



Bcl-2 Overexpression Induces Neurite Outgrowth via the *Bmp4/Tbx3/NeuroD1* Cascade in H19-7 Cells

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Abstract

Bcl-2 is overexpressed in the nervous system during neural development and plays an important role in modulating cell survival. In addition to its anti-apoptotic function, it has been suggested previously that *Bcl-2* might act as a mediator of neuronal differentiation. However, the mechanism by which *Bcl-2* might influence neurogenesis is not sufficiently understood. In this study, we aimed to determine the non-apoptotic functions of *Bcl-2* during neuronal differentiation. First, we used microarrays to analyze the whole-genome expression patterns of rat neural stem cells overexpressing *Bcl-2* and found that *Bcl-2* overexpression induced the expression of various neurogenic genes. Moreover, *Bcl-2* overexpression increased the neurite length as well as expression of *Bmp4*, *Tbx3*, and proneural basic helix–loop–helix genes, such as *NeuroD1*, *NeuroD2*, and *Mash1*, in H19-7 rat hippocampal precursor cells. To determine the hierarchy of these molecules, we selectively depleted *Bmp4*, *Tbx3*, and *NeuroD1* in *Bcl-2*-overexpressing cells. *Bmp4* depletion suppressed the upregulation of *Tbx3* and *NeuroD1* as well as neurite outgrowth, which was induced by *Bcl-2* overexpression. Although *Tbx3* knockdown repressed *Bcl-2*-mediated neurite elaboration and downregulated *NeuroD1* expression, it did not affect *Bcl-2*-induced *Bmp4* expression. While the depletion of *NeuroD1* had no effect on the expression of *Bcl-2*, *Bmp4*, or *Tbx3*, *Bcl-2*-mediated neurite outgrowth was suppressed. Taken together, these results demonstrate that *Bcl-2* regulates neurite outgrowth through the *Bmp4/Tbx3/NeuroD1* cascade in H19-7 cells, indicating that *Bcl-2* may have a direct role in neuronal development in addition to its well-known anti-apoptotic function in response to environmental insults.

Keywords *Bcl-2* · Neurite outgrowth · *Bmp4* · *Tbx3* · *NeuroD1*

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Abbreviations

NPCs Neural precursor cells
bHLH Basic helix–loop–helix
CNS Central nervous system
bFGF Basic fibroblast growth factor

Introduction

Bcl-2 gene was identified at the breakpoint of the t(14;18) (q32;q21) chromosomal translocation that is associated with human follicular lymphoma, and since then, it has been shown that the *Bcl-2* protein is mainly located on the mitochondrial outer membrane and is responsible for the regulation of programmed cell death (Pegoraro et al. 1984; Hockenbery et al. 1990). Currently, it is recognized that *Bcl-2* can not only modulate apoptosis by interacting with other pro- or anti-apoptotic *Bcl-2* family members, but it also has an anti-autophagy function by directly binding

with Beclin-1 (Adams and Cory 1998; Pattingre et al. 2005). Consequently, Bcl-2 is considered to be an arbiter of cell survival for development, tissue homeostasis, protection against diverse insults, and various diseases including cancer (Adams and Cory 1998).

In mice, Bcl-2 is highly expressed in the organs related to the immune system (such as the thymus and the spleen) and the brain (Hockenbery et al. 1991; Abedohmae et al. 1993). During brain development, the mRNA levels of *Bcl-2* are the highest on embryonic day 15, which is the stage of neurogenesis, indicating that Bcl-2 may have a considerable impact on the process of neuronal development in the CNS (central nervous system) (Abedohmae et al. 1993; Merry et al. 1994). According to previous reports, overexpression of *Bcl-2* prevents neurotrophic factor deprivation-induced neuronal apoptosis in embryonic neurons (Allsopp et al. 1993). Moreover, *Bcl-2* transgenic mice are protected against middle cerebral artery occlusion-induced ischemia (Martinou et al. 1994), and *Bcl-2*-deficient mice exhibit progressive degeneration of motor, sympathetic, and sensory neurons during early postnatal development (Michaelidis et al. 1996). In addition to these neuroprotective functions, Bcl-2 has also been shown to influence neurogenesis in pheochromocytoma and neuroblastoma cell lines (Sato et al. 1994; Hanada et al. 1993). Zhang et al. (1996) reported that Bcl-2 directly modulated neuronal differentiation in human neural crest cells, and Hilton et al. (1997) suggested that Bcl-2 had an impact on the axonal growth rate of the embryonic sensory neurons. Moreover, Bcl-2 promotes regeneration of injured axons in the mammalian CNS (Chen et al. 1997), indicating that Bcl-2 may have a direct function on neurogenesis in addition to its well-documented role as a suppressor of apoptosis. Nevertheless, the precise non-apoptotic functions of Bcl-2 during neuronal differentiation still remain unclear.

Neurogenesis is the differentiation process for neuronal lineage commitment of multipotent neural stem cells either during the development of the fetal nervous system or during the regeneration of an impaired adult nervous system, which is spatiotemporally coordinated by a variety of intrinsic and extrinsic factors in stem cell niches (Gage 2000; Paridaen and Huttner 2014). Proneural bHLH proteins, including NeuroDs and neurogenins, are essential transcriptional regulators for cell fate specification in neural stem cell niches (Paridaen and Huttner 2014; Ross et al. 2003). Moreover, deregulated expression or mutation of the bHLH genes occurs in brain cancers, as well as neurodevelopmental, neuropsychiatric, and neurodegenerative disorders (Dennis et al. 2019). Their expression is also regulated by various signaling networks such as Notch, Wnt, and BMP (Dennis et al. 2019). However, the signaling pathway that couples Bcl-2 to the regulation of bHLH transcription factors during neuronal differentiation is not yet fully understood.

Here, we aimed to clarify the non-apoptotic functions of Bcl-2 during neuronal differentiation and to explain the mechanism by which Bcl-2 regulates neurite formation. Using gain- or loss-of-function studies, we showed that the neurite lengths of differentiating H19-7 cells were affected by the modulation of the *Bcl-2* gene. Moreover, we observed that *Bcl-2* overexpression influenced various neurogenic factors by analyzing whole-genome expression patterns obtained through microarrays. In conclusion, we demonstrated that *Bcl-2* overexpression promoted neurite outgrowth through the Bmp4/Tbx3/NeuroD1 cascade in the H19-7 cells, indicating that Bcl-2 may have a direct role in neuronal development in addition to its well-known anti-apoptotic function.

Materials and Methods

Materials

The cell culture materials, such as Dulbecco's modified Eagle's medium (DMEM) with L-glutamine and low glucose, fetal bovine serum (FBS), phosphate-buffered saline (PBS), penicillin/streptomycin, and trypsin/EDTA, were purchased from WISENT (St. Bruno, QC, Canada). G-418 was obtained from Duchefa (Haarlem, Netherlands). RNAiso Plus for RNA extraction was purchased from Takara Bio (Otsu, Japan), Reverse Transcription Master Mix for cDNA synthesis was obtained from Elpis Bio (Daejeon, Korea), and GoTaq® DNA polymerase kits were purchased from Promega (Madison, WI, USA). SensiFAST™ SYBR® No-ROX kits were purchased from Bioline (London, UK). The antibodies used were purchased as follows: Bcl-2 (SC-7382) from Santa Cruz Biotechnology (Santa Cruz, CA, USA), Calnexin (ADI-SPA-860) from Enzo Life Sciences (Farmingdale, NY, USA); Bmp4 (ab39973), Tbx3 (ab99302), and NeuroD1 (ab16508) from Abcam (Cambridge, UK); GFP (11814460001) from Roche (Indianapolis, IN, USA), β -tubulin type III (TUBJ1, 802001) from BioLegend (San Diego, CA, USA), Alexa Flour® 488-conjugated goat anti-rabbit IgG (A11008) from Thermo Fisher Scientific (Rockford, IL, USA), and Cy™ 3-conjugated AffiniPure goat anti-rabbit IgG (H+L) (111-165-144) from Jackson ImmunoResearch (West Grove, PA, USA). All other chemicals were of analytical grade.

