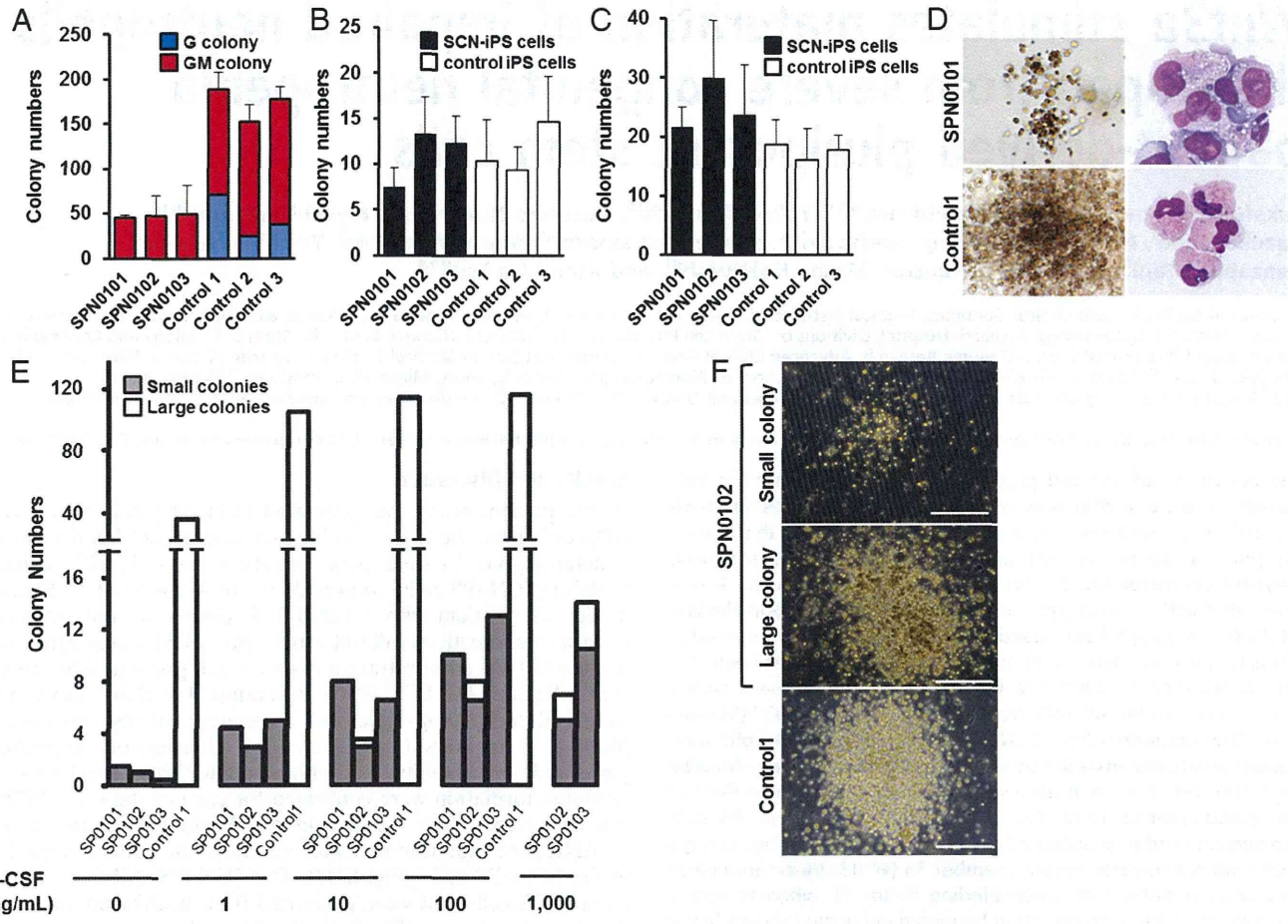

Fig. 1. Impaired neutrophil development from SCN-iPS cells. (*A–C*) A hematopoietic colony assay was performed by using 1×10^4 $CD34^+$ cells derived from three SCN-iPS cell clones (SPN0101, SPN0102, and SPN0103) and three control iPS cell clones (controls 1, 2, and 3) in the presence of a cytokine mixture. Colonies were sorted as myeloid (*A*), erythroid (*B*), and mixed-lineage (Mix) (*C*). Data are shown as mean ± SD. (*D*) Photographs of colonies (*Left*; 100×) and cells in a GM colony (*Right*; 400×; May–Grünwald–Giemsa staining). (*E*) A hematopoietic colony assay with dose escalation of G-CSF was performed by using 1×10^5 $CD34^+$ cells derived from SCN-iPS and control iPS cells. Filled and open bars indicate small colonies consisting of <100 cells and large colonies consisting of >100 cells, respectively. Data are shown as the average of three independent experiments. (*F*) Photographs of a small colony derived from SCN-iPS cells (SPN0102) in the presence of 10 ng/mL G-CSF, large colonies derived from SCN-iPS cells in the presence of 1,000 ng/mL G-CSF, and large colonies derived from control iPS cells (control 1) in the presence of 10 ng/mL G-CSF. (Scale bars, 200 μm.)

and *D*). In particular, only a few SCN-iPS cell-derived granulocyte (G) colonies—myeloid colonies consisting of only granulocytes—were detected (Fig. 1*A*). SCN-iPS cell-derived granulocyte–macrophage (GM) colonies—myeloid colonies consisting of macrophages/monocytes with/without granulocytes—contained a few immature myeloid cells in addition to macrophages/monocytes, whereas control iPS cell-derived GM colonies included a substantial number of mature, segmented, and band neutrophils (Fig. 1*D*).

We also found that Mix colonies derived from SCN-iPS cells, but not control iPS cells, contained immature myeloid cells and few mature neutrophils (Fig. S2 *C* and *D*). Next, we conducted a hematopoietic colony assay using various concentrations of G-CSF alone instead of the cytokine mixture to examine the G-CSF dose dependency of neutrophil differentiation from SCN-iPS and control iPS–$CD34^+$ cells. For all concentrations of G-CSF used (1–1,000 ng/mL), the SCN-iPS cell-derived myeloid colonies were significantly lower in number and smaller in size than the control iPS cell-derived myeloid colonies (Fig. 1*E*). Myeloid colony formation from control iPS cells reached a plateau at ~1–10 ng/mL G-CSF, whereas the number and size of those from SCN-iPS cells gradually increased with increasing concentrations of G-CSF. However, the values observed for SCN-iPS cells did not reach those for the control iPS cells, even at the highest dose of G-CSF used (1,000 ng/mL). Furthermore, large colonies consisting of >100 cells derived from SCN-iPS cells were only found with higher concentrations of G-CSF (Fig. 1*F*). Thus, granulopoiesis initiated from SCN-iPS cells was relatively insensitive to G-CSF, reflecting the inadequate in vivo response of neutrophils to G-CSF in SCN patients (14, 15). Therefore, these results support the applicability of the SCN-iPS cells established herein as a disease model for SCN.

