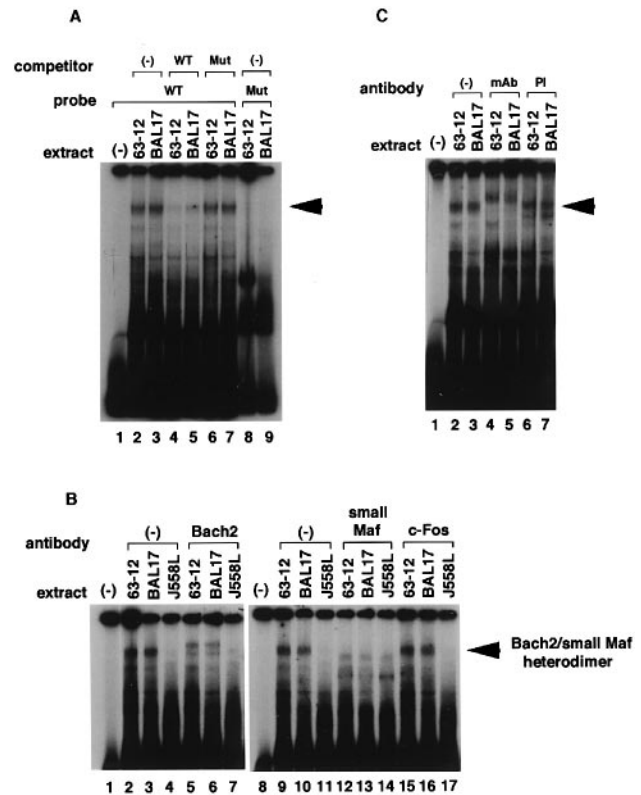
Hence, the Bach2–small-Maf heterodimer may represent the first example of a cell-lineage-restricted negative effector of MAREs, and might be involved in the repression of immunoglobulin genes at earlier stages of B-cell differentiation.

## Results

### *Bach2* binds to MARE in IgH 3' enhancer regions

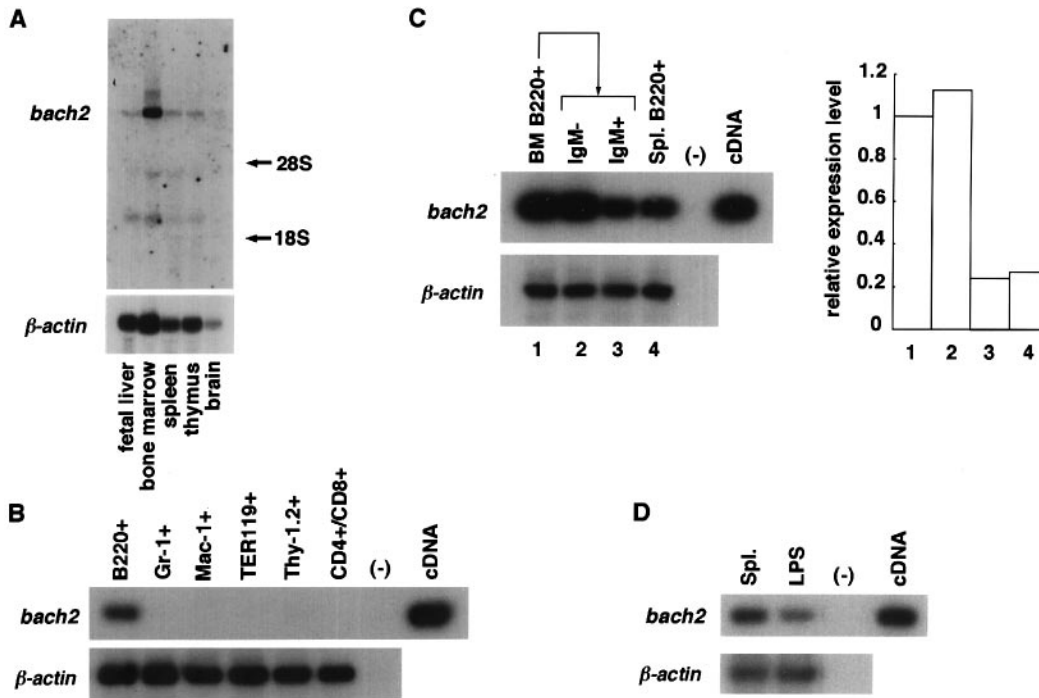
Several TREs have been identified in the 3' enhancer/locus control region (LCR) of the immunoglobulin heavy chain (IgH) gene (Pettersson *et al.*, 1990; Lieberson *et al.*, 1991; Matthias and Baltimore, 1993; Madisen and Groudine, 1994; Grant *et al.*, 1995; Chauveau and Cogne, 1996). At least two of them, located in the Cα3'E and HS3, are identical to the MARE consensus sequence (Figure 1). It should be noted that Cα3'E is composed of an inverted repeat of HS3 (Chauveau and Cogne, 1996), and hence it contains an identical MARE. To examine whether Maf dimers bind to these elements in B cells, we carried out electrophoretic mobility shift assays (EMSA) using nuclear extracts from various B cell lines (Figure 2). The DNA probe which we used is a 29 bp fragment that was derived from IgH HS3 and contains one putative MARE.

As shown in Figure 2A, EMSA and competition assays revealed the presence of only one specific DNA-binding protein complex in the nuclear extracts prepared from the pro-B cell line 63-12 and from the mature B cell line BAL17 (Figure 2A, lanes 2–5). An oligonucleotide containing mutations in the MARE failed to compete with the bound complex (Figure 2A, lanes 6 and 7). Furthermore, the mutated DNA did not generate a corresponding protein–DNA complex when it was radiolabeled and incubated with the nuclear extracts (Figure 2A, lanes 8 and 9). These results established specific binding of the complex to the MARE. This MARE-binding complex was