Cell Culture

H19-7 cells, which are conditionally immortalized rat hippocampal precursor cells with a temperature-sensitive SV40 large T antigen, were maintained in DMEM supplemented with 10% (v/v) heat-inactivated FBS, 100 units/mL penicillin, and 100 μ g/mL streptomycin under 0.2 mg/mL G-418

selection at 33 °C (the temperature at which the SV40 large T antigen is functional) in a humidified incubator with 5% CO₂. To induce differentiation, the medium was changed to N2 medium supplemented with 20 ng/mL bFGF (R&D Systems, Minneapolis, MN, USA), and the cells were incubated at 39 °C for 2 days. Neural precursor cells (NPCs) were obtained from pregnant Sprague–Dawley rats. Protocols were reviewed and approved by the Institutional Animal Care and Use Committee of Hanyang Laboratory Animal Research Center (2014-0126A). The embryonic brain cortices from E14 rat embryos were mechanically triturated in a Ca²⁺/Mg²⁺-free Hank's balanced salt solution (HBSS; Gibco, Grand Island, NY, USA), seeded at 2 × 10⁵ cells in 100-mm culture dishes (Corning Life Sciences, Acton, MA, USA), pre-coated with 15 µg/mL poly-L-ornithine (Sigma-Aldrich, St. Louis, MO, USA) and 1 µg/mL fibronectin (Invitrogen, Carlsbad, MO, USA), and cultured for 5 to 6 days in N2 medium supplemented with bFGF. The cell clusters generated were dissociated in HBSS, plated on fresh culture dishes, and induced for additional proliferation in N2 + bFGF up to 70 to 80% cell confluency before the cells were subjected to differentiation for 2 days.

Gene Expression Profiling Using cDNA Microarrays

Microarray analysis was performed using tools from the commercial microarray service Ebiogen (Seoul, Korea) and deposited in the NCBI Gene Expression Omnibus (GEO, <http://www.ncbi.nlm.nih.gov/geo>) repository (accession number GSE130481). In brief, the gene expression profiles of rat NPCs from the vector + bFGF group (proliferation control), the vector – bFGF group (differentiation control), and the *Bcl-2* + bFGF group (*Bcl-2* overexpression) were compared using cDNA microarrays. NPCs derived from the E14 rat embryos were transiently transfected with 4 µg of either MSCV-IRES-EGFP or *rBcl-2*-MSCV-IRES-EGFP using a Nucleofector™ kit (Lonza, Walkersville, MD, USA) according to the manufacturer's protocol. Total RNA was then isolated and amplified. The amplified cRNA was hybridized to an Agilent Rat Oligo Microarray (44 K) (Agilent Technology, Palo Alto, CA, USA) at 65 °C for 17 h in an Agilent DNA microarray hybridization oven and then washed. The hybridized images were scanned using an Agilent DNA microarray scanner and quantified using Feature Extraction software (Agilent Technology). The data normalization and selection of the genes that had undergone fold changes were performed using GeneSpring GX software, version 7.3 (Agilent Technology). The gene classification was performed using BioCarta (<http://www.biocarta.com>), GenMAPP (<http://www.genmapp.org>), and DAVID (<http://david.abcc.ncifcrf.gov>). To obtain insights into the biological processes related with neural development, Gene Ontology (GO) analysis was performed. Using GO terms

corresponding to 'nervous system development,' the neural development-related genes were selected for further analysis. All microarray analyses and visualization were conducted using R software, version 3.4.1 (www.r-project.org).

Retroviral Construction and Infection

Rat *Bcl-2* cDNA was amplified from NPCs of E14 Sprague–Dawley rat embryos using PCR and cloned into the retroviral vector MSCV-IRES-EGFP. The construct was obtained using a forward primer containing a BglII site (5'-GAAGATCTATGGCGCAAGCCGGGAGA-3') and a reverse primer containing an EcoRI site (5'-GGAATTCTCACTTGTGGCCAGGTATGCAC-3'). PCR mixtures contained 1 µL of cDNA from NPCs, 5 µL of 10X PCR buffer, 5 µL of dNTP mix (2.5 mM), 1 µL of Taq polymerase (10 units/µL, Pyrobest, Takara Bio) adjusted to 50 µL with distilled water. The PCR amplification consisted of denaturation for 5 min at 95 °C followed by 30 cycles of 30 s at 95 °C, 30 s at 60 °C, and 90 s at 72 °C, with a final extension for 7 min at 72 °C. The PCR product was separated via electrophoresis on a 1.5% agarose gel and visualized using a 3UV™ transilluminator (UVP, Upland, CA, USA). The DNA band of the expected size was excised, purified using a FavorPrep™ GEL/PCR purification mini kit (Favorgen Biotech, Pingtung, Taiwan), and digested with the appropriate restriction enzymes (BglII and EcoRI; New England Biolabs, Beverly, MA, USA) at 37 °C. The digested sample was then ligated into the MSCV-IRES-EGFP retroviral vector. The cloned rat *Bcl-2* was confirmed using sequencing (Cosmo Genetech, Seoul, Korea), and the sequence was aligned with the NCBI rat *Bcl-2* mRNA sequence (NM_016993.1) using the Genomatix pairwise comparison program (<http://www.genomatix.de/cgi-bin/dialign/dialign.pl>). The viral particles were produced by transfecting the retrovirus packaging cell line 293GPG with the cloned vector using polyethylenimine (PEI; Sigma-Aldrich), and supernatants containing viral particles were harvested after incubation for 48 h. For viral infection, H19-7 cells were incubated with a viral suspension (4 × 10⁶ particles/mL) containing polybrene (1 µg/mL; Sigma-Aldrich) for 4 h followed by transfer to fresh medium.

Transient Transfection with Small Interfering RNAs

Bcl-2, *Bmp4*, *Tbx3*, and *NeuroD1* siRNAs, as well as control siRNA (Bioneer, Daejeon, Korea), were transiently transfected into H19-7 cells for loss-of-function studies. The siRNA sequences were as follows: *Bcl-2* (5'-GAAUCAAGUGUUCGUCUAUA-3' and 5'-UAUGACGAACACUUGAUUC-3'), *Bmp4* (5'-GACUACUGGACACCAGACU-3' and 5'-AGUCUGGUGUCCAGUAGUC-3'), *Tbx3* (5'-CUGGAUAAAAGGCCAAGU-3' and 5'-ACUUGGCCUUUU

UAUCCAG-3'), and *NeuroD1* (5'-GAAACAUGACCAAU CAUA-3' and 5'-UAUGAUUUGGUCAUGUUUC-3'). Each siRNA (100 nM) was introduced into the cells using PEI transfection reagent.

Immunostaining and Measurement of Neurite Outgrowth

Cells were washed with PBS and fixed with 4% (w/v) paraformaldehyde (PFA; Sigma-Aldrich) for 15 min followed by washing three times with 0.1% bovine serum albumin (BSA; Sigma-Aldrich) in PBS at 25 °C. The cells were permeabilized with 0.3% Triton X-100 in PBS for 20 min and blocked with 10% normal goat serum in PBS for 1 h at room temperature. Next, the cells were incubated with anti-TUJ1 antibody (1:2000) and anti-GFP antibody (1:500) at 4 °C followed by incubation with CyTM 3-conjugated AffiniPure goat anti-rabbit IgG (H+L) (1:200) and Alexa Flour[®] 488-conjugated goat anti-rabbit IgG (1:500) for 1 h before mounting with Vectashield (Vector Laboratories, Burlingame, CA, USA) containing 4, 6-diamidino-2-phenylindole (DAPI). The immunoreacted cells were imaged using a fluorescence microscope (Leica Microsystems, Wetzlar, Germany), and the morphological characteristics were quantified using ImageJ software (NIH; <http://rsb.info.nih.gov/ij/>). The neurite length was defined as the distance from the soma to the tip of the branch. The neurite length data were obtained from ten randomly selected areas from at least three independent experiments, and more than 100 cells were counted for each group in each experiment.