To examine neutrophil development from SCN-iPS cells in more detail, SCN-iPS and control iPS–$CD34^+$ cells (1×10^4 cells each) were cocultured in suspension with AGM-S3 cells in the presence of neutrophil differentiation medium (*SI Materials and Methods*). The number of nonadherent cells derived from SCN-iPS–$CD34^+$ cells was lower than that from control iPS–$CD34^+$ cells on day 14 of culture (SCN-iPS cells, $9.77 \times 10^4 \pm 1.65 \times 10^4$ cells; control iPS cells, $52.48 \times 10^4 \pm 23.13 \times 10^4$ cells; $P < 0.05$) (Fig. 2*A*). The proportion of mature neutrophils among the nonadherent cells was also significantly lower for SCN-iPS cells relative to control iPS cells on day 14 (SPN-iPS cells, 15.53% ± 4.33%; control iPS cells, 71.285 ± 3.30%; $P < 0.05$) (Fig. 2 *B* and *C*), indicating that myeloid cells derived from SCN-iPS cells revealed the maturation arrest in the neutrophil development. We then examined a possibility that the maturation arrest in SCN-

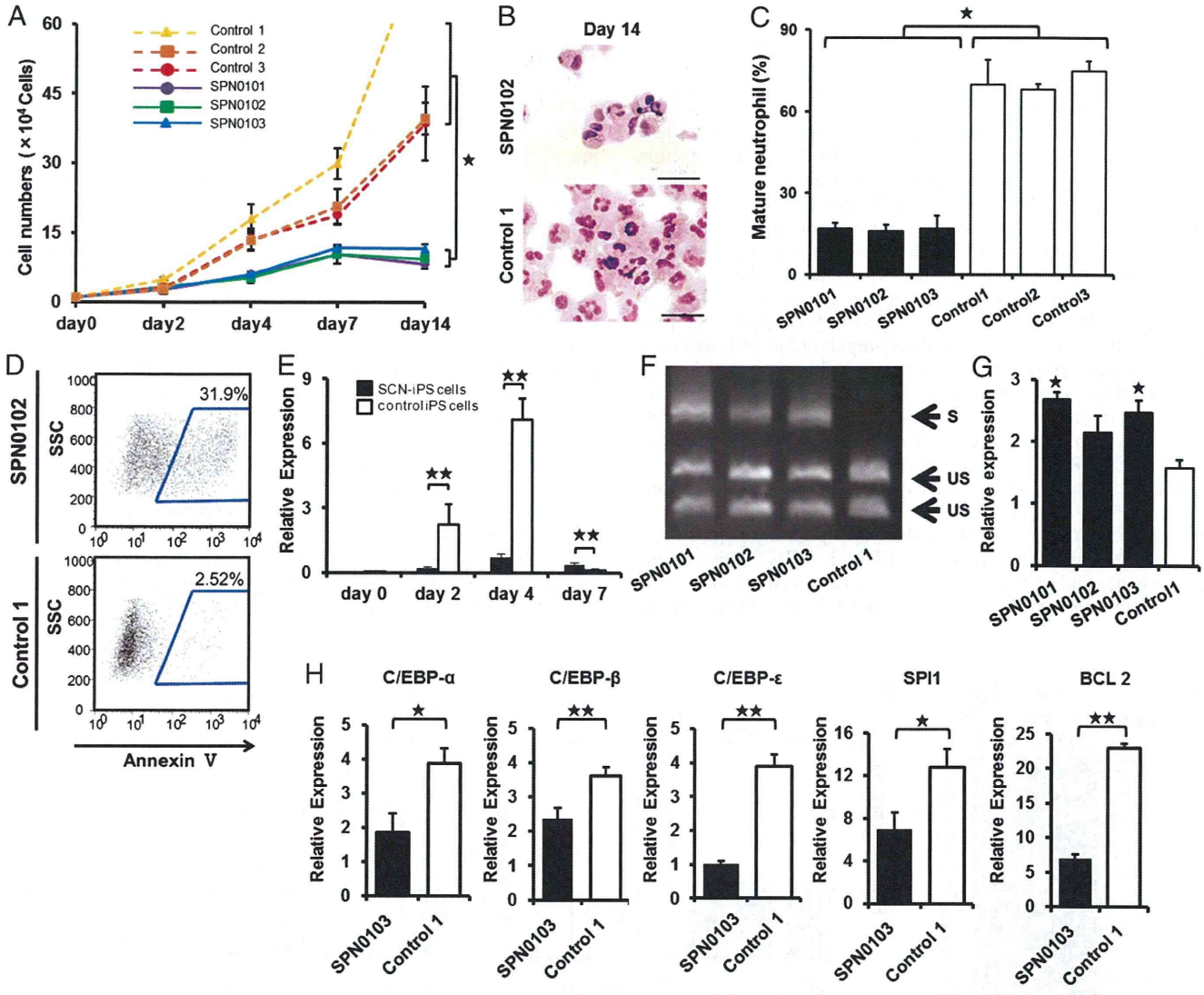

Fig. 2. Analysis of impaired neutrophil development from SCN-iPS cells. (*A*) Total number of nonadherent cells in the suspension culture of 1×10^4 $CD34^+$ cells derived from SCN-iPS and control iPS cells. Data are shown as mean ± SD. $^*P < 0.01$. (*B*) Photographs of nonadherent cells derived from SCN-iPS (SPN0103) and control iPS cells (control 1) on day 14 of culture (400×; May–Grünwald–Giemsa staining; scale bars, 50 μm.) (*C*) Filled and open bars show the proportion of mature neutrophils among the cells derived from SCN-iPS (filled bars) and control iPS (open bars) cells on day 14 of suspension culture. Data are shown as mean ± SD. $^*P < 0.05$. (*D*) Flow cytometric analysis of annexin V expression on cultured cells from SCN-iPS cells (SPN0102) or control iPS cells (control 1) on day 7. (*E*) Sequential qRT-PCR analysis of the relative expression of ELANE mRNA [ELANE/hypoxanthine–guanine phosphoribosyltransferase (HPRT) expression]. Data obtained from independent experiments using three SCN-iPS cell clones (SPN0101, SPN0102, and SPN0103) and three control iPS cell clones are shown as mean ± SD. $^{**}P < 0.01$. (*F* and *G*) $CD34^+$ cells derived from SCN-iPS or control iPS cells were cultured in neutrophil differentiation medium (see text). On day 7, nonadherent cells were collected and analyzed. (*F*) Representative gel showing spliced (S) and unspliced (US) XBP-1 bands on day 7. (*G*) qRT-PCR analysis of the relative mRNA expression (target/HPRT expression) of BiP on day 7. Data are shown as mean ± SD. $^*P < 0.05$; different from control 1). (*H*) qRT-PCR analysis of the relative mRNA expression (target / HPRT expression) of C/EBP-α, C/EBP-β, C/EBP-ε, SPI1, and BCL2 genes in non-adherent cells derived from SCN-iPS cells (filled bars, SPN0103) and control iPS cells (open bars, control 1) on day 2 of suspension culture. Data are shown as the mean ± the s.d. ($^{**}P < 0.01$, $^*P < 0.05$).

iPS cell-derived myeloid cells might be caused by their apoptosis. In flow cytometric analysis, SCN-iPS cell-derived myeloid cells contained a significantly higher proportion of annexin V-positive cells than control iPS-derived myeloid cells on day 7 of culture, suggesting that the maturation arrest in myeloid cells derived from SCN-iPS cells might be caused by their apoptosis (Fig. 2*D*).

We next examined ELANE mRNA expression levels in nonadherent cells derived from SCN-iPS vs. control iPS cells (Fig. 2*E*). ELANE expression was significantly lower in nonadherent cells derived from SCN-iPS vs. control iPS cells on days 2 and 4 of culture ($P < 0.01$), as reported (16, 17). However, the former was a little higher than the latter on day 7 ($P < 0.01$). This result may be explained by the existence of SCN-iPS cell-derived myeloid cells arrested at an early stage along the neutrophil differentiation pathway even on day 7 of culture. We also examined the expression of proteinase 3 and azurocidin, which comprise a family of closely related genes encoding neutrophil granule proteins along with ELANE, and found these genes were more highly expressed on day 4 (Fig. S3).