**Fig. 2.** MARE-binding complex in B-cell extracts. (A) EMSA was carried out with oligonucleotide probe which contains the MARE in the HS3/Cα3'E (lanes 1–7) or its derivative containing mutations in the MARE (lanes 8 and 9). Nuclear extracts were from pro-B cell line 63-12 (lanes 2, 4, 6 and 8) and mature-B cell line BAL17 (lanes 3, 5, 7 and 9). Unlabeled wild-type or mutated competitor DNAs (lanes 4–5 and 6–7, respectively) were added at 100-fold molar excess prior to addition of the radiolabeled probe. The arrow indicates the specific MARE-binding complex in the B-cell extracts. (B) Effects of various antibodies were examined. EMSA was carried out with nuclear extracts of 63-12 cells (lanes 2, 5, 9, 12 and 15), BAL17 cells (lanes 3, 6, 10, 13 and 16) and J558L plasmacytoma cells (lanes 4, 7, 11, 14 and 17) in the presence (lanes 5–7 and 12–17) or absence (lanes 2–4 and 9–11) of various antibodies. Antibodies were anti-Bach2 (lanes 5–7), anti-small-Maf (lanes 12–14) and anti-Fos (lanes 15–17). Bach2–small-Maf complex is indicated with an arrow. (C) The effect of anti-Bach2 monoclonal antibody was examined as above. EMSA was carried out with nuclear extracts of 63-12 cells (lanes 2, 4 and 6) or BAL17 cells (lanes 3, 5 and 7) in the presence of Bach2 monoclonal antibody 2G11-11 (lanes 4–5) or preimmune rabbit serum (lanes 6–7).

not detected using nuclear extracts from the plasmacytoma cell line J558L (Figure 2B, lane 4), indicating its stage-specific activity. To reveal constituents of the complex, we utilized antibodies that recognize various factors that could bind to a MARE. Formation of the specific protein–DNA complex was inhibited by anti-Bach2 as well as by anti-small-Maf antisera (Figure 2B, lanes 5, 6, 12 and 13). On the other hand, preimmune sera did not show any effect on complex formation (Figure 2C, lanes 6–7). Furthermore, anti-Fos antibodies, which react with c-Fos, FosB, Fra-1 and Fra-2, or anti-Jun antibodies, which recognize c-Jun, JunB and JunD, did not have any effects (Figure 2B, lanes 15–16; data not shown). Finally, involvement of Bach2 in the MARE-binding complex was confirmed using an anti-Bach2 monoclonal antibody (Figure 2C): addition of the Bach2 monoclonal antibody supershifted the MARE-binding complex. These results estab-



**Fig. 3.** Expression of *bach2* mRNAs in hematopoietic tissues. (A) Total RNAs (20  $\mu$ g) were hybridized with a *bach2*-specific DNA probe after separation on 1.0% agarose-formaldehyde gel and transfer onto a nylon membrane. RNAs were from 13.5 days post-coitus fetal liver, adult bone marrow, spleen, thymus and brain. Relative levels of *bach2* mRNA, normalized for  $\beta$ -actin mRNA, are 0.5, 2.6, 0.8, 0.7 and 1.0, respectively. Positions of 28S and 18S ribosomal RNAs are indicated with arrows. (B) Hematopoietic cells were fractionated depending on the surface marker expression, and *bach2* expression in each fraction was determined by RT-PCR analysis. B220<sup>+</sup> (B cell), Gr-1<sup>+</sup> (granulocyte), Mac-1<sup>+</sup> (mono-macrophage) and TER-119<sup>+</sup> (erythroid) fractions were from bone marrow, the Thy-1.2<sup>+</sup> (mature T-cell) fraction from spleen, and the CD4/CD8-double positive (immature T-cell) fraction from thymus. (C) The relationship between *bach2* mRNA expression and B cell differentiation was examined by RT-PCR. Bone marrow B220<sup>+</sup> cells (lane 1) were further fractionated into B220<sup>+</sup>/IgM<sup>-</sup> and B220<sup>+</sup>/IgM<sup>+</sup> cells (lanes 2 and 3, respectively). Spleen B220<sup>+</sup> fraction was also compared as the most differentiated B cell fraction (lane 4). Relative levels of *bach2* mRNA, normalized for  $\beta$ -actin mRNA, are shown on the right side. (D) Primary spleen B cells were stimulated with LPS and *bach2* mRNA expression was determined by RT-PCR.

lished that the TRE within the 3' enhancers C $\alpha$ 3'E and HS3 of the IgH gene is actually a MARE and bound by a heterodimer of Bach2 and one or another of the small Maf proteins in B-cell extracts.

#### Expression of *Bach2* in hematopoietic cells

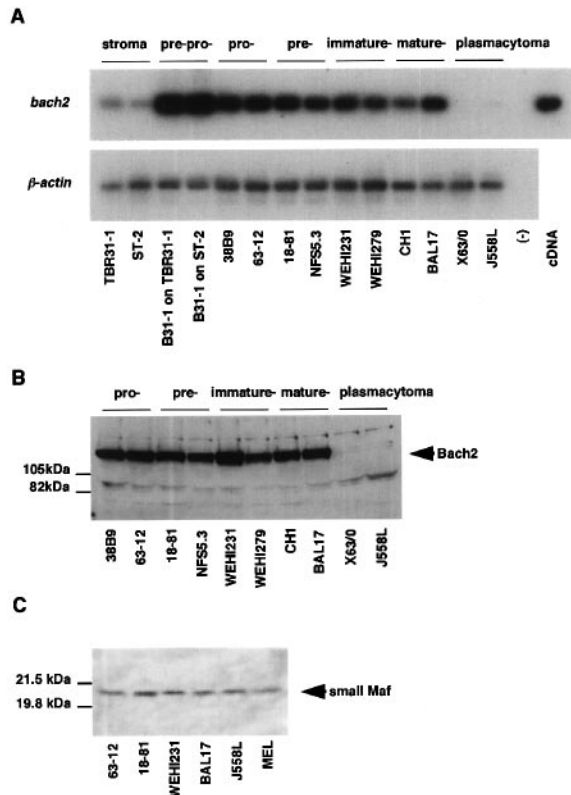
We have reported previously that expression of *bach2* mRNA in mice is restricted to the brain and spleen. To determine the possible role played by Bach2 during hematopoiesis, we isolated total RNA samples from bone marrow, thymus and spleen of adult mice as well as from fetal livers (13.5 days post-coitus embryos), and performed RNA blotting analysis (Figure 3A). Hematopoietic cells in the adult bone marrow revealed a 2.5-fold higher level of *bach2* mRNA expression compared with that of other hematopoietic tissues or brain.

To determine the cell-lineage specificity of Bach2 expression *in vivo*, we fractionated hematopoietic cells from bone marrow, spleen and thymus into various lineages using lineage-specific monoclonal antibodies (mAbs) and made comparisons by RT-PCR (Figure 3B). Only the B220-positive (B220<sup>+</sup>) B cells isolated from bone marrow showed a high level of Bach2 expression. Mac-1<sup>+</sup> cells (mono-macrophage lineage) did not express Bach2. These results clearly established that Bach2 is a B-cell-restricted transcription factor.