Reverse Transcription (RT)-PCR and Real-Time PCR

Total RNA was isolated using RNAiso Plus according to the manufacturer's protocol. Next, 1 µg of isolated total RNA was incubated with Reverse Transcription Master Premix kit for 60 min at 37 °C. The cDNA was mixed with specific primers and GoTaq[®] DNA polymerase, and the mixtures were amplified using a thermocycler (Takara Bio). The primer sequences used were as follows: *Bcl-2* (5'-CCTGGC ATCTTCTCCTTCCA-3' and 5'-CACCCCATCCCTGAA GAGTT-3'), *Gapdh* (5'-GGCATTGCTCTCAATGACAA-3' and 5'-AGGGCCTCTCTTGCTCTC-3'), *Bmp4* (5'-GAG ATCGCCACCTACAGGAA-3' and 5'-GCTCCTGCTTCG ACTCCTTA-3'), *Tbx3* (5'-TTTGGCCATGTCGCCTTT TG-3' and 5'-GAGCGGCTATTTCAGTTCCGA-3'), *NeuroD1* (5'-CTCAGTTCTCAGGACGAGGA-3' and 5'-TAG TTCTTGCCAAGCGCAG-3'), *NeuroD2* (5'-TTCTCG CTCAAGCAGGACTC-3' and 5'-GCGTTGAGCTCCTCG TACAT-3'), *Mash1* (5'-GGCTCAACTTCAGTGGCTTC-3' and 5'-TGGAGTAGTTGGGGGAGATG-3'). The PCR conditions were as follows: denaturation at 95 °C for 30 s, annealing at 60 °C (*NeuroD1*, 58 °C) for 30 s, and extension

at 72 °C for 40 s (*Bcl-2*, 28 cycles; *Gapdh*, 25 cycles; *Bmp4*, *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1*, 33 cycles). The PCR products were analyzed on a 1.5% agarose gel. For real-time PCR, 1 µL of cDNA was amplified in duplicate in a final volume of 20 µL using the SensiFAST[™] SYBR NO-ROX[®] kit and the RT-PCR primers listed above. Thermocycling conditions were 95 °C for 10 min followed by 40 cycles of 95 °C for 15 s and 58 °C (*NeuroD1*) or 60 °C (all other genes) for 1 min. The primer sequences for real-time PCR were the same as for RT-PCR.

Western Blot Analysis

Protein expression was analyzed by immunoblotting as described previously (Zhang et al. 2019; Pan et al. 2017). The cells were lysed in 20 mM Tris/HCl at pH 7.5 with 150 mM NaCl, 1 mM EDTA, 1 mM EGTA, 2.5 mM sodium pyrophosphate, 1% Triton X-100, and 1 mM PMSF. Samples containing 30 µg of total protein were loaded onto 12% SDS-PAGE gels, electrophoresed, and transferred onto nitrocellulose membranes (Amersham Biosciences, Piscataway, NJ, USA). After blocking with 5% nonfat dried milk for 1 h, the membranes were incubated with primary antibodies followed by a horseradish peroxidase (HRP)-conjugated secondary antibody (1:2000; Jackson ImmunoResearch). Specific bands were detected using enhanced chemiluminescence (ECL) (Thermo Fisher Scientific), and band intensities were quantified using ImageJ software.

Statistical Analysis

Statistical analysis was performed with SPSS software, version 18.0 (SPSS Inc., Chicago, IL, USA). The data were expressed as the mean ± SD of at least three independent experiments. Comparisons between groups were made using the unpaired Student's *t* test. *p* values < 0.05 were considered statistically significant.

Results

Bcl-2 Affects Neuronal Differentiation of Rat Hippocampal Progenitor Cells

We previously reported that phospholipase D1 (PLD1), a membrane-anchored enzyme that hydrolyzes phosphatidylcholine into phosphatidic acid, which acts as a lipid second messenger, and the polar head group choline (Park and Han 2018), increases Bcl-2 expression via the PLA2/Cox2/EP4/PKA/p38MAPK/CREB cascade in rat NPCs and via the JNK/STAT3 pathway in rat hippocampal progenitor cells during neuronal differentiation (Park et al. 2014; Yoon et al. 2012). Next, we sought to determine

how *Bcl-2* influences the process of neuronal differentiation. To investigate whether the modulation of *Bcl-2* impacts neurite outgrowth, control or *Bcl-2* siRNA was transfected into H19-7 cells and then stimulated using N2 medium supplemented with 20 ng/mL bFGF for neuronal differentiation. As shown in Fig. 1a and b, bFGF-induced neurite outgrowth was repressed by *Bcl-2* depletion compared to the bFGF-treated control siRNA group. Inversely,

Bcl-2 was overexpressed through retroviral transduction with MSCV-IRES-EGFP or *rBcl-2*-MSCV-IRES-EGFP followed by stimulation with bFGF. As shown in Fig. 1c and d, the neurite length of GFP⁺ cells was significantly potentiated compared with the bFGF-treated vector group. Moreover, these phenomena could be completely reproduced in E14 rat cortical NPCs (Fig. S1). These results suggest that *Bcl-2* might be directly involved in neuronal differentiation.

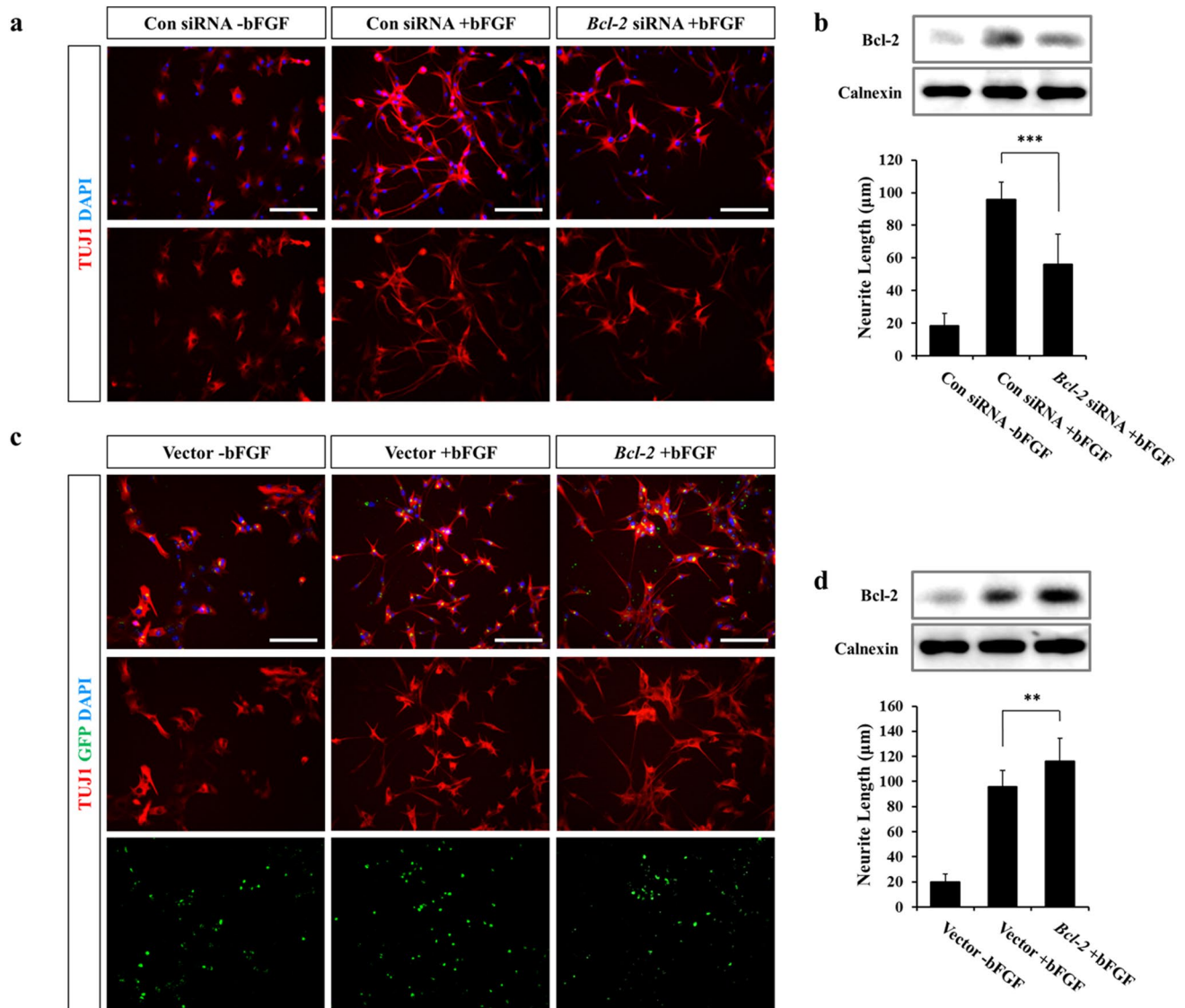


Fig. 1 Effect of *Bcl-2* gene modulation during neuronal differentiation in H19-7 cells. **a** H19-7 cells were transfected with control or *Bcl-2* siRNA for 2 days, after which the medium was changed to N2 medium supplemented with 20 ng/mL bFGF and the temperature shifted to 39 °C for 2 days. The cells were immunostained with TUJ1. Scale bar, 100 μm. **b** Immunoblotting was performed to verify the knockdown efficiency, and the neurite lengths of the TUJ1⁺ cells were measured from 10 randomly selected areas from at least

three independent experiments and presented as the mean ± SD. *** $p < 0.001$. **c** MSCV-IRES-EGFP or *rBcl-2*-MSCV-IRES-EGFP vectors were introduced into the cells through retroviral transduction for 2 days, followed by stimulation with bFGF and shifting the temperature to 39 °C for 2 days. **d** Cells were then immunostained with TUJ1 and GFP. Scale bar, 100 μm. The results are presented as the mean ± SD of three independent experiments. ** $p < 0.01$