It has been reported that induction of the endoplasmic reticulum stress (ER) response and the unfolded protein response (UPR) has been advanced as a potential explanation for the molecular pathogenesis of SCN (18, 19). Thus, we examined activation of the UPR by X-box binding protein 1 (XBP-1) mRNA splicing on day 7. As shown in Fig. 2*F*, SPN-iPS cells induced XBP-1 mRNA splicing. We also found the up-regulation of BiP

(also known as GRP78 or HSPA5) (Fig. 2*G*). These results suggested that ER stress response and UPR might be involved in the pathogenesis in SCN.

To examine further the differences in gene expression between the two cell types, a microarray analysis was carried out by using $CD34^+$ cells derived from SCN-iPS and control iPS cells (three clones of each) in suspension culture on day 2. At this early time point, differences in cell number and morphology were not yet readily discernible between SCN-iPS and control iPS cells, as shown in Fig. 2*A*. However, the microarray analysis revealed a differential expression of various genes between the two cell types. Transcription factor genes, which were related to neutrophil development [e.g., CCAAT/enhancer-binding protein (C/EBP)-α (20), C/EBP-β (21), C/EBP-ε (22), and SPI1 (also known as PU.1) (23)], were all down-regulated in SCN-iPS cells. B-cell chronic lymphocytic leukemia/lymphoma 2, which regulates cell death under ER stress through the core mitochondrial apoptosis pathway (24), was also down-regulated (Fig. 3*A*). These findings were confirmed by quantitative reverse-transcriptional PCR (qRT-PCR), as shown in Fig. 2*H*.

Notably, the down-regulation of the genes in SCN-iPS cells related to and regulated by the wingless-type mmtv integration site family, member 3a (Wnt3a)/β-catenin pathway [e.g., Wnt3a, lymphoid enhance-binding factor (LEF)-1, BIRC5 (also known as survivin), and cyclin D1] was also uncovered by microarray analysis and qRT-PCR (Fig. 3 *A*–*C* and Fig. S4). Therefore, we examined the effect of enhancement of Wnt3a/β-catenin signaling by exogenous Wnt3a addition on the neutrophil development of $CD34^+$ cells derived from SCN-iPS and control iPS cells. Although Wnt3a did not stimulate the survival, proliferation, and differentiation of $CD34^+$ cells derived from both iPS cells in the absence of cytokines stimulating myelopoiesis including G-CSF, the addition of Wnt3a to the neutrophil differentiation medium induced a dose-dependent increase in the percentage of mature neutrophils among the cultured cells, as shown in Fig. 3 *D* and *E*. Furthermore, when Wnt3a was added concurrently with 1,000ng/mL G-CSF, the proportion of mature neutrophils increased more than it did with Wnt3a or 1,000 ng/mL G-CSF alone, reaching a value comparable with that observed for control iPS cells (Fig. 4 *A* and *B*).

The reduced expression of LEF-1 (as regulated by the Wnt3a/β-catenin pathway) reportedly plays a critical role in the defective maturation of neutrophils in SCN patients (25). Therefore, we next examined LEF-1 mRNA expression in SCN-iPS–$CD34^+$ cells cultured in the presence of Wnt3a, G-CSF (1,000 ng/mL), or both. Wnt3a and G-CSF both enhanced LEF-1 mRNA expression, but the most significant increase was observed in the presence of Wnt3a plus G-CSF. LEF-1 expression in SCN-iPS–$CD34^+$ cells in response to Wnt3a plus G-CSF was almost the same as that in control iPS–$CD34^+$ cells (Fig. 4*C*). These results substantiate the importance of LEF-1 in neutrophil development and the pathogenesis of SCN, as shown (25). Moreover the