#### Expression of *Bach2* during B-cell differentiation

The relative expression levels in bone marrow and spleen suggests that Bach2 is expressed during the earlier stages of B-cell differentiation. This possibility has been addressed by fractionating the B220<sup>+</sup> cells into two populations, depending on the cell surface expression of IgM. The B220<sup>+</sup>/IgM<sup>-</sup> fraction contains pro- and pre-B cells, whereas the B220<sup>+</sup>/IgM<sup>+</sup> fraction contains immature- and mature-B cells (Hardy *et al.*, 1991; Rolink and Melchers, 1991). As a source of mature B-cell population we also assessed B220<sup>+</sup> cells from spleen. As shown in Figure 3C, the B220<sup>+</sup>/IgM<sup>-</sup> fraction, which represents an early stage of B-cell lineage development, showed the highest level of expression of *bach2* mRNA, whereas the B220<sup>+</sup>/IgM<sup>+</sup> bone marrow cells and B220<sup>+</sup> spleen cells expressed less *bach2* mRNA. The mitogen lipopolysaccharide (LPS) is known to induce proliferation and differentiation of resting B cells. Upon LPS treatment of spleen B cells, Bach2 expression was further down-regulated (to 50%, Figure 3D). Taken together, these results indicated that Bach2 expression decreases during the maturation of B cells.

The relationship between Bach2 expression and B-cell development was further examined using various B cell lines at different stages of B-cell differentiation (Figure 4A). Among the cell lines examined, B31-1 is a stroma-dependent B-cell line and is at the earliest stage (N.Yanai

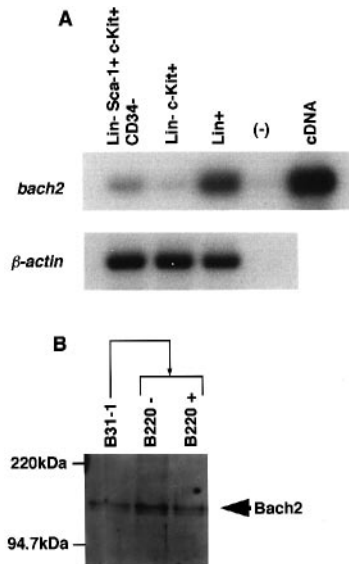


**Fig. 4.** Expression of Bach2 in B cell lines. **(A)** Expression of *bach2* mRNA in various B cell lines was examined by RT-PCR. Cell lines were stromal cell lines TBR31-1 and ST-2, pre-pro-B cell line B31-1, pro-B cell lines 3B9 and 63-12, pre-B cell lines 18-81 and NFS5.3, immature-B cell lines WEHI 231 and WEHI 279, mature-B-cell lines CH1 and BAL17, and plasmacytoma cell lines X63/0 and J558L. The PCR products of  $\beta$ -actin mRNA are shown at the bottom. **(B)** Immunoblotting analysis of the expression of Bach2 protein in the B-cell lines. Twenty-five micrograms of whole-cell extracts prepared from each B-cell line were separated with 7.5% of SDS-polyacrylamide gel, transferred onto membranes, and reacted with anti-Bach2 antiserum. Positions of mol. wt markers are shown at the left-hand side. **(C)** Immunoblotting analysis of the expression of small Maf proteins in B cell lines. Whole-cell extracts of indicated cell lines as well as MEL cells were examined for the presence of small Maf proteins with anti-small-Maf antiserum. The ~20 kDa antigen is indicated with an arrow. Positions of mol. wt markers are shown on the left-hand side.

and M.Obinata, unpublished observations). When cultured with the stromal cell line TBR31-1, B31-1 cells are a mixture of B220<sup>-</sup> and B220<sup>+</sup> fractions, both of which express the pre-pro-B-cell-surface-marker-pattern like c-Kit<sup>+</sup>, CD43<sup>-</sup>, HSA (CD24)<sup>-</sup> and IgM<sup>-</sup> (N.Yanai and M.Obinata, unpublished observations). RT-PCR analysis revealed that *bach2* was expressed abundantly at the earliest stage of B-cell development (i.e. B31-1 on TBR31-1; Figure 4A) and, in addition, in the stroma-independent pre-B, pro-B, immature-B and mature-B cell lines. In contrast, it was not detected in two different plasmacytoma cell lines, X63/0 (X63-Ag8.653) and J558L. Two stromal cell lines (TBR31-1 and ST-2) expressed the *bach2* gene at a low level, raising the possibility that Bach2 may play some roles in stromal cells as well.

Immunoblotting analysis with an anti-Bach2 antiserum confirmed that Bach2 is expressed in the pro-B, pre-B, immature-B and mature-B cell lines, and that it is absent in the plasmacytoma cell lines (Figure 4B). Furthermore,