***Bcl-2* Overexpression Increases Expression of Various Neurogenic Factors in NPCs**

To investigate whether *Bcl-2* overexpression regulates the expression of neurogenic factors, we examined the gene expression patterns of NPCs derived from the cerebral cortex of E14 rat embryos by using microarrays. We found that the expression of 4762 genes was upregulated by *Bcl-2* overexpression, and of these, 3537 genes overlapped with the genes upregulated by the differentiation stimuli (Fig. 2a). On the other hand, out of the 6116 genes that were decreased by *Bcl-2* overexpression, 4989 of them overlapped with the genes downregulated by differentiation stimulation (Fig. S2). Additionally, 706 genes were identified as genes involved in the nervous system development through GO term analysis (Fig. 2b). Among them, *Bcl-2* overexpression upregulated 372

genes and downregulated 334 genes (Table S1). As in the differentiated control group (–bFGF), a variety of neurogenic marker genes, such as *Map2*, *Mapt*, *Synj1*, and *Snap25*, were increased by *Bcl-2* overexpression (Fig. 2b). Moreover, neurogenic bHLH transcription factors, including *NeuroD2* and *Ascl1* (*Mash1*), as well as *Bmp4* and *Tbx3* were increased by *Bcl-2* overexpression (Fig. 2b). Next, we verified whether the microarray results could be reproduced in H19-7 cells. As shown in Fig. 3a and b, *Bcl-2* overexpression induced a significant increase in neurite outgrowth. Moreover, the genes identified in the microarrays (*Bmp4*, *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1*) showed significantly increased mRNA levels (Fig. 3c, d). The expression of the *Bmp4*, *Tbx3*, and *NeuroD1* proteins also showed a similar tendency (Fig. 3e, f). In summary, *Bcl-2* overexpression upregulates the expression of various neurogenic factors, such as *Bmp4*, *Tbx3*, and *NeuroD1*, and increases neurite outgrowth.

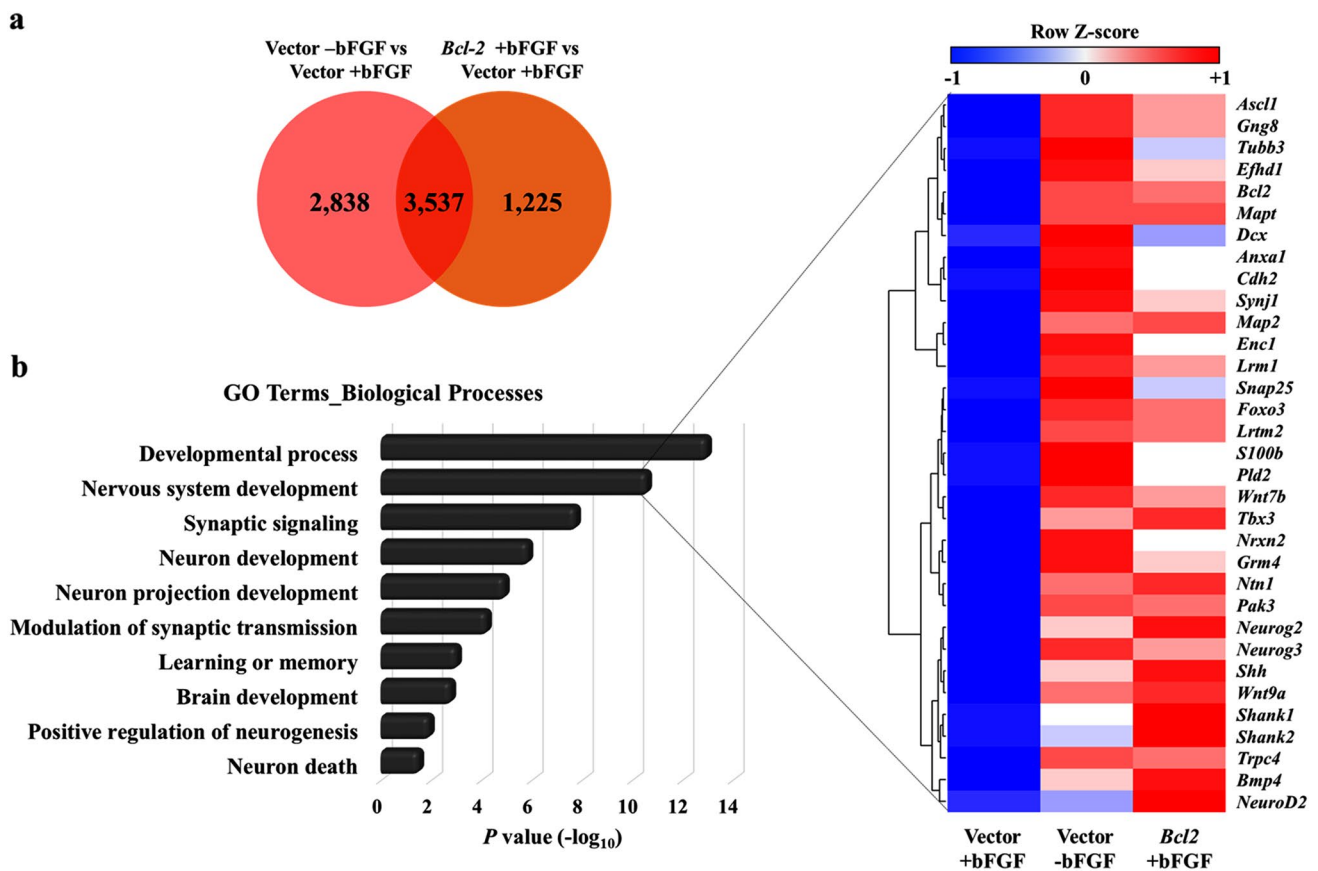


Fig. 2 Microarray analysis of the genes upregulated by *Bcl-2* overexpression in rat NPCs. **a** Whole-genome expression profiles were analyzed using cDNA microarrays of rat NPCs. The number of genes upregulated 1.2-fold by differentiation stimuli or by *Bcl-2* overexpression is shown in the Venn diagram. **b** Upregulated genes were categorized using Gene Ontology (GO) analysis based on the biological

processes. The genes corresponding to the nervous system development are expressed in the heat map (right panel). The columns represent the individual groups, and the rows represent each upregulated gene. The relative expression value for each gene is depicted by Z-score, with red indicating high expression and blue indicating low expression