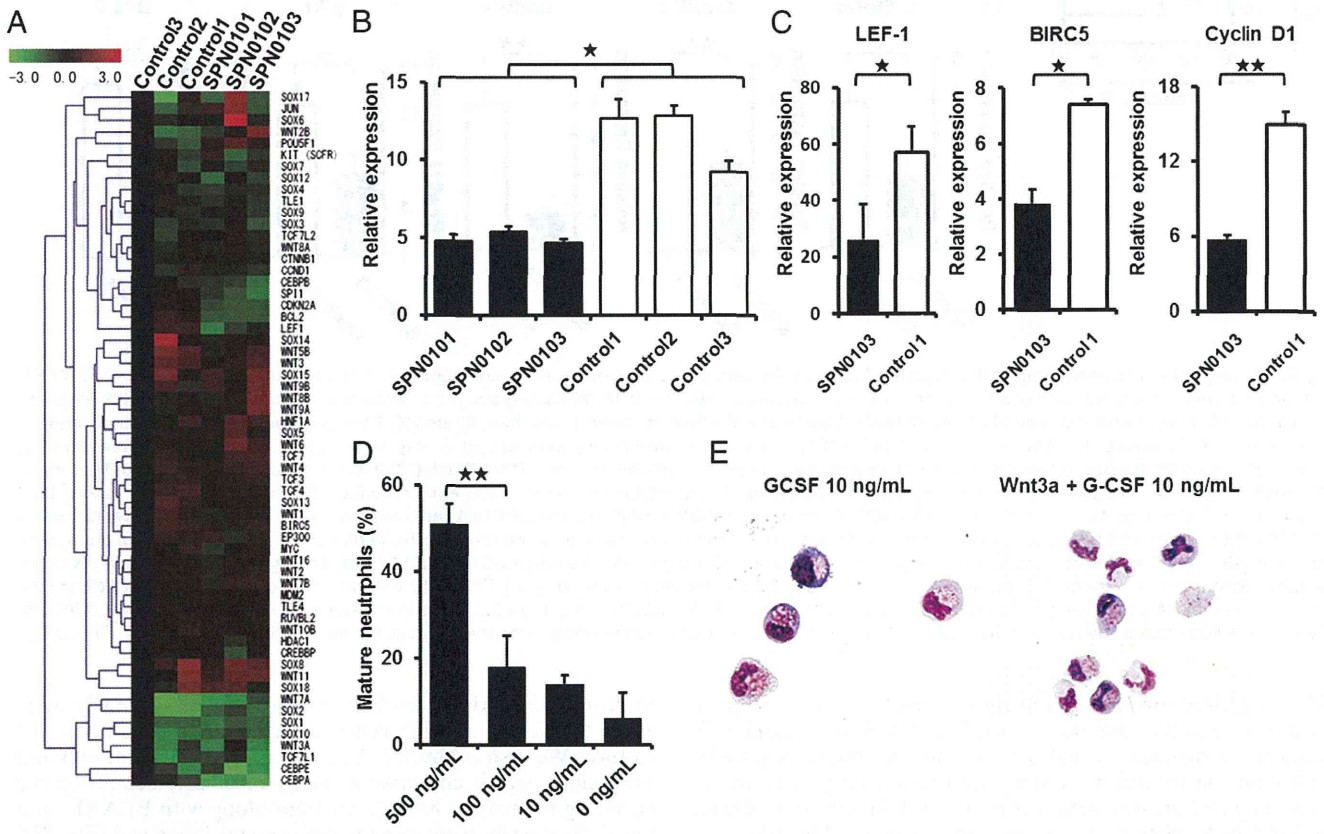

Fig. 3. Effects of Wnt3a on neutrophil development from SCN-iPS cells. (*A*) Heat map showing differential gene expression among SCN-iPS and control iPS cells on day 2. Red, high gene expression; blue, low gene expression compared with gene expression in control 3. (*B*) qRT-PCR analysis of the relative mRNA expression (target/HPRT expression) of Wnt3a on day 2. Filled and open bars indicate experiments using SCN-iPS cells (SPN0101, SPN0102, and SPN0103) and control iPS cells (controls 1, 2, and 3), respectively. Data are shown as mean ± SD. $^{\star}P < 0.05$. (*C*) qRT-PCR analysis of the relative expression (target/HPRT expression) of genes regulated by the Wnt3a/β-catenin pathway (LEF-1, survivin, and cyclin D1) in SCN-iPS cells (filled bars, SPN0103) vs. control iPS cells (open bars, control 1) on day 2 of suspension culture. Data are shown as mean ± SD. $^{\star\star}P < 0.01$; $^{\star}P < 0.05$. (*D*) Proportion of mature neutrophils among the cells derived from SCN-iPS cells (SPN0102) on day 14 of suspension culture with dose escalation of Wnt3a. Data are shown as mean ± SD. $^{\star\star}P < 0.01$. (*E*) Photographs of nonadherent cells on day 7 of suspension culture with or without Wnt3a (500 ng/mL) (400×; May–Grünwald–Giemsa staining).

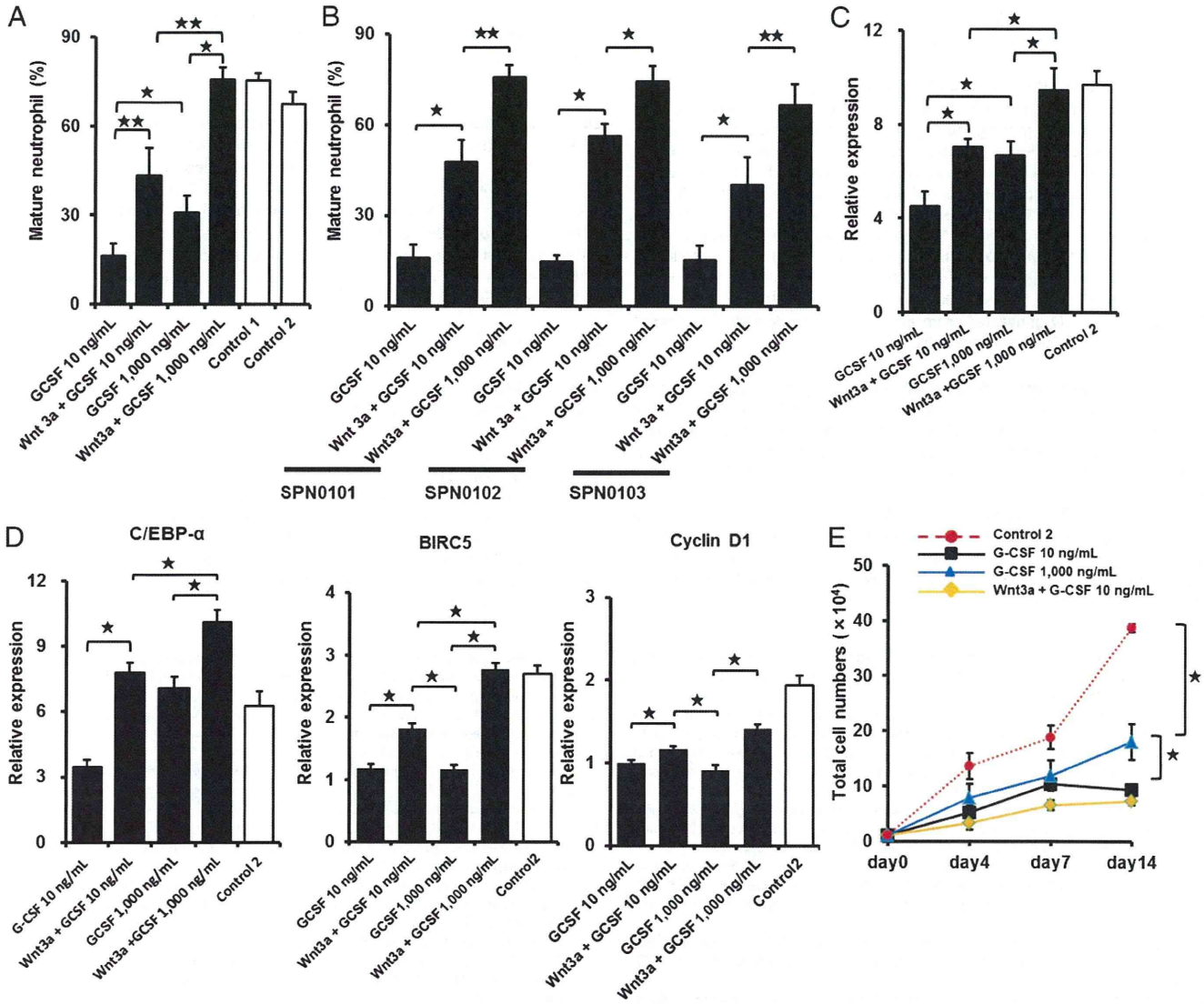

Fig. 4. Effects of Wnt3a in combination with high-dose G-CSF. (*A*) Filled and open bars show the proportion of mature neutrophils among the cells derived from SCN-iPS cells (SPN0101) on day 14 of suspension culture in the presence of neutrophil differentiation medium containing 10 ng/mL G-CSF (GCSF 10 ng/mL); 500 ng/mL Wnt3a and 10 ng/mL G-CSF (Wnt3a+GCSF 10 ng/mL); 1,000 ng/mL G-CSF (GCSF 1,000 ng/mL); or 500 ng/mL Wnt3a and 1,000 ng/mL G-CSF (Wnt3a + GCSF 1,000 ng/mL); and that from control iPS cells (controls 1 and 2) cultured in the neutrophil differentiation medium containing 10 ng/mL G-CSF, respectively. Data are shown as mean ± SD. $^{**}P < 0.01$; $^{*}P < 0.05$. (*B*) The proportion of mature neutrophils among the cells derived from three SCN-iPS cell clones (SPN0101, SPN0102, and SPN0103) on day 14 of suspension culture in the presence of neutrophil differentiation medium containing 10 ng/mL G-CSF (GCSF 10 ng/mL); 500 ng/mL Wnt3a and 10 ng/mL G-CSF (Wnt3a+GCSF 10 ng/mL); or 500 ng/mL Wnt3a and 1,000 ng/mL G-CSF (Wnt3a + GCSF 1,000 ng/mL). Data are shown as mean ± SD. $^{**}P < 0.01$; $^{*}P < 0.05$. (*C*) Filled and open bars show the relative expression (target/HPRT expression) of LEF-1 mRNA in SCN-iPS cells (SPN0101) on day 2 of suspension culture in the presence of differentiation medium containing the same combinations of Wnt3a and G-CSF as shown in *A* and that from control iPS cells (control 2), respectively. Data are shown as mean ± SD. $^{**}P < 0.01$; $^{*}P < 0.05$. (*D*) Filled and open bars show the relative expression (target/HPRT expression) of C/EBP-α, BIRC5, or cyclin D1 mRNA in SCN-iPS cells (SPN0101) on day 2 of suspension culture in the presence of differentiation medium containing the same combinations of Wnt3a and G-CSF as shown in *A* and that from control iPS cells (control 2), respectively. Data are shown as mean ± SD. $^{**}P < 0.01$; $^{*}P < 0.05$. (*E*) Total cell numbers of nonadherent cells in suspension cultures of 1×10^4 $CD34^+$ cells derived from control iPS cells (control 2; red broken line) and SCN-iPS cells (SPN0101) in the presence of neutrophil differentiation medium (black line) and those from SCN-iPS cells in the presence of neutrophil differentiation medium containing 500 ng/mL Wnt3a (yellow line) or 1,000 ng/mL G-CSF (black line). Data are shown as mean ± SD. $^{**}P < 0.05$.