#### B-cell-specific-Maf DNA-binding complex

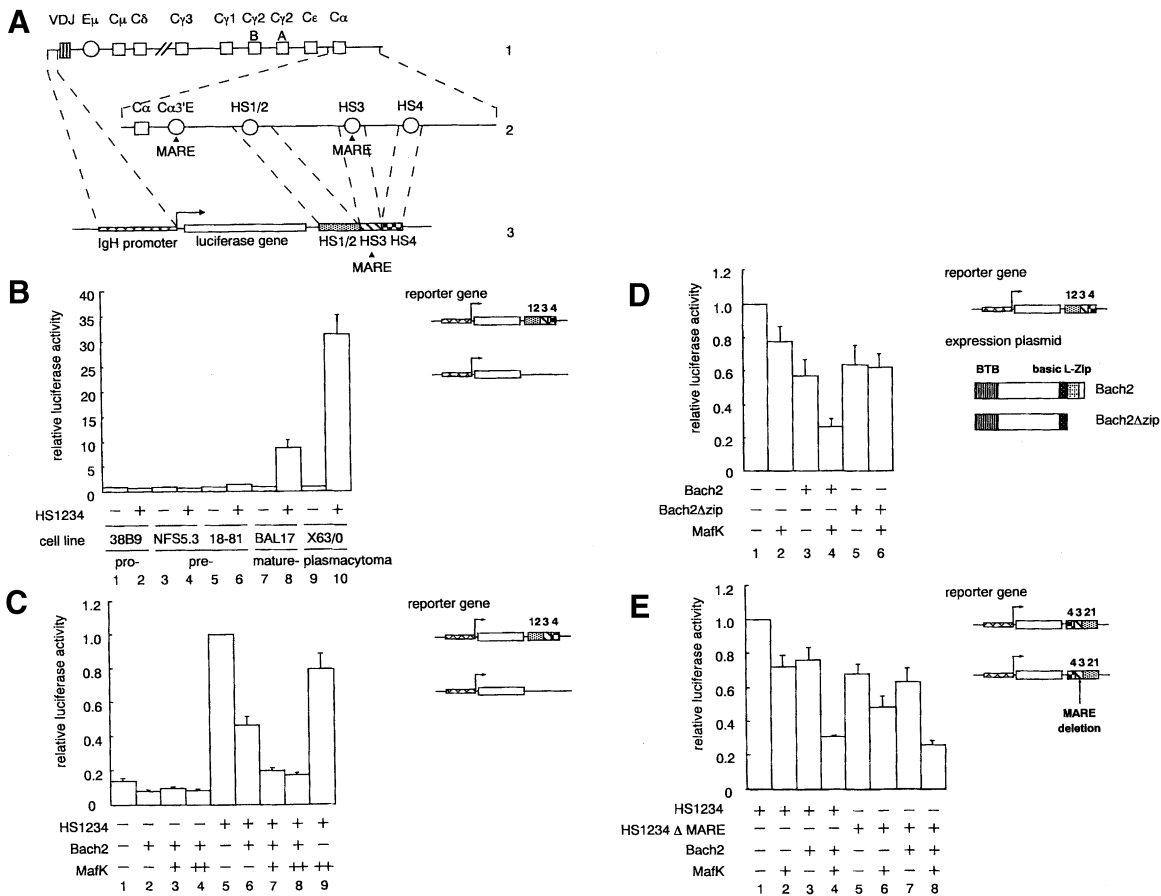


**Fig. 5.** Expression of Bach2 during B cell commitment. **(A)** Lin<sup>-</sup>/Sca-1<sup>+</sup>/c-Kit<sup>+</sup>/CD34<sup>-</sup> (lane 1), Lin<sup>-</sup>/c-Kit<sup>+</sup> (lane 2) and Lin<sup>+</sup> (lane 3) fractions were sorted from bone marrow cells of adult mice. *bach2* expression in each fraction was examined by RT-PCR. **(B)** Pre-pro B cell line B31-1 cells cultured on stromal ST-2 cells were fractionated into B220<sup>-</sup> and B220<sup>+</sup> fractions. Twenty-five micrograms of whole-cell extracts were separated with SDS-7.5% polyacrylamide gel and examined for Bach2 expression with anti-Bach2 antiserum.

the expression profile of Bach2 in the different B-cell lines correlates well with the presence or absence of the MARE-binding complex, as shown in the EMSA studies (Figure 2). On the other hand, the anti-small-Maf antibody reacted with an ~20 kDa antigen which was present in all of the B-cell lines including plasmacytoma, as well as in the murine erythroleukemic (MEL) cells, in which *mafK* is known to be expressed (Andrews *et al.*, 1993b; Igarashi *et al.*, 1995a,b; Figure 4C; data not shown). Hence, Bach2 determines the B-cell lineage and stage-specificity of MARE effectors by interacting with more broadly expressed small Maf proteins. Such a B-cell- and stage-specific Bach2 heterodimer will most probably play an important role during B-cell development and differentiation.

#### Expression of Bach2 during B-cell commitment

To determine at which point Bach2 expression commences during the differentiation of B cells, we examined hematopoietic stem cells (c-Kit<sup>+</sup>/Sca-1<sup>+</sup>/CD34 low or negative/lineage markers negative). A single cell of the stem cell fraction was shown previously to be able to reconstitute bone marrow cells in lethally irradiated mice (Osawi *et al.*, 1996). Expression of Bach2 was compared with those in more differentiated c-Kit<sup>+</sup>/Lin<sup>-</sup> cells, which include progenitor cells of various lineages as well as in lineage-markers-positive (Lin<sup>+</sup>) differentiated cells. As shown in Figure 5A, a significant level of *bach2* mRNA could be detected in the stem cell fraction, whereas the c-Kit<sup>+</sup>/Lin<sup>-</sup> cells expressed Bach2 at low levels. Considering the fact that the Lin<sup>+</sup> fraction contained differentiated cells of various lineages and that Bach2 expression in this fraction is restricted to the B220<sup>+</sup> cells, the expression level in the stem-cell fraction was estimated to be relatively



**Fig. 6.** Repression of IgH 3' enhancer activity by Bach2. (A) Schematic representation of reporter plasmid (line 3) that has IgH promoter (line 1) and a set of IgH 3' HS1/2, -3 and -4 (Madisen and Groudine, 1994; lines 1 and 2). HS1234 fragments were linked in both orientations relative to the promoter, and both reporter genes gave essentially similar results in experiments described below. HS1234 (-) reporter plasmid carries only IgH promoter. (B) Enhancer activity of HS1234 in different cell background. IgH promoter reporter plasmids with or without the HS1234 mini-enhancer (1 μg) were transfected into the indicated B cell lines. Relative expression was determined by comparing normalized reporter gene levels induced by HS-containing plasmid with that by an enhancerless control (promoter only). Values represent the averages and standard errors of four transfections. (C) Cooperative repression of HS1234 activity by Bach2 and MafK. Bach2- and MafK-expression plasmids were transfected into X63/0 cells in various combinations, as shown below, together with reporter plasmids (0.1 μg) that carried (lanes 5-9) or lacked (lanes 1-4) the HS1234. Amounts of MafK expression plasmid were titrated (0, 0.45 or 0.9 μg) in the presence or absence of Bach2-expression plasmid (0.9 μg). The results are means of four independent experiments, each carried out in duplicate, and standard errors are indicated with thin lines. (D) Cooperative repression by Bach2 and MafK requires their interaction. Effects of co-transfection with MafK (0.9 μg) and wild-type Bach2 (0.1 μg, lanes 3-4) or a Bach2 derivative that lacked the leucine zipper (0.1 μg, lanes 5-6) were compared. (E) HS3 MARE is not the sole target of Bach2/MafK. The MARE within HS3 was deleted from the HS1234 reporter gene, and its response to Bach2 (0.1 μg) and MafK (0.9 μg) expression (lanes 5-8) was compared with the wild-type reporter plasmid (lanes 1-4).

low compared with expression in B220<sup>+</sup> cells in the Lin<sup>+</sup> fraction.