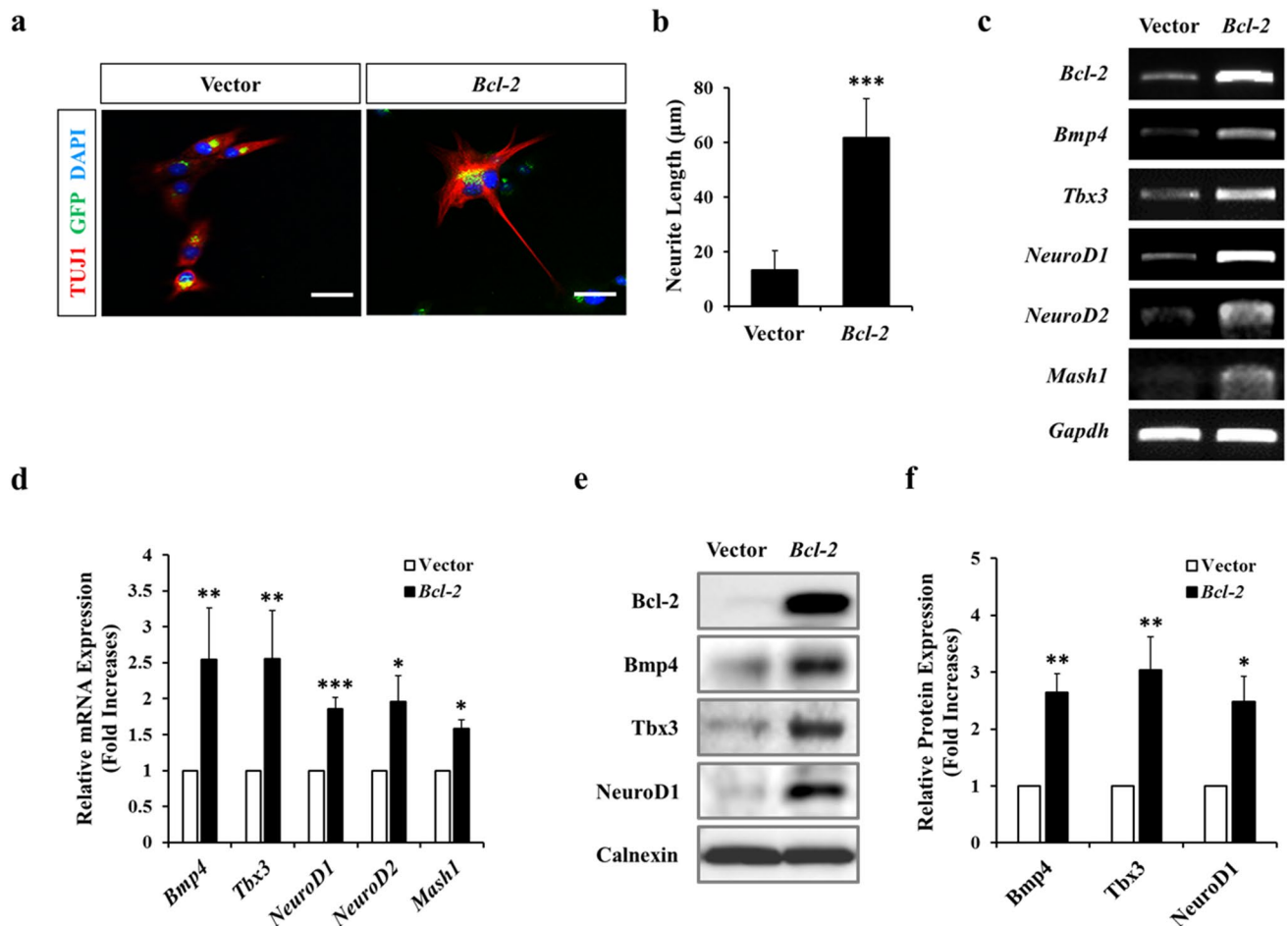


Fig. 3 *Bcl-2* overexpression induces neurite outgrowth as well as expression of several genes. **a** H19-7 cells were infected with MSCV-IRES-EGFP or *rBcl-2*-MSCV-IRES-EGFP using retroviral transduction for 2 days. Immunofluorescence images for TUJ1 and GFP were used to determine neurite outgrowth. Scale bar, 50 µm. **b** The neurite length of TUJ1⁺ cells was measured from ten randomly selected areas from at least three independent experiments and presented as the mean ± SD. ****p* < 0.001. **c, d** Total RNA was isolated using Trizol reagent, and mRNA levels of *Bcl-2*, *Bmp4*, *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1* were determined using RT-PCR (c) and real-time RT-PCR (d). The results are presented as the mean ± SD of three independent experiments. **p* < 0.05, ***p* < 0.01, ****p* < 0.001. **e, f** Cells were lysed and analyzed using immunoblotting with anti-*Bcl-2*, anti-*Bmp4*, anti-*Tbx3*, anti-*NeuroD1*, and anti-Calnexin antibodies. The band intensity was quantified with ImageJ software. The results are presented as the mean density (as a fold increase) ± SD from three independent experiments. **p* < 0.05, ***p* < 0.01

Bmp4 is Involved in the Process of Neurite Outgrowth Induced by *Bcl-2* Overexpression

Bone morphogenetic proteins (BMPs) are extracellular secretory proteins belonging to the transforming growth factors-β (TGF-β) superfamily and mediate developmental processes, including morphogenesis, proliferation, lineage commitment, differentiation, and apoptosis in the nervous system (Mehler et al. 1997). In particular, *Bmp4* is highly expressed in the embryonic cortex of the developing dorsal forebrain (Furuta et al. 1997) and triggers neuronal differentiation of the NPCs in the neocortical ventricular zone (Li et al. 1998; Moon et al. 2009). However, many reports suggest that BMPs and their signaling pathways are involved

in the commitment of the astroglial fate during neuronal development in a subclass-specific manner (Mehler et al. 1997; Gross et al. 1996). To investigate the relationship of *Bcl-2* overexpression-induced *Bmp4* with other genes, we transfected 100 nM of control or *Bmp4* siRNA into *Bcl-2*-overexpressing H19-7 cells. *Bcl-2*-induced neurite elaboration was significantly repressed by *Bmp4* depletion (Fig. 4a, b). Additionally, the *Bcl-2*-induced expression of *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1* was strikingly downregulated by *Bmp4* knockdown at both the mRNA (Fig. 4c, d) and protein levels (Fig. 4e, f). These results indicate that *Bmp4* participates in *Bcl-2*-mediated neurite outgrowth by controlling the expression of *Tbx3* and neurogenic bHLH transcription factors.

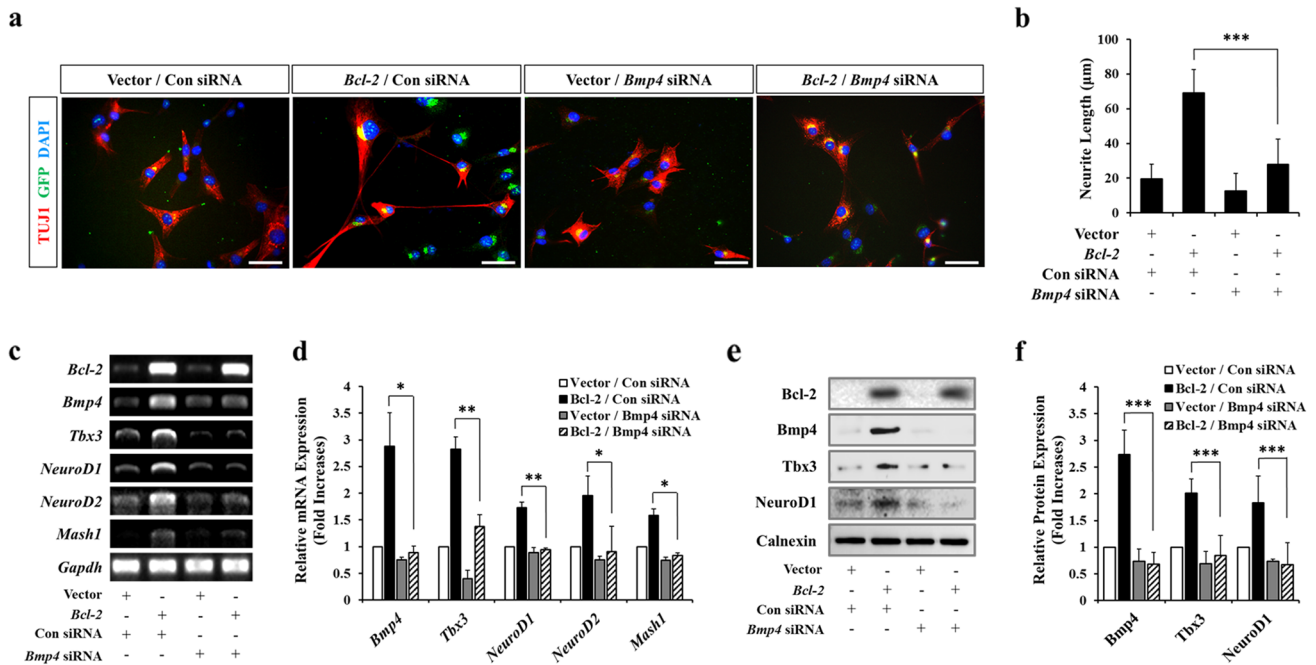


Fig. 4 Effect of *Bmp4* gene depletion in *Bcl-2*-overexpressing H19-7 cells. **a** Cells were infected with MSCV-IRES-EGFP or *rBcl-2*-MSCV-IRES-EGFP using retroviral transduction for 2 days followed by transfection with control or *Bmp4* siRNA. The cells were then immunostained for TUJ1 and GFP. Scale bar, 50 µm. **b** Neurite length was measured. The results are presented as the mean \pm SD of three independent experiments. *** $p < 0.001$. **c, d** Total RNA was isolated using Trizol reagent, and mRNA levels of *Bcl-2*, *Bmp4*, *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1* were determined using RT-PCR (c) and real-time RT-PCR (d). The results are presented as the mean \pm SD of three independent experiments. * $p < 0.05$, ** $p < 0.01$. **e, f** Cells were lysed, and immunoblotting was performed using anti-*Bcl-2*, anti-*Bmp4*, anti-*Tbx3*, anti-*NeuroD1*, and anti-Calnexin antibodies. The results are presented as the mean density (as a fold increase) \pm SD from three independent experiments. *** $p < 0.001$