administration of Wnt3a led to up-regulate C/EBP-α, cyclin D1, and BIRC5/survivin in addition to LEF-1 in the presence of G-CSF (Fig. 4*D*). These results suggested that the up-regulation of LEF-1 expression might promote granulopoiesis by increasing the expressions of cyclin D1, BIRC5/survivin, and C/EBP-α and its binding to LEF-1 in accordance with the previous report (25). Interestingly, Wnt3a did not stimulate the proliferation of myeloid cells, whereas 1,000 ng/mL G-CSF did to a certain extent (Fig. 4*E*). Hence, Wnt3a was capable of stimulating the maturation of impaired neutrophils in the presence of G-CSF, but not the proliferation of myeloid cells from SCN-iPS cells.

Importantly, aside from providing new insights into the mechanisms behind impaired neutrophil development in SCN patients, the present study demonstrates that agents activating the Wnt3a/β-catenin pathway are potential candidates for new drugs for SCN with mutations in the ELANE gene. Because endogenous G-CSF is readily increased in SCN patients (26), these activating agents may be viable alternatives to exogenous G-CSF treatment.

Materials and Methods

Additional information is available in *SI Materials and Methods*.

Generation of Human iPS Cells. BM fibroblasts from a patient with SCN and skin dermal fibroblasts from a healthy donor were acquired after obtaining informed consent after getting the approval by the Ethics Committee of the Institute of Medical Science, University of Tokyo, in accordance with the Declaration of Helsinki. The SCN patient presented with a heterozygous mutation in the ELANE gene in the 707 region of exon 5. SCN-iPS cells were established from the SCN-BM fibroblasts by transfection with the pMX retroviral vector, as described (10). This vector expressed the human transcription factors OCT3/4, SOX2, KLF4, and c-MYC. Control iPS cell clones, control 1 (TkDN4-M) and control 3 (201B7), were gifts from K. Eto and S. Yamanaka (Kyoto University, Kyoto), respectively (10, 11). Control 2 (SPH0101) was newly generated from another healthy donor's skin dermal fibroblasts by using the same methods.

Hematopoietic Colony Assay. A hematopoietic colony assay was performed in an aliquot of culture mixture, which contained 1.2% methylcellulose (Shin-Etsu Chemical), 30% (vol/vol) FBS, 1% (vol/vol) deionized fraction V BSA, 0.1 mM 2-mercaptoethanol (2-ME), α-minimum essential medium, and a cytokine mixture consisting of 100 ng/mL human stem cell factor (hSCF) (Wako), 100 ng/mL fusion protein 6 [FP6; a fusion protein of interleukin (IL)-6 and IL-6 receptor] (a gift from Tosoh), 10 ng/mL human IL-3 (hIL-3) (a gift from Kirin Brewery), 10 ng/mL human thrombopoietin (hTPO) (a gift from Kirin Brewery), 10 ng/mL human G-CSF (a gift from Chugai Pharmaceutical), and 5 U/mL human erythropoietin (a gift from Kirin Brewery). For dose escalation experiments, various concentrations (0, 1, 10, 100, and 1,000 ng/mL) of G-CSF were used instead of the cytokine mixture described above. Colony types were determined according to established criteria on day 14 of culture by in situ observations under an inverted microscope (IX70; Olympus) (27).

Suspension Culture and Neutrophil Differentiation Assay. $CD34^+$ cells (1×10^4 cells) were cocultured with irradiate confluent AGM-S3 cells in neutrophil differentiation medium containing Iscove's modified Dulbecco's medium, 10% FBS, 3 mM L-glutamine, 1×10^{-4} M 2-ME, 1×10^{-4} M nonessential amino acids solution, 100 ng/mL hSCF, 100 ng/mL FP6, 10 ng/mL hIL-3, 10 ng/mL hTPO, and 10 or 1,000 ng/mL human G-CSF. Wnt3a (10, 100, or 500 ng/mL) (R&D) was then added. The medium was replaced with an equivalent volume of fresh medium every 4 d. Living, nonadherent cells were counted following 0.4% trypan blue staining.

PCR primer. All primer sets used in this study are shown in Table S1.

Statistical Analysis. All data are presented as mean ± SD. $P < 0.05$ was considered significant. Statistical analyses were performed by using Prism software (GraphPad).

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1. Zeidler C, Germeshausen M, Klein C, Welte K (2009) Clinical implications of *ELA2*-, *HAX1*-, and G-CSF-receptor (*CSF3R*) mutations in severe congenital neutropenia. *Br J Haematol* 144(4):459–467.
2. Freedman MH, et al. (2000) Myelodysplasia syndrome and acute myeloid leukemia in patients with congenital neutropenia receiving G-CSF therapy. *Blood* 96(2):429–436.
3. Dale DC, et al. (1993) A randomized controlled phase III trial of recombinant human granulocyte colony-stimulating factor (filgrastim) for treatment of severe chronic neutropenia. *Blood* 81(10):2496–2502.
4. Rosenberg PS, et al.; Severe Chronic Neutropenia International Registry (2006) The incidence of leukemia and mortality from sepsis in patients with severe congenital neutropenia receiving long-term G-CSF therapy. *Blood* 107(12):4628–4635.
5. Xia J, et al. (2009) Prevalence of mutations in ELANE, GFI1, HAX1, SBDS, WAS and G6PC3 in patients with severe congenital neutropenia. *Br J Haematol* 147(4):535–542.
6. Horwitz MS, et al. (2007) Neutrophil elastase in cyclic and severe congenital neutropenia. *Blood* 109(5):1817–1824.
7. Hajjar E, Broemstrup T, Kantari C, Witko-Sarsat V, Reuter N (2010) Structures of human proteinase 3 and neutrophil elastase—so similar yet so different. *FEBS J* 277(10): 2238–2254.
8. Fouret P, et al. (1989) Expression of the neutrophil elastase gene during human bone marrow cell differentiation. *J Exp Med* 169(3):833–845.
9. Pham CT (2006) Neutrophil serine proteases: Specific regulators of inflammation. *Nat Rev Immunol* 6(7):541–550.
10. Takayama N, et al. (2010) Transient activation of c-MYC expression is critical for efficient platelet generation from human induced pluripotent stem cells. *J Exp Med* 207(13):2817–2830.
11. Takahashi K, et al. (2007) Induction of pluripotent stem cells from adult human fibroblasts by defined factors. *Cell* 131(5):861–872.
12. Germeshausen M, Ballmaier M, Welte K (2007) Incidence of CSF3R mutations in severe congenital neutropenia and relevance for leukemogenesis: Results of a long-term survey. *Blood* 109(1):93–99.
13. Ma F, et al. (2007) Novel method for efficient production of multipotential hematopoietic progenitors from human embryonic stem cells. *Int J Hematol* 85(5):371–379.
14. Konishi N, et al. (1999) Defective proliferation of primitive myeloid progenitor cells in patients with severe congenital neutropenia. *Blood* 94(12):4077–4083.
15. Nakamura K, et al. (2000) Abnormalities of primitive myeloid progenitor cells expressing granulocyte colony-stimulating factor receptor in patients with severe congenital neutropenia. *Blood* 96(13):4366–4369.
16. Skokowa J, Fobiwe JP, Dan L, Thakur BK, Welte K (2009) Neutrophil elastase is severely down-regulated in severe congenital neutropenia independent of ELA2 or HAX1 mutations but dependent on LEF-1. *Blood* 114(14):3044–3051.
17. Kawaguchi H, et al. (2003) Dysregulation of transcriptions in primary granule constituents during myeloid proliferation and differentiation in patients with severe congenital neutropenia. *J Leukoc Biol* 73(2):225–234.
18. Köllner I, et al. (2006) Mutations in neutrophil elastase causing congenital neutropenia lead to cytoplasmic protein accumulation and induction of the unfolded protein response. *Blood* 108(2):493–500.
19. Grenda DS, et al. (2007) Mutations of the ELA2 gene found in patients with severe congenital neutropenia induce the unfolded protein response and cellular apoptosis. *Blood* 110(13):4179–4187.
20. Pabst T, et al. (2001) AML1-ETO downregulates the granulocytic differentiation factor C/EBPalpha in t(8;21) myeloid leukemia. *Nat Med* 7(4):444–451.
21. Hirai H, et al. (2006) C/EBPbeta is required for 'emergency' granulopoiesis. *Nat Immunol* 7(7):732–739.
22. Bedi R, Du J, Sharma AK, Gomes I, Ackerman SJ (2009) Human C/EBP-ε activator and repressor isoforms differentially reprogram myeloid lineage commitment and differentiation. *Blood* 113(2):317–327.
23. Friedman AD (2007) Transcriptional control of granulocyte and monocyte development. *Oncogene* 26(47):6816–6828.
24. Hetz C (2012) The unfolded protein response: Controlling cell fate decisions under ER stress and beyond. *Nat Rev Mol Cell Biol* 13(2):89–102.
25. Skokowa J, et al. (2006) LEF-1 is crucial for neutrophil granulocytopoiesis and its expression is severely reduced in congenital neutropenia. *Nat Med* 12(10):1191–1197.
26. Mempel K, Pietsch T, Menzel T, Zeidler C, Welte K (1991) Increased serum levels of granulocyte colony-stimulating factor in patients with severe congenital neutropenia. *Blood* 77(9):1919–1922.
27. Nakahata T, Ogawa M (1982) Hemopoietic colony-forming cells in umbilical cord blood with extensive capability to generate mono- and multipotential hemopoietic progenitors. *J Clin Invest* 70(6):1324–1328.