B220 is known as one of the earliest markers expressed in the B-cell lineage (Li *et al.*, 1996). To determine the timing of Bach2 induction during B-cell development, we took advantage of the fact that the B31-1 cells, grown on the TBR31-1 stromal cells, are a mixture of B220<sup>-</sup> and B220<sup>+</sup> cells, and that B220<sup>-</sup> cells give rise to B220<sup>+</sup> cells *in vitro* (N.Yanai and M.Obinata, unpublished observations). Each population was purified and examined for the presence of Bach2 protein by immunoblot analysis. As shown in Figure 5B, expression of Bach2 in the less-differentiated B220<sup>-</sup> fraction is more abundant than it is in the B220<sup>+</sup> fraction, suggesting that B220<sup>-</sup> B31-1 cells, which are already committed to the B-cell lineage, express Bach2 at a high level. Taken together, these results indicate that Bach2 is expressed at low levels in uncommitted hematopoietic stem cells, and that its expression is up-regulated during, or soon after, commitment of stem

cells to the B-cell lineage. The commitment to other hematopoietic cell lineages might then lead to the down-regulation of *bach2*.

### Bach2 negatively regulates IgH 3' enhancer activity

To examine an effect of Bach2 on the IgH 3' enhancer activity, the HS1, -2, -3 and -4 were cloned in combination as described previously, downstream of the luciferase gene under the control of IgH promoter (Figure 6A). HS3 contains an inverted repeat of the Cα3'E and carries an identical MARE that binds Bach2-small-Maf heterodimer (Figure 1). Hence, the HS1234 reporter plasmid contains at least one functional MARE. The HS1234 mini-enhancer was shown previously to be active in plasmacytoma cells but relatively inactive in pre-B cells (Madisen and Groudine, 1994). Accordingly, the HS1234 mini-enhancer failed to activate IgH promoter-driven reporter gene expression in pro-B- and pre-B-cell lines (Figure 6B). In

contrast, the ability of the HS1234 to enhance transcription from the IgH promoter in plasmacytoma cells was evident, as shown in Figure 6B (compare lanes 9 and 10). Its stimulating activity was lower in mature B cells than in plasmacytoma cells (compare lanes 8 and 10).

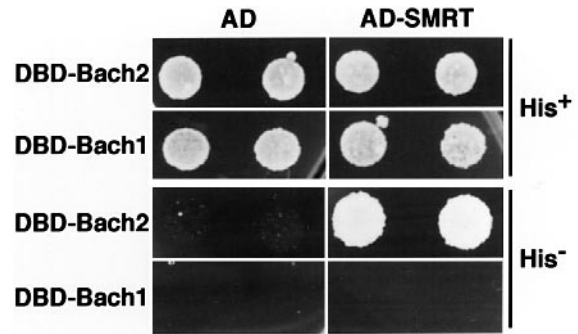
To examine the regulatory role of Bach2 in B-cell differentiation, we carried out co-transfection experiments (Figure 6C). In this experiment, we used 0.1  $\mu$ g of reporter plasmid (1  $\mu$ g was used in Figure 6B). Co-transfection of Bach2-expression plasmid into the plasmacytoma cells repressed reporter gene activity driven by the HS1234 (Figure 6C, lane 6). Expression of MafK alone resulted in only weak inhibition of the reporter gene activity (Figure 6C, lane 9). Interestingly, co-transfection of both Bach2- and MafK-expression plasmids resulted in more efficient repression that virtually abolished the effect of the HS1234 enhancer (Figure 6C, lanes 7 and 8), indicating that Bach2 and MafK cooperatively repressed gene expression. Neither of them showed significant repression of reporter gene in the absence of the HS1234, indicating that effects of Bach2 and MafK were mediated by HS1234.

To verify the interaction of Bach2 and MafK in the observed cooperative transcription repression, we examined a Bach2 derivative that lacked the leucine zipper (Bach2 $\Delta$ zip), and hence could not form a heterodimer with a small Maf protein (Figure 6D). In this experiment, we used 0.1  $\mu$ g of Bach2-expression plasmid per transfection (0.9  $\mu$ g was used in Figure 6C). Both wild-type Bach2 and Bach2 $\Delta$ zip repressed the reporter gene activity to 60% in the absence of MafK. However, Bach2 $\Delta$ zip did not exert synergistic transcription repression with MafK, whereas Bach2 did exert such an effect (compare lanes 4 and 6). The results indicated that a heterodimer of Bach2 and MafK was responsible for the observed cooperative repression of transcription. The residual repression activity of Bach2 $\Delta$ zip that was independent of dimer formation may be due to its interaction with other proteins through remaining regions such as the BTB domain. Such an interaction could inhibit the function of other transcription factors that are involved in enhancer activity of the HS1234.

In order to examine roles of the MARE within HS3 in the context of the large *cis*-regulatory region, we deleted the MARE from the 6.6 kb HS1234 mini-enhancer ( $\Delta$ MARE). As shown in Figure 6E, the deletion caused a modest decrease in the reporter gene expression (compare lanes 1 and 5). Co-expression of Bach2 and MafK still showed some synergistic repression of such a reporter gene activity, even though its extent was reduced. Based on these observations, we could draw two conclusions. First, in plasmacytoma cells, the enhancer function of the HS1234 is partly dependent on the MARE within the HS3. Secondly, the HS3 MARE is not the sole target of the Bach2–small-Maf heterodimer. Other functional MAREs appear to be present within the IgH 3' enhancer regions (see Discussion). The results described in Figure 6D and E, taken together, strongly implicated Bach2 as a negative regulator of IgH 3' enhancer that functions by forming a heterodimer with small Maf proteins.

#### **Bach2 binds to a co-repressor**

Since several BTB-domain-containing proteins have been shown to bind to co-repressors like SMRT, and because



**Fig. 7.** Bach2 binds to the corepressor SMRT. Various combinations of plasmids encoding GAL4 DNA-binding domain (DBD) and activation domain (AD) fusion proteins were introduced into the reporter yeast strain, and the resulting transformants were examined for the His<sup>+</sup> phenotype by spotting onto His<sup>+</sup> and His<sup>-</sup> plates.

we had shown that Bach2 functions as a transcription repressor, we examined whether Bach2 interacts with SMRT in a yeast two-hybrid system. Bach2 was fused to the GAL4 DNA binding domain, and the fusion protein was then expressed in yeast cells. The Bach2 fusion protein did not activate the GAL4-dependent *HIS3* reporter gene (Figure 7). However, when it was co-expressed together with SMRT–GAL4 activation domain fusion protein, the Bach2–GAL4 fusion activated the reporter gene, resulting in histidine autotrophy. In contrast to the Bach2 fusion, the Bach1 fusion did not show any interaction with SMRT, as evidenced by its failure to support yeast growth in the presence of the SMRT fusion. These results thus indicate that Bach2 but not Bach1 binds specifically to SMRT.