The Upregulation of *Bmp4* Induced by *Bcl-2* Overexpression is Independent of Canonical *Bmp/Smad* Pathway

BMPs are secreted extracellularly and bind to their specific receptor leading to the phosphorylation of the Smad1/5/8 protein complex and translocation into the nucleus. The Smad1/5/8 protein complex then acts as a transcription factor and induces the expression of several target genes (Wrana 2013). One of those target genes, *Id*, represses neuronal differentiation of the NPCs and induces astroglial lineage commitment by preventing DNA binding to neurogenic bHLH transcription factors or by promoting their degradation through ubiquitin-mediated proteolysis (Miyazono and Miyazawa 2002). In addition to these canonical pathways, BMPs also can activate LIMK or the small GTPase Cdc42 instead of phosphorylating Smad. These Smad-independent pathways stimulate cell migration and axon growth (Wrana 2013; Yam and Charron 2013). To examine whether *Bcl-2*-mediated neurite outgrowth is dependent on *Bmp/Smad* signaling, we used anti-*Bmp4* antibody to neutralize the secreted *Bmp4*. As shown in Fig. S3, *Bcl-2*-induced upregulation of *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1* was reduced by *Bmp4* neutralization in a dose-dependent

manner. However, neither *Bcl-2* overexpression nor *Bmp4* neutralization affected the expression of both *Id1* and *Id2* in H19-7 cells. These results indicate that while *Bmp4* induced by *Bcl-2* overexpression can act in an autocrine or paracrine manner after being secreted into the extracellular space, the Smad-dependent canonical pathway is not associated with *Bcl-2*-mediated neurite formation.

Tbx3 is Also Associated with the Process of Neurite Outgrowth Induced by *Bcl-2* Overexpression

Tbx3 is Also Associated with the Process of Neurite Outgrowth Induced by *Bcl-2* Overexpression

The T-box family of transcription factors, which are characterized by a common DNA binding motif termed as the T-box, are involved in embryonic developmental processes by regulating cell differentiation and migration (Naiche et al. 2005; Papaioannou 2014). In particular, several subfamilies of T-box genes are essential for brain development and their mutations are associated with neurodevelopmental disorders such as autism spectrum disorders (Mihalas and Hevner 2017). Among them, *Tbx3* is involved in various signaling pathways related to the pluripotency network and has a critical role in the maintenance of the embryonic stem cells during early cell fate specification (Russell et al. 2015). In order to investigate how *Tbx3* impacts other genes during

Bcl-2-mediated neurite outgrowth, we transfected 100 nM of control or *Tbx3* siRNA into *Bcl-2*-overexpressing H19-7 cells. We observed that *Bcl-2*-induced neurite outgrowth was significantly repressed by *Tbx3* depletion (Fig. 5a, b). Moreover, *NeuroD1*, *NeuroD2*, and *Mash1* that were induced by *Bcl-2* overexpression were downregulated by *Tbx3* knock-down, while there was no significant change in the expression of *Bcl-2* and *Bmp4* (Fig. 5c, d). These alterations also coincided with changes in protein levels (Fig. 5e, f). We demonstrated that *Tbx3* could mediate the neurite outgrowth by controlling the expression of neurogenic bHLH genes downstream of *Bmp4* during Bcl-2-mediated neuronal differentiation.

NeuroD1 is a Key Downstream Regulator of Bcl-2-Mediated Neurite Outgrowth in H19-7 Cells

bHLH proteins possess an HLH domain that enables dimerization and a basic domain for DNA binding (Dennis et al. 2019). bHLH transcription factors are hetero-dimerized with E proteins, which in turn bind to the E-box DNA elements to promote the expression of neurogenic target genes, and their transcriptional activities are inhibited by interaction with the

Hes or Id families (Ross et al. 2003). As mentioned previously, we established that Bcl-2 regulated neurite outgrowth by increasing the levels of the proneural bHLH transcription factors, including *NeuroD1*, *NeuroD2*, and *Mash1*, without changing the expression of Id. *NeuroD1* is highly accumulated in late development stage of the nervous system and is an essential participant in terminal differentiation, neuronal maturation, and survival (Gao et al. 2009). *NeuroD1* also triggers neuronal specification by reprogramming the transcription factor and chromatin landscapes at regulatory elements of neurogenic target genes (Pataskar et al. 2016). To verify the function of *NeuroD1*, we transfected 100 nM of *NeuroD1* siRNA into *Bcl-2*-overexpressing H19-7 cells. *Bcl-2*-induced neurite elaboration was significantly suppressed by *NeuroD1* knockdown (Fig. 6a, b). However, *NeuroD1* depletion did not influence the expression of other genes (*Bcl-2*, *Bmp4*, *Tbx3*, *NeuroD2*, and *Mash1*) at the mRNA level (Fig. 6c, d). This indicates that *NeuroD1* functions independently from other bHLH genes during Bcl-2-mediated neurite outgrowth. Moreover, we found that the protein expression levels of Bcl-2, *Bmp4*, and *Tbx3* did not show any significant changes by the *NeuroD1* knockdown (Fig. 6e, f). In conclusion, we demonstrated that *Bcl-2* overexpression