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Acute kidney injury after myeloablative cord blood transplantation in adults: the efficacy of strict monitoring of vancomycin serum trough concentrations

H. Mae, J. Ooi, S. Takahashi, S. Kato, T. Kawakita, Y. Ebihara, K. Tsuji, F. Nagamura, H. Echizen, A. Tojo. Acute kidney injury after myeloablative cord blood transplantation in adults: the efficacy of strict monitoring of vancomycin serum trough concentrations. Transpl Infect Dis 2013: **15**: 181–186. All rights reserved

Abstract: *Background.* Acute kidney injury (AKI) is a common medical complication after myeloablative allogeneic stem cell transplantation (SCT). We have previously performed a retrospective analysis of AKI after cord blood transplantation (CBT) in adults, and found that the maximum of vancomycin (VCM) trough levels were significantly higher in patients with AKI. Following these results, we have monitored VCM serum trough concentrations more strictly, to not exceed 10.0 mg/L, since 2008.
Methods. In this report, we performed an analysis of AKI in a new group of 38 adult patients with hematological malignancies treated with unrelated CBT after myeloablative conditioning between January 2008 and July 2011.
Results. Cumulative incidence of AKI at day 100 after CBT was 34% (95% confidence interval 19–50). The median of the maximum value of VCM trough was 8.8 (4.5–12.2) mg/L. In multivariate analysis, no factor was associated with the incidence of AKI. No transplant-related mortality was observed. The probability of disease-free survival at 2 years was 83%.
Conclusion. These findings suggest that strict monitoring of VCM serum trough concentrations has a beneficial effect on outcomes of CBT.

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Key words: vancomycin; myeloablative conditioning; cord blood transplantation; acute kidney injury

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Acute kidney injury (AKI) is a common medical complication early after myeloablative allogeneic stem cell transplantation (SCT). The incidence of AKI, defined as a 2-fold rise in serum creatinine (sCr) concentration from baseline, has been reported ranging from 36% to 72% in SCT in a myeloablative setting (1–7), and about 20% required hemodialysis. We have previously reported a retrospective analysis of AKI in a group of 54 adult patients with hematological malignancies who received unrelated cord blood transplantation (CBT) after myeloablative conditioning between 2004 and 2007 (8). A statistically significant decrement of renal function from baseline was observed between days 11 and 20. Among the 54 patients, AKI occurred in 27.8% and was associated with a high mortality rate. Although no difference was seen in maximum cyclosporine (CYA) trough levels, the maximum vancomycin (VCM) trough levels were significantly higher in patients with AKI (8). Following these results, we have monitored VCM serum trough concentrations more strictly. In this report, we performed an analysis of AKI in a new group of 38 adult patients with hematological malignancies treated with unrelated CBT after myeloablative conditioning between January 2008 and

July 2011. The main purpose of this retrospective single-center study was to confirm the efficacy of strict monitoring of VCM serum trough concentrations, as well as to identify factors related to the incidence of AKI.

Patients and methods

Patients

This was a retrospective single-center analysis. Between January 2008 and July 2011, 39 consecutive adult patients with hematological malignancies were treated with unrelated CBT at The Institute of Medical Science, University of Tokyo. We excluded 1 patient who experienced primary engraftment failure. A total of 38 patients were analyzed. Patients qualified as standard risk if they were in first or second complete remission, had chronic-phase chronic myelogenous leukemia or refractory anemia of myelodysplastic syndrome, or had no high-risk cytogenetics. Patients in third complete remission, in relapse, or in refractory disease, with chronic myelogenous leukemia beyond chronic phase, or with high-risk cytogenetics were classified as high risk. Analyses of data were performed in December 2011. Written informed consent for treatment was obtained from all patients.

Conditioning

All patients received 4 fractionated 12 Gy total body irradiation on days −8 and −7, in addition to cytosine arabinoside (Ara-C) and cyclophosphamide. Ara-C was administered intravenously (IV) over 2 h at a dose of 3 g/m^2 every 12 h on day −5 and −4 (total dose 12 g/m^2). In patients with myeloid malignancies, recombinant human granulocyte colony-stimulating factor (G-CSF) was combined with Ara-C. G-CSF was administered by continuous infusion at a dose of 5 μg/kg/day. Infusion of G-CSF was started 12 h before the first dose of Ara-C and stopped at the completion of the last dose. Cyclophosphamide was administered IV over 2 h at a dose of 60 mg/kg once daily on days −3 and −2 (total dose 120 mg/kg). Two days after the completion of conditioning, patients received a CBT.

Graft-versus-host disease (GVHD) prophylaxis

All patients received standard CYA and methotrexate as GVHD prophylaxis. CYA was given IV every day starting on day −1 at a dose of 3 mg/kg/day. Methotrexate (15 mg/m^2 IV) was given on day 1, and 10 mg/m^2 on day 3 and 6. Once oral intake could be tolerated, patients were administered oral CYA at a dose of 1:2, in 2 divided doses per day, based on the last intravenous dose. CYA was reduced when sCr levels rose above 1.5 times baseline, or other serious agent-associated toxicities occurred. Physicians could freely modify the CYA dose for patients experiencing severe acute GVHD (aGVHD) or risk of disease relapse. Corticosteroid-based treatment was considered when grade II or higher severe aGVHD occurred (0.5–2 mg/kg).