## **Discussion**

The results of the RT–PCR assay and EMSA, shown in this study, have established that Bach2 functions in B cells as a major MARE-binding factor. In terms of cell differentiation, B cell is the second hematopoietic cell lineage in which partners of MARE-effectors have been identified, with a precedent being NF-E2 p45 in erythroid cells (Andrews *et al.*, 1993a,b; Igarashi *et al.*, 1994). This is somewhat surprising in view of our previous observation that, among various hematopoietic cell lines tested, Bach2 expression was detected in the monocytic leukemic cell line M1 but not in BaF3 cells, which are supposed to have a pro-B status (Oyake *et al.*, 1996). However, in this study we examined Bach2 expression in primary B cells and in a large set of established B-cell lines, and the results clearly indicate that Bach2 is in fact a B-cell-specific factor. The specific deployment of Bach2 in B cells suggests that Bach2 and its interacting bZip proteins are important regulators of B-cell differentiation.

We can conclude that the partner molecule for Bach2 in B cells is one of the small Maf proteins, for the following reasons. First, antiserum raised against MafK abolished formation of the Bach2 DNA-binding complex in EMSA (Figure 2). Secondly, the small Maf-related antigen detected in B cells by immunoblotting analysis was the same as that detected in MEL cells known to express MafK (Igarashi *et al.*, 1995a,b; Figure 4C). However, because the MafK antiserum reacts with recombinant MafF, MafG and MafK proteins (unpublished

observation), we could not determine which of the small Maf proteins actually interacts with Bach2 in B cells. Interestingly, the small Maf antigen was detected also in plasmacytoma cells, which do not express Bach2 (Figure 4C). The switching of MARE effectors from the Bach2–small-Maf heterodimers to other dimers, such as small Maf homodimers, will probably change the pattern of gene expression during B cell differentiation. Because small Maf proteins lack any functional domains other than the bZip domain, occupation of MAREs by small Maf homodimers should keep the element in a silenced status (Engel, 1994), in a way similar to a situation described for the Myc–Max–Mad transcription factor network (Amati and Land, 1994).

The results presented here allow us to articulate several hypotheses for the potential function of Bach2 during differentiation of B cells. Our study shows for the first time the existence of functional MAREs within the IgH 3' enhancer region. Since this enhancer region, together with the MAREs, are evolutionarily conserved (Mills *et al.*, 1997), important roles would be expected in IgH gene expression. Furthermore, the two MAREs within the 3' enhancer of the mouse IgH gene are bound by Bach2–small-Maf heterodimers in B-cell extracts (Figure 2). Finally, we show here that Bach2 is expressed at high levels in immature B cells but not in terminally differentiated B cells that express high levels of the IgH gene (plasmacytes; Figure 4). A similar expression profile of Bach2 was also evident in human B-lineage cells (E.Ito, T.Toki and K.Igarashi, unpublished observation). Since Bach2 does not act as a transcriptional activator and rather represses activity of the IgH 3' enhancer regions (Figure 6), we interpret our findings to show that Bach2 functions by inhibiting premature initiation of robust transcription of the IgH locus in undifferentiated B cells. Consistent with this model, the IgH 3' enhancer is inactive before terminal differentiation where Bach2 is expressed abundantly, but is very active in plasmacytoma or myeloma cells, in which Bach2 is not expressed (Madisen and Groudine, 1994; this study).

The present results established that Bach2 represses the IgH 3' enhancer by forming a heterodimer with a small Maf protein, because synergistic repression with MafK of the enhancer activity was lost upon deletion of the leucine zipper from Bach2 (Figure 6D). However, the MARE within the HS3 is not the only target *cis*-element. This was indicated by the results that deletion of the HS3 MARE did not completely abolish cooperative transcription repression by Bach2 and MafK (Figure 6E). In this regard, it should be noted there are several other TREs within HS1, HS2, HS3 and HS4 (Pettersson *et al.*, 1990; Lieberson *et al.*, 1991; Matthias and Baltimore, 1993; Madisen and Groudine, 1994; Grant *et al.*, 1995; Chauveau and Cogne, 1996). Because MARE is closely related to TRE, some of these TREs may actually be a MARE and bind Bach2–small-Maf heterodimer within cells. Indeed, Maf family members can bind to sequences that diverge considerably from the consensus MARE (Ho *et al.*, 1996). We are currently trying to identify other Bach2 target sites within the 3' enhancer regions.

We examined the effect of the HS3 MARE deletion in pro-B and pre-B cells because there was a possibility that the deletion would relieve repression and activate HS1234

enhancer activity in these early-stage cells. However, the HS3 MARE deletion did not cause activation of the reporter gene expression in these cells (data not shown). As the HS1234 is more than 6 kb in length and contains many *cis*-elements, its enhancer activity may not reflect function of a singular *cis*-element. Rather, output may be determined as a combination of activities of positive and negative *cis*- and *trans*-elements. Regarding repression, another candidate effector is BASP/Pax5 which is known to repress IgH 3' enhancer activity in early B cells (Singh and Birshtein, 1993).

An interesting possibility is that Bach2 could modulate the activity of the IgH locus through its BTB domain, which is one of the hallmarks of Bach proteins and distinguishes them from other p45-related factors (Oyake *et al.*, 1996). The BTB domain has been implicated in transcription repression by the transcription factors BCL6 and PLZF (Chen *et al.*, 1993; Ye *et al.*, 1993). These proteins interact with co-repressor molecules like SMRT through the BTB domain (Dhordain *et al.*, 1997; Grignani *et al.*, 1998; Lin *et al.*, 1998). Bach2 indeed binds to SMRT in a yeast two hybrid assay (Figure 7), raising the possibility that it recruits the co-repressor to the IgH locus. In the transfection assay, Bach2 repressed the IgH 3' HS1234 mini-enhancer reporter gene that contains multiple binding sites for various B cell transcription factors. Such a dominant effect of Bach2 might be explained by its interaction with co-repressors like SMRT. We examined effect of histone deacetylase inhibitor trichostatin A, and found that it does not abrogate transcription repression by Bach2 (A.Muto and K.Igarashi, unpublished observation). Because trichostatin A inhibits some, but not all, of histone deacetylase (Carmen *et al.*, 1996), further studies are necessary to reveal the mechanism by which Bach2 represses transcription.