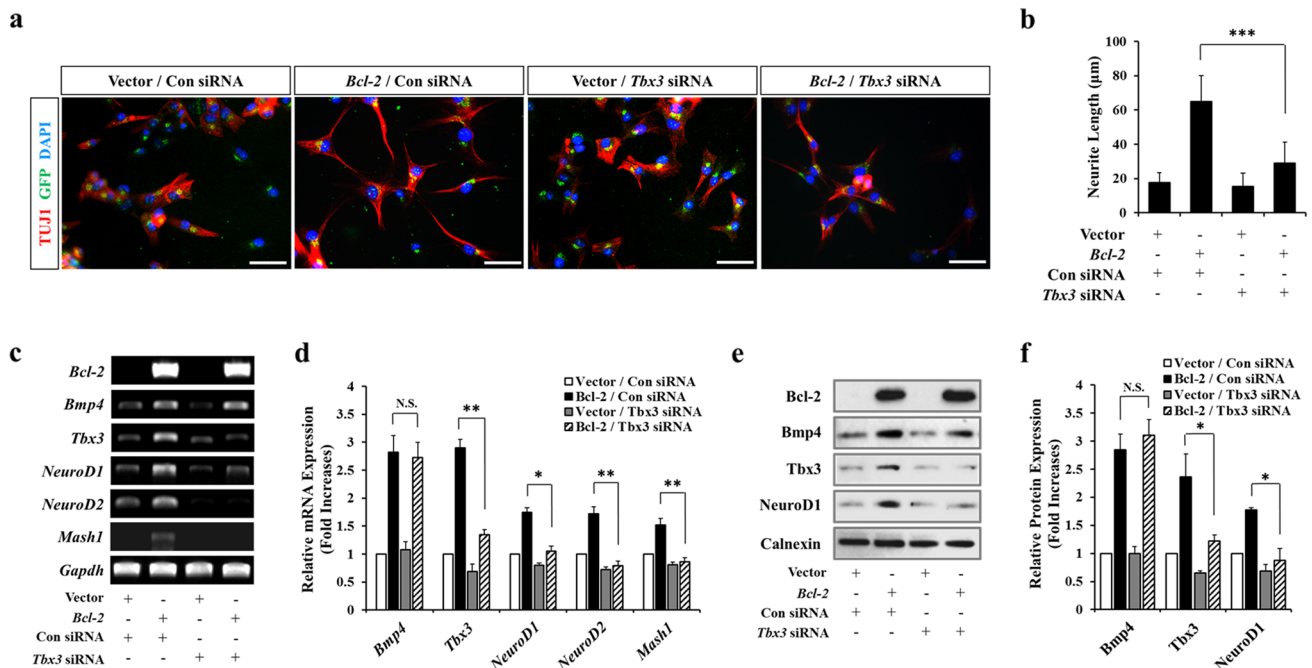


Fig. 5 Effect of *Tbx3* gene depletion in *Bcl-2*-overexpressing H19-7 cells. **a** Cells were infected with MSCV-IRES-EGFP or *rBcl-2*-MSCV-IRES-EGFP via retroviral transduction for 2 days followed by transfection with control or *Tbx3* siRNA. The cells were then immunostained for TUJ1 and GFP. Scale bar, 50 μm. **b** Neurite length was measured. The results are presented as the mean ± SD of three independent experiments. *** $p < 0.001$. **c, d** Total RNA was isolated using Trizol reagent, and mRNA levels of *Bcl-2*, *Bmp4*, *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1* were determined using RT-PCR (c) and real-time RT-PCR (d). The results are presented as the mean ± SD of three independent experiments. * $p < 0.05$, ** $p < 0.01$. **e, f** Cells were lysed, and immunoblotting was performed using anti-Bcl-2, anti-Bmp4, anti-Tbx3, anti-NeuroD1, and anti-Calnexin antibodies. The results are presented as the mean density (as a fold increase) ± SD from three independent experiments. * $p < 0.05$

roD1, *NeuroD2*, and *Mash1* were determined using RT-PCR (c) and real-time RT-PCR (d). The results are presented as the mean ± SD of three independent experiments. * $p < 0.05$, ** $p < 0.01$. **e, f** Cells were lysed, and immunoblotting was performed using anti-Bcl-2, anti-Bmp4, anti-Tbx3, anti-NeuroD1, and anti-Calnexin antibodies. The results are presented as the mean density (as a fold increase) ± SD from three independent experiments. * $p < 0.05$

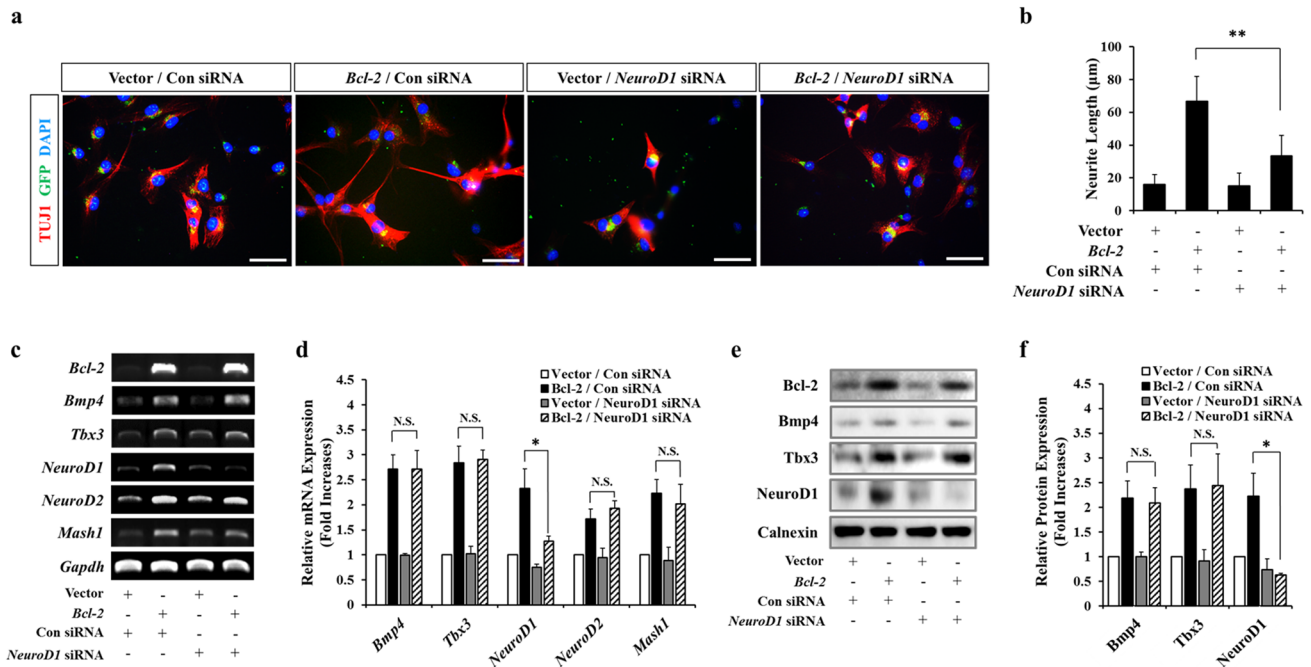


Fig. 6 Effect of *NeuroD1* gene depletion in *Bcl-2*-overexpressing H19-7 cells. **a** Cells were infected with MSCV-IRES-EGFP or *rBcl-2*-MSCV-IRES-EGFP through retroviral transduction for 2 days followed by transfection with control or *NeuroD1* siRNA. The cells were then immunostained for TUJ1 and GFP. Scale bar, 50 μm. **b** Neurite length was measured. The results are presented as the mean ± SD of three independent experiments. ** $p < 0.01$. **c, d** Total RNA was isolated using Trizol reagent, and mRNA levels of *Bcl-2*,

Bmp4, *Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1* were determined using RT-PCR (**c**) and real-time RT-PCR (**d**). The results are presented as the mean ± SD of three independent experiments. * $p < 0.05$. **e, f** Cells were lysed, and immunoblotting was performed using anti-*Bcl-2*, anti-*Bmp4*, anti-*Tbx3*, anti-*NeuroD1*, and anti-Calnexin antibodies. The results are presented as the mean density (as a fold increase) ± SD from three independent experiments. * $p < 0.05$

promotes neurite formation via the *Bmp4*/*Tbx3*/*NeuroD1* pathway in H19-7 cells.

Discussion

Multipotent neural stem cells can give rise to all types of neural cells through asymmetric cell division, including neurons, astrocytes, and oligodendrocytes in the mammalian nervous system (Gage 2000; Paridaen and Huttner 2014). They are spatiotemporally controlled by intrinsic or extrinsic factors found in the neural stem cell niche (Paridaen and Huttner 2014). In particular, bFGF is a necessary stem cell mitogen required for proliferation and neurogenesis during the development of the nervous system (Raballo et al. 2000). It interacts with receptor tyrosine kinase FGFRs (FGF receptors) on the cell surface and triggers various cellular processes by activating downstream molecules including Ras, phospholipase C, and phosphoinositide 3-kinase via tyrosine phosphorylation of the adaptor protein FRS2 (FGF receptor substrate 2) (Schlessinger 2004). We previously reported that PLD1 plays an important role in bFGF signaling involved in neuronal differentiation in rat hippocampal

progenitor cells. PLD1 is activated by Src and Ras during bFGF-induced neurite outgrowth and regulates neurotrophin-3 expression through the RhoA/ROCK/JNK/EI1 pathway in H19-7 cells (Oh et al. 2007; Choi et al. 2012). Furthermore, PLD1 upregulates *Bcl-2* expression through the PLA2/Cox2/EP4/PKA/p38MAPK/CREB cascade in rat NPCs and through the JNK/STAT3 pathway in H19-7 cells during neuronal differentiation (Park et al. 2014; Yoon et al. 2012). This indicates that PLD1-mediated *Bcl-2* expression is required in bFGF signaling for neuronal fate determination of NPCs. However, the mechanism by which *Bcl-2* influences neuronal differentiation is not fully understood.