Supportive care

All patients received G-CSF by intravenous infusion starting on day 1 until durable granulocyte recovery was achieved. The supportive care regimen, including prophylaxis for infection was the same as previously reported (8, 9).

Monitoring

All patients were monitored retrospectively 10 days before, and after the first 100 days, of CBT. Daily laboratory data collecting and the detecting method of VCM and CYA trough concentration were the same as previously reported (8). Therapeutic drug monitoring for VCM by assessing serum trough concentration was done twice in weekly, and modified to not exceed 10.0 mg/L.

End-points and definitions

AKI was defined as 2-fold rise in sCr concentration on daily laboratory results from the baseline (the average of days −10 to 0). Myeloid engraftment was defined as the first of 3 consecutive days, during which the absolute neutrophil count was at least 0.5×10^9/L. Platelet recovery time was achieved on the first of 3 days when the platelet count was higher than 50×10^9/L without transfusion support. The aGVHD was graded according to previously published criteria (10). Transplant-related mortality was defined as death from any cause except relapse. Relapse was defined by morphologic evidence of disease in peripheral blood, bone marrow, or extramedullary sites. Disease-free survival was defined as the time from CBT to relapse, death, or the last observation.

Statistical analysis

Continuous variables are expressed as median and their range. For dichotomous variables, the frequencies of positive occurrence are given along with their corresponding percentages. Continuous variables were divided into high or low with their median values, and a single VCM trough concentration of 10.0 mg/L was defined as a threshold level for analysis. Cumulative incidence of AKI was estimated with competing risk setting, of which death and relapse were defined as competing risk events. Variables considered in univariate analysis were body weight, age, recipient gender, recipient cytomegalovirus serology, disease status at transplant (standard or high risk), total nucleated cell dose, CD34+ cell dose, baseline sCr levels, VCM use, VCM trough levels, CYA trough levels, foscarnet use, aminoglycosides use, days of neutrophil engraftment, aGVHD grade 3–4, and positive blood culture result. Variables with a *P*-value <0.1 for cumulative incidence of AKI were tested in multivariate analysis using Cox proportional hazards models, and *P*-values <0.05 were considered to be statistically significant. The probability of disease-free survival was estimated from the time of CBT according to the Kaplan–Meier method. Endpoints were calculated at the last contact, the date of the last follow-up being December 1, 2011. Statistical software R, version 2.12.2, was used for analysis.

Results

Characteristics of patients and cord blood units

The characteristics of 38 patients and cord blood units are shown in Table 1. Among the patients, the median age was 41.5 years (range, 18–52 years), the median weight was 59.5 kg (range, 39–76 kg), the median number of cryopreserved nucleated cells was 2.8×10^7/kg (range, 1.7–5.7 $\times 10^7$/kg), and the median number of cryopreserved CD34+ cells was 0.9×10^5/kg (range, 0.4–2.6 $\times 10^5$/kg). All patients received a single and human leukocyte antigen-mismatched cord blood unit.

Time courses of changing renal function

No patient had confirmed renal dysfunction before transplantation. The changes of renal function as variations (%) of sCr from baseline levels observed on days 11–20 were greatest and significant (+15.8%,

Characteristics and clinical course

Characteristics	
Patients, *n*	38
Male/Female, *n*	25/13
Median age, years (range)	41.5 (18–52)
Median weight, kg (range)	59.5 (39–76)
Median number of cryopreserved nucleated cells, $\times 10^7$/kg (range)	2.8 (1.7–5.7)
Median number of cryopreserved CD34+ cells, $\times 10^5$/kg (range)	0.9 (0.4–2.6)
Recipient CMV status, Positive/Negative, *n*	32/6
Diagnosis	
AML, *n*	12
MDS-related secondary AML, *n*	6
RAEB, *n*	3
RA, *n*	2
CML, *n*	3
ALL, *n*	11
NHL, *n*	1
Disease status at transplant	
Standard risk, *n*	10
High risk, *n*	28
Conditioning regimen	
TBI + Ara-C/G-CSF + CY, *n*	26
TBI + Ara-C + CY, *n*	12
GVHD prophylaxis	
CYA + MTX, *n*	38
Baseline sCr, mg/dL (range)	0.62 (0.33–0.87)
Neutrophil >0.5 $\times 10^9$/L, days (range)	21 (17–30)
Patients with positive blood culture, *n* (%)	6 (16)
Patients taking aminoglycosides, *n* (%)	32 (84)
Patients taking foscarnet, *n* (%)	10 (26)
Patients taking liposomal amphotericin, *n* (%)	16 (42)
Maximum CYA trough value, μg/L (range)	258.5 (40–453)
Patients taking VCM, *n* (%)	32 (84)
Duration of VCM therapy, days (range)	54 (6–100)
Maximum VCM trough value, mg/L (range)	8.8 (5.2–12.2)
Patients with maximum VCM trough value, >10.0 mg/L, *n* (%)	9 (24)
Patient requiring hemodialysis, *n* (%)	0 (0)

CMV, cytomegalovirus; AML, acute myelogenous leukemia; MDS, myelodysplastic syndrome; RAEB, refractory anemia with excess blasts; RA, refractory anemia; CML, chronic myelogenous leukemia; ALL, acute lymphoblastic leukemia; NHL, non-Hodgkin's lymphoma; TBI, total body irradiation; Ara-C, cytosine arabinoside; G-CSF, recombinant human granulocyte colony-stimulating factor; CY, cyclophosphamide; GVHD, graft-versus-host disease; CYA, cyclosporine; MTX, methotrexate; sCr, serum creatinine; VCM, vancomycin.

Table 1

0.57 ± 0.18 mg/dL to 0.71 ± 0.24 mg/dL, $P < 0.001$). No obvious recovery occurred of declined renal function, which remained until day 100.

Incidence and risk factors of AKI

Cumulative incidence of AKI at day 100 after CBT was 34% (95% CI 19–50) (Fig. 1). The median of the maximum value of VCM trough was 8.8 (4.5–12.2) mg/L. In univariate analysis, baseline sCr levels and foscarnet use were associated with the incidence of AKI (Table 2). In multivariate analysis, no factor was associated with the incidence of AKI (Table 2).

Transplant outcomes

All patients had myeloid reconstitution, and the median time to >0.5 × 10^9/L absolute neutrophil count was 21 days (range, 17–30 days). A self-sustained platelet count >50 × 10^9/L was achieved in 37 patients at a median time of 45.5 days (range, 34–127 days). In 37 of 38 evaluable patients, aGVHD occurred. The grading of aGVHD was grade I in 7 patients, grade II in 25, grade III in 4, and grade IV in 1. No one experienced hepatic veno-occlusive disease. Six of 38 patients (16%) had positive blood culture; however, no one had confirmed hypotension, indicated with decrease in systolic blood pressure >10 mmHg to <90 mmHg. Of 6 patients with positive blood cultures, 4 patients were not administered VCM. The total number of positive blood cultures was 13 of 998 specimens. Ten of 13 bacterial pathogens from blood cultures were gram-positive cocci (Table 3). Vancomycin-resistant *Enterococci* were detected in 1 patient from blood culture, however, this had been continuously detected from stool specimens since admission. No patients required hemodialysis. Among the 38 patients, no patient died of transplant-related causes (transplant-related mortality 0%). Six patients relapsed. Of these 6 patients, 5 patients died of relapse. A total of 32 of 38 patients are alive and free of disease at between 139 and 1400 days (median: 634 days) after CBT. The probability of disease-free survival at 2 years was 83% and 77% at 3 years (Fig. 2).