It will also be interesting to analyze whether Bach2 participates in the function of the IgH 3' enhancer in terms of altering the chromatin structure of the locus, thereby contributing to the LCR activity of this element (Madisen and Groudine, 1994). BTB-domain-containing proteins have previously been shown to be involved in regulating chromatin structure (Albagli *et al.*, 1995). We showed recently that Bach1 is a candidate molecule that binds to the  $\beta$ -globin LCR. Bach1 functions as a novel type of architectural transcription factor that mediates interactions among multiple MAREs within the  $\beta$ -globin LCR depending on the protein interaction through the BTB domain (Igarashi *et al.*, 1998). In this sense, it should be noted that IgH 3' LCR also contains at least two separated MAREs (Figure 1) and other putative target sites. Hence Bach2 may orchestrate assembly of a regulatory complex on this region by mediating interactions among the *cis*-elements.

Previous results suggest that stem cells express various genes at low levels that later become up-regulated when the stem cells differentiate into a specific hematopoietic cell lineage (Hu *et al.*, 1997). The commitment and differentiation of stem cells, which express these 'differentiation markers' at low levels, toward a particular cell lineage occurs by the induction and repression of specific sets of genes (Hu *et al.*, 1997). From this point of view, the up-regulation of Bach2 during differentiation of stem cells into B220<sup>+</sup>/IgM<sup>-</sup> bone marrow cells, as well as its

high expression in B220<sup>+</sup> B31-1 cells, indicates a potential role of Bach2 in lineage commitment of B cells. Several transcription factor genes have been shown to be essential for proper development of B cells (Fitzsimmons and Hagman, 1996). Among these factors, EBF and BSAP/Pax5 show a very similar expression pattern to that of Bach2 (Barberis *et al.*, 1990; Hagman *et al.*, 1993). Expression of these proteins is restricted to the B cell lineage; they are turned on at an early stage of B cell development and down-regulated upon maturation to plasma cells. Ikaros, another hematopoietic-specific transcription factor, is required for development of both B and T cells, and is expressed in the stem-cell fraction as well (Georgopoulos, 1997). Bach2 may act together with these B- and lymphoid-specific transcription factors, leading to the differentiation of B cells from uncommitted stem cells.

In conclusion, the present study has identified Bach2 as a B cell-specific component of a small Maf heterodimer and implicated Bach2 in the regulation of B cell-specific gene expression. The results thus provide crucial information and together with further studies will enhance our ability to understand how the development of B cells is regulated by members of the bZip family of transcription factors.

## Materials and methods

### B-cell cultures

Pro-B cell lines 63-12 and 38B9 (Alt *et al.*, 1981; Shinkai *et al.*, 1992), pre-B cell lines NFS5.3 and 18-81 (Rosenberg and Baltimore, 1978; Hardy *et al.*, 1986), immature-B cell lines WEHI 231 and WEHI 279 (Warner *et al.*, 1979; Sibley *et al.*, 1980), mature-B cell lines CH1 and BAL17 (Lynes *et al.*, 1978; Kim *et al.*, 1979), and plasmacytoma lines X63/0 (X63-Ag8.653) and J558L (Kearney *et al.*, 1979; Oi *et al.*, 1983) were maintained in Iscove's modified Dulbecco's medium (IMDM, Gibco-BRL) supplemented with 10% fetal bovine serum, penicillin (100 U/ml), streptomycin (0.1 mg/ml) and 2-mercaptoethanol ( $5 \times 10^{-5}$  M). B31-1 cell line, a bone marrow stromal-cell-(TBR-31-1)-dependent B cell line which contains B220<sup>+</sup> and B220<sup>-</sup> cells deriving from the B220<sup>-</sup> cells was cultured with  $\alpha$ -MEM supplemented with 10% fetal bovine serum, 50  $\mu$ M 2-mercaptoethanol, penicillin and streptomycin (Koguma *et al.*, 1998). From B31-1 cells, B220<sup>-</sup> and B220<sup>+</sup> cells were fractionated by B220 using an immunomagnetic bead system (Miltenyi Biotech).

Spleen cell suspensions were treated with ammonium chloride lysis buffer (pH 7.4) which contained 155 mM NH<sub>4</sub>Cl, 10 mM KHCO<sub>3</sub> and 10 mM Na<sub>2</sub>-EDTA to deplete erythroid cells.  $1 \times 10^7$  treated spleen cells were cultured with RPMI-1640 supplemented with 10% fetal bovine serum, 100 U/ml penicillin, 0.1 mg/ml streptomycin and  $5 \times 10^{-5}$  M 2-mercaptoethanol. Lipopolysaccharide (Sigma) was added to cultures to a final concentration of 50  $\mu$ g/ml. After 4 days in culture, cells were harvested to prepare mRNA as described below.

### EMSA

An oligonucleotide probe was from the IgH HS3 (5'-GCTGAGGGCAGCTGAGTCATCCTGAGCCT-3'), or its derivative-containing mutations (5'-GCTGAGGGCAGCCTTTCATCCTGAGCCT-3', mutations are underlined). The double-stranded oligonucleotide was labeled with [ $\gamma$ -<sup>32</sup>P]ATP and T4 Polynucleotide Kinase (TOYOBO). Incubation of B cell extracts with the DNA probe was carried out at 37°C for 10 min under the conditions described previously (Kataoka *et al.*, 1994b). Where indicated, antibodies were added to the binding reaction at dilutions of 1/10 or 1/20, with incubation for 30 min before addition of DNA. The reaction products were electrophoresed on 4% polyacrylamide gels. Nuclear extracts of B cells were prepared from  $10^7$  cells as described previously (Andrews and Faller, 1991). The anti-small Maf antiserum and anti-Bach2 antiserum (F69-2) have been described previously (Igarashi *et al.*, 1995a; Oyake *et al.*, 1996). Anti-Bach2 monoclonal antibody (2G11-11) was raised against recombinant mouse Bach2 and does not react with Bach1 or other known CNC family proteins. Its

characterization will be described elsewhere (T.Oyake and K.Igarashi, in preparation). Anti-Fos antibodies which react with c-Fos, FosB, Fra1, Fra2 and anti-Jun antibodies, which react with c-Jun, JunB and JunD, were obtained from Santa Cruz (California).