Bcl-2 is generally regarded as an anti-apoptotic protein that prevents the cytosolic release of apoptogenic factors, including cytochrome *c*, in the mitochondrial outer membrane (Adams and Cory 1998; Pan et al. 2014, 2015). Many previous reports have shown the neuroprotective effects of *Bcl-2* against environmental insults such as ischemia (Martinou et al. 1994). Moreover, the interaction of *Bcl-2* with calcineurin can inhibit Ca^{2+} release by suppressing IP₃R (inositol 1,4,5-triphosphate receptor) through the phosphatase cascade of DARPP-32 (dopamine and cAMP-regulated phosphoprotein-32)/PP1α (protein phosphatase 1

alpha) on the endoplasmic reticulum (ER) (Tang et al. 2003; Erin et al. 2003). These mechanisms may also be involved in neuropsychiatric disorders. *Bcl-2* rs956572 polymorphism has been found to be associated with dysfunction of intracellular Ca^{2+} homeostasis and the cortical glutamatergic system in the pathophysiology of type I bipolar disorder (Uemura et al. 2011; Soeiro-de-Souza et al. 2013). Moreover, mood-stabilizing agents, such as lithium and valproate, increase *Bcl-2* expression in the rat CNS (Chen et al. 1999). *Bcl-2* family proteins are involved in the development of resistance against therapy-induced apoptosis during the treatment of several types of brain cancers such as malignant glioblastoma (Strik et al. 1999; Fels et al. 2000). Taken together, this strongly indicates the possibility that *Bcl-2* can be a potential therapeutic target. Recently, the use of the BH3-mimetic drug Venetoclax (ABT-199) is on the rise as a *Bcl-2* inhibitor in various fields including clinical lymphoma therapy (King et al. 2017). However, it still needs to be confirmed whether this drug can also be used to treat brain cancer. In addition, studies using various cancer models have suggested that *Bcl-2* expression is intimately regulated by PLD1, indicating that targeting PLD1 might have robust anticancer effects via the inhibition of *Bcl-2* function (Cho et al. 2008). The small-molecule PLD1 inhibitor FIPI shows remarkable preclinical efficacy for the treatment of colorectal cancer (Kang et al. 2015), and the peptide drug TVTSP, a PLD1-specific inhibitor, was recently verified as an efficient therapeutic agent for several types of cancer and other inflammatory conditions (Cho et al. 2011; Lee et al. 2018). Therefore, detailed research needs to be done in the future to evaluate if these drugs can also be considered as potential therapeutics for several brain disorders.

Apart from its neuroprotective function, *Bcl-2* mediates neurogenesis for the developing CNS and the regenerating adult nervous system (Michaelidis et al. 1996; Zhang et al. 1996; Hilton et al. 1997; Chen et al. 1997). However, it is unclear whether *Bcl-2* exerts its neuroprotective effect by merely providing sufficient time for neurogenesis of NPCs by protecting them from cell death. Loss of *Bcl-2* function represses neurite elaboration in response to differentiation stimuli, and inversely, gain of *Bcl-2* function enhanced neurite outgrowth (Fig. 1), indicating that *Bcl-2* is strongly involved in the neuronal differentiation process. Next, we sought to determine how *Bcl-2* impacts neurite outgrowth. According to previous reports, *Bcl-2* overexpression increases synaptosomal-associated protein 25 (SNAP-25) in a dopaminergic neuronal cell line (Oh et al. 1996). Moreover, Suzuki and Tsutomi (1998) suggested that *Bcl-2* controls neuronal differentiation by accelerating polymerization of neurofilament chains, and Chang et al. (2007) reported that *Bcl-X_L* overexpression induces proneural bHLH genes (*Ngn1*, *NeuroD1*, and *Mash1*) and suppresses anti-neuronal bHLH genes (*Hes1/5* and *Id1/2/3*) without

changing the expression of the Notch signaling genes. Therefore, we analyzed the whole-genome expression profiles of rat NPCs to compare the genes that were altered by differentiation stimuli and the genes affected by *Bcl-2* overexpression. Similar to the differentiated control group, *Bcl-2* overexpression increased many neurogenic marker genes (Fig. 2b). In particular, proneural bHLH genes, including *NeuroD2*, *Neurog2*, and *Mash1*, were upregulated. When *Bcl-2* was overexpressed in H19-7 cells, neurite length was significantly increased, and *NeuroD1*, *NeuroD2*, and *Mash1* were also upregulated (Fig. 3). However, the expression of *Neurog1* and *Neurog2* was not affected (data not shown). These results imply that *Bcl-2* overexpression has a direct impact on the neuronal differentiation through upregulation of neurogenic bHLH genes. Additionally, we found that *Bcl-2* overexpression significantly increased *Bmp4* and *Tbx3* expression, indicating that *Bmp4*, *Tbx3*, and several bHLH transcription factors are included in *Bcl-2*-mediated neurite outgrowth.

To investigate the hierarchy of these molecules, we selectively depleted *Bmp4*, *Tbx3*, or *NeuroD1* in *Bcl-2*-overexpressing H19-7 cells. When *Bmp4* was depleted, *Bcl-2*-mediated neurite formation was significantly repressed, and *Tbx3* and *NeuroD1* were downregulated (Fig. 4), indicating that *Bmp4* is required for *Bcl-2*-mediated neurite outgrowth by regulating *Tbx3* and *NeuroD1*. *Bmp4* induces neuronal differentiation in the neocortical ventricular zone (Li et al. 1998; Moon et al. 2009). However, many reports suggest that BMPs might induce astroglial fate specification (Mehler et al. 1997; Gross et al. 1996). It is thought that this discrepancy occurs due to the dependency of *Bmp4* on Smad. Extracellularly secreted *Bmp4* activates Smad1/5/8 protein by binding to BMP receptors on the cell surface, which facilitates Smad1/5/8 to act as a transcriptional regulator and induce the expression of the target genes including *Id* (Wrana 2013; Miyazono and Miyazawa 2002). Conversely, *Bmp4* can induce axon growth by activating LIMK or the small GTPase *Cdc42* without Smad phosphorylation (Wrana 2013; Yam and Charron 2013). In this study, *Bmp4* neutralization downregulated its downstream genes (*Tbx3*, *NeuroD1*, *NeuroD2*, and *Mash1*) without affecting the expression of *Id1* and *Id2* (Fig. S3). In addition, Smad1 was not phosphorylated by *Bcl-2* overexpression (data not shown). These results indicate that although the Smad-dependent canonical pathway might not be associated with *Bcl-2*-mediated neurite formation, *Bmp4* functions in an autocrine or paracrine manner after being secreted into the extracellular space. *Bcl-2* also increases stroke-induced striatal neurogenesis in adult brains by modulating *Bmp4* function via activation of β -catenin signaling (Lei et al. 2012). The expression of *Bmp4* induced by *Bcl-2* overexpression has been thought to be mediated by Wnt/ β -catenin signaling. We also found that *Tbx3* acts downstream of *Bmp4* and controls neurite

outgrowth by increasing the expression of the neurogenic bHLH genes during Bcl-2-mediated neuronal differentiation (Fig. 5). Bmp4 has been shown to induce Tbx3 expression in the pathophysiology of glomerular diseases (Wensing and Campos 2014), and β -catenin reinforces the pluripotency by activating Oct-4 via a TCF-independent mechanism, which induces the expression of Tbx3 as a Oct-4 target gene (Kelly et al. 2011). Moreover, Tbx3 mediates TGF- β 1-induced anti-proliferative and pro-migratory effects in breast epithelial cells by repressing Tbx2 transcription, which allows for the derepression of p21 and a G1 cell cycle arrest (Li et al. 2013). Finally, while Bcl-2-mediated neurite outgrowth was significantly suppressed by *NeuroD1* knockdown, the expression of other genes was not altered (Fig. 6). This indicates that *NeuroD1* functions independently of other bHLH genes during Bcl-2-mediated neurite outgrowth and that *Bcl-2* overexpression promotes neurite elaboration via the Bmp4/Tbx3/*NeuroD1* pathway. Taken together, this study shows that Bcl-2 may have a direct role in neuronal differentiation in addition to its well-known anti-apoptotic function in response to environmental insults.

Conclusions

We demonstrated that *Bcl-2* overexpression induces neurite outgrowth through the Bmp4/Tbx3/*NeuroD1* cascade, thereby contributing to understanding of the non-apoptotic function of Bcl-2 during neuronal differentiation.

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Author Contributions YY Lee conceptualized and designed of the study, collected and assembled the data, analyzed and interpreted the results, and wrote the manuscript. H-J Choi conceptualized and designed the study and provided financial support. SY Lee analyzed the microarray data and performed some of the experiments. S-Y Park analyzed and interpreted the results. M-J Kang conducted some of the experiments. J Han analyzed the microarray data. J-S Han conceptualized and designed the study, analyzed and interpreted the data, wrote the manuscript, and provided financial support. All authors read and approved the final manuscript.

Compliance with Ethical Standards

Conflict of interest The authors declare that they have no conflicts of interest.

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