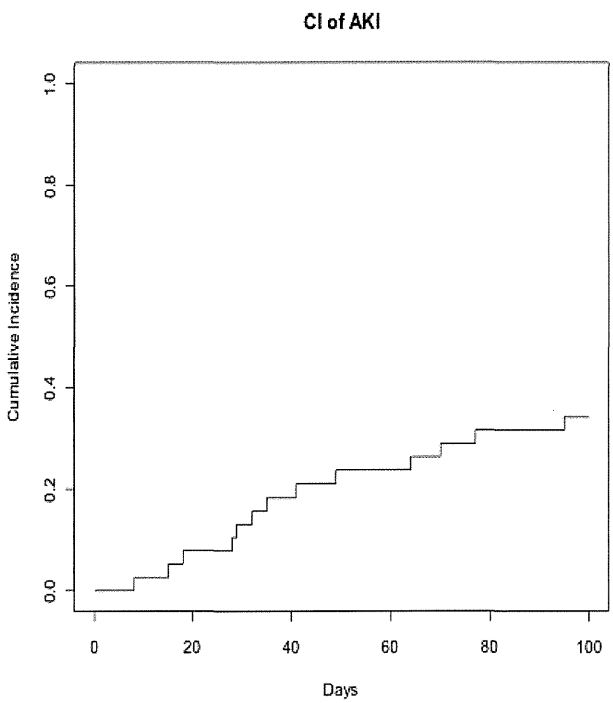

Fig. 1. Cumulative incidence (CI) of acute kidney injury (AKI).

Discussion

In this study, similar trends were observed in the time course of renal function changes as previously reported (8). However, the elevation in sCr was lower in this study, especially in days 11–20 (from 35.0% [8] to 15.8% in this study). Cumulative incidence of AKI was 34%; however, this was not assessed in our previous study (8). When we assessed the incidence of AKI with an identical definition to the previous

Univariate and multivariate analysis of factors associated with acute kidney injury

	Univariate analysis		Multivariate analysis	
	Hazard ratio (95% CI)	*P*	Hazard ratio (95% CI)	*P*
Baseline sCr, mg/dL				
>0.62	0.27 (0.08–0.98)	0.047	0.33 (0.08–1.32)	0.12
<0.62	1		1	
Foscarnet				
(+)	3.11 (1.07–9.05)	0.037	2.45 (0.71–8.42)	0.15
(−)	1		1	
VCM trough, >10.0 mg/L				
(+)	2.68 (0.89–8.09)	0.081	2.64 (0.76–9.19)	0.13
(−)	1		1	

CI, confidence interval; sCr, serum creatinine; VCM, vancomycin.

Table 2

Isolated bacterial pathogens from blood cultures

Pathogens	*n*
Enterococcus faecalis	3
Vancomycin-resistant *Enterococcus faecium*	3
Methicillin-resistant *Staphylococcus* species	1
Methicillin-resistant *Staphylococcus epidermidis*	3
Stenotrophomonas maltophilia	1
Bacillus species	1
Bacillus cereus	1

Table 3

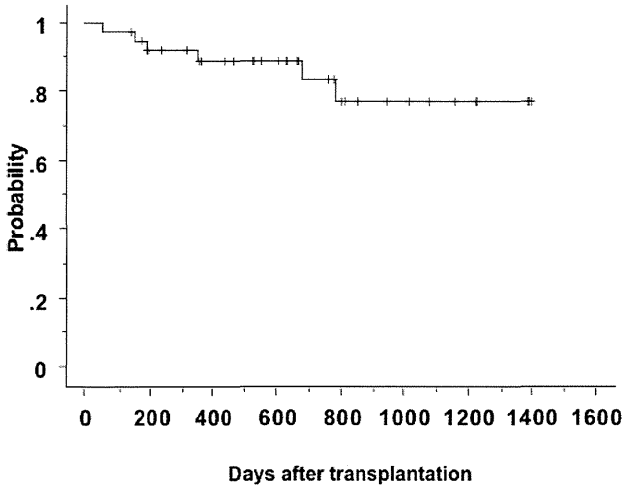

Fig. 2. Probability of disease-free survival after cord blood transplantation.

study, defined as just a 2-fold rise in sCr of 10 days average before and after transplantation, the incidence of AKI decreased to 11% in this study. In our previous study, the maximum VCM trough levels were significantly higher in patients with AKI (8); therefore, we have monitored VCM serum trough concentrations more strictly to not exceed 10.0 mg/L since 2008 in this study period. The average maximum value of VCM trough levels was lowered to 8.7 ± 2.1 mg/L from 12.2 ± 4.6 mg/L in the previous study, and proportion of patients with trough levels >10.0 mg/L was also decreased from 57% to 24%. Although baseline sCr levels and foscarnet use were associated with the incidence of AKI, VCM trough levels were not associated with AKI in univariate analysis. No factor was associated with AKI in multivariate analysis. Parikh et al. (11) reported AKI significantly affects survival after myeloablative allogeneic SCT in their meta-analysis, and more recently, Kagoya et al. (7) as well as Gooley et al. (12) reported the association of severity of AKI classification and non-relapse mortality within 100 days after transplantation. Although cumulative incidence of AKI was 34% in this study, no patients required hemodialysis or died of transplant-related causes. Recently, Yazaki et al. (13) reported the association of overall mortality and early bacterial infection of CBT in adults. They reported that cumulative incidence of early bacterial infection at day 100 was 21%, early bacterial infection had a negative effect on survival for adults, and the median day of development was 10 days after transplant, suggesting that prevention of bacterial infection in the very early post-CBT phase is important. Recently, a shift has occurred in the type of infecting organisms that cause bacteremia from predominantly gram-negative organisms to gram-positive cocci. The same trend is confirmed in the CBT (13, 14). VCM has an important role for infection control of gram-positive bacteremia, and was given to almost all the patients in this study. The reduced susceptibility of staphylococci for VCM has been reported since the mid 1990s, and prolonged exposure to lower VCM concentration has been associated with resistance (15). Although very few studies about pharmacokinetics and pharmacodynamics of VCM are available, several studies revealed area under the curve/minimum inhibitory concentration (AUC/MIC) as a preferred parameter, and AUC/MIC >400 associated with successful outcome and prevention of resistance (15, 16). Because of the difficulty of determining multiple concentrations for calculating AUC in the clinical setting, VCM trough concentrations have been recommended as the best surrogate marker for AUC/MIC, and concentrations of 15–20 mg/L – higher than the 5–15 mg/L previously recommended – is recommended as the target range (16). However, because an increased risk of nephrotoxicity with elevated VCM trough concentrations has been reported, and no appropriate pharmacokinetic/pharmacodynamic parameters for VCM have been determined (15, 17, 18), careful assessments are needed for using VCM at high target concentrations. Although we controlled VCM levels to not exceed 10.0 mg/L in this study, no patient died of bacterial infections. Further studies are required to determine the optimal VCM trough concentrations. Few reports are available about monitoring VCM trough concentrations for preventing AKI in allogeneic SCT in adults. Despite the limitations associated with this retrospective review of a small number of patients, our results suggest that strict monitoring of VCM serum trough concentrations has a beneficial effect on outcomes of CBT.