### Cell staining and sorting

Fluorescence-conjugated monoclonal antibodies to TER119, B220, Mac-1, Gr-1, Thy1.2, surface-IgM, CD4, CD8 and Sca-1 and biotinylated lineage mixture antibodies to TER-119, B220, Mac-1, Gr-1 and CD3- $\epsilon$  were obtained from PharMingen. Monoclonal antibodies to CD34 and c-Kit were as described previously (Osawa *et al.*, 1996). Cells ( $1 \times 10^7$ ) in single-cell suspensions, obtained from bone marrow, spleen or thymus of C57BL/6 or BALB/c mice (5–10 weeks), were incubated with appropriate mAbs on ice for 30 min. Cells were washed with staining medium (SM, phosphate-buffered saline containing 0.05% NaN<sub>3</sub> and 3% fetal bovine serum), and resuspended in SM containing 1  $\mu$ g/ml of propidium iodide. Cells were sorted using a four-color fluorescence-activated cell sorter (FACS Vantage, Becton Dickinson) and  $6 \times 10^3$  to  $1 \times 10^5$  cells were collected for each fraction. RNA was prepared from each fraction as described above. cDNA was synthesized by random hexamer priming and PCR was carried out with specific primers for Bach2 (J2020F; 5'-CGCTGTCGAAAGAGGAAGCTGGAC-3' and J2209R; 5'-CCTGGATCTGCTCTGGACTCTGGA-3') and  $\beta$ -actin ( $\beta$ -actin-1; 5'-TGCCCATCTATGAGGGTTACG-3' and  $\beta$ -actin-2; 5'-AAAGCTGGTCCAGCCGTTC-3'). The amplicon derived from the genomic *bach2* DNA is much larger than that derived from cDNA because of the presence of an intron (unpublished observation). The amount of templates used were normalized for relative levels of  $\beta$ -actin cDNA. All PCRs were carried out in 20  $\mu$ l reactions using 1.25 U of ExTaq DNA polymerase (Takara) and 20 pmol of each primer, with a thermal cycler (Perkin Elmer 9600) and a profile of 94°C for 1 min, 55°C for 1 min and 72°C for 1 min. At least two different protocols (typically 26 and 30 cycles) were employed to ensure linearity of amplification. Products were resolved on 2% agarose gels, transferred onto ZetaProbe membranes (Bio-Rad) and hybridized with radiolabeled DNA fragments that are specific for each target cDNA.

### Immunoblotting analysis

Whole cell extracts, prepared from B-cell lines as described previously (Pagano *et al.*, 1992), were separated on sodium dodecyl sulfate (SDS)-polyacrylamide gels. Proteins were transferred onto polyvinylidene difluoride membranes (Waters) and processed for reaction with the antiserum against Bach2 (F69-2) or anti-small-Maf antiserum. Secondary anti-rabbit IgG antibodies were conjugated with horseradish peroxidase (ZYMED). Detection of peroxidase activity was carried out with the enhanced chemiluminescence system (Amersham).

### Plasmids

An internal control sea pansy luciferase plasmid was constructed, using the luciferase assay system (TOYO-INIKI), by inserting the *NheI*-*Bam*HI 1.2 kb fragment of pRL-SV40 into the *Eco*RI site of pEF-BssHII, a modified version of pEF-Bos (Mizushima and Nagata, 1990). The resulting plasmid pEF-SP carries a sea pansy luciferase gene driven by the promoter of human polypeptide chain elongation factor 1 $\alpha$  gene. To construct IgH promoter/3' enhancer reporter plasmid, an *Eco*RI-*Nco*I 2.2 kb DNA fragment containing the IgH promoter was cloned in the *Xho*I-*Nco*I site of pGL3 promoter vector (Promega), resulting in pIGHP. Then the 6.5 kb chimeric mini-3' enhancer (HS1, -2, -3 and -4 fusion; Madisen and Groudine, 1994) of IgH gene was cloned in the *Bam*HI site of the pIGHP-luc, resulting in pIGHHS1-4. The MARE was deleted from the enhancer using PCR. The resulting plasmid, pIGHHS1-4MARE, carried a 37 bp deletion within the HS3, including the MARE. pCMV-Bach2(F) has been described previously (Oyake *et al.*, 1996). The leucine-zipper-coding domain was deleted from the pCMV-Bach2(F) using an *Eco*47III site, located just before the leucine zipper, and a *Not*I site in the vector plasmid. To construct a yeast expression plasmid for Bach2-GAL4 DNA-binding-domain fusion, the entire Bach2 coding sequence (reconstituted J/F-type; see Oyake *et al.*, 1996) was isolated by PCR and inserted into the *Eco*RI site of pGBT9 (Clontech), resulting in pGBT-Bach2 with the entire *bach2* ORF fused in-frame to the DNA-binding domain of GAL4. pGBT1A1 carries *bach1* ORF fused to the DNA-binding domain of GAL4 as described previously (Oyake *et al.*, 1996). pACT-SMRT encodes residues 194–657 of SMRT fused to the activation domain of GAL4, and has been described previously (Dhordain *et al.*, 1997).



**Transfection assay**

Cultured B cell lines were transfected using FuGENE 6 reagent (Boehringer Mannheim) according to the manufacturer's protocol. Amounts of transfected plasmids are indicated in the figure legends. Preparation of cell lysates and luciferase assays were carried out using TOYO-INKI, following the supplier's protocol, with a Lumat LB950 luminometer (Berthold). Fire-fly luciferase activity was normalized for transfection efficiency as determined by the control sea pansy luciferase activity.

**Acknowledgements**

We thank J.D.Engel and J.Bungert for critical reading of the manuscript and discussions. Further thanks go to T.Oyake for monoclonal antibody, Y.Matsuzaki for help with the FACS, P.Dhordain for SMRT plasmids, and M.Nishizawa, E.Ito and A.Kobayashi for stimulating discussion. This work was supported by the International Scientific Research Program and Grants-in-aid from the Ministry of Education, Science, Sport and Culture of Japan, an RFTF grant from the Japanese Society for the Promotion of Science, and grants from the Mochida Memorial Foundation, the Ciba-Geigy Foundation Japan, the Naito Foundation and the National Institutes of Health (NIH) of USA.

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Received March 31, 1998; revised July 29, 1998;  
accepted August 3, 1998