derived hematopoiesis in our method occurs through clonogenic hematopoietic stem/progenitor cells. We are in the process of determining in vivo repopulating ability of cells harvested from our culture by using serial transplantation into immunodeficient mice to assess the possibility of inducing feasible cell sources for various clinical applications, such as cell therapies and disease investigation.

Finally, time-lapse imaging strongly indicated crosstalk between hematopoietic cells and the autologous microenvironment composed of non-hematopoietic cells. Emerged blood cells move about actively and generate colonies in surrounding cell layers, suggesting the importance of a direct interaction between blood cells and microenvironmental cells for the maintenance, proliferation, and differentiation of stem or progenitor cells (Movie S3). In fact, a model of hematopoietic disorders triggered by mutation in the bone marrow microenvironment has been recently reported [55]. However, further investigation is necessary to identify the mechanisms responsible for such phenomena. Our culture may aid these investigations as it facilitates simple and sequential harvest of hematopoietic cells with minimal contamination by autologous adherent cell layers.

In conclusion, this study presents novel methods for analyzing the mechanisms of normal hematopoiesis in a robust, reproducible, and stepwise manner. Furthermore, employing gene-manipulated ES cells or disease-specific iPS cells will supply in vitro models of disease pathology, thereby providing further insights into hematological defects in conditions such as aplastic anemia and myelodysplastic syndromes.

Supporting Information

Movie S1 Time-lapse microscopic movie showing the morphological change in a single colony from day 0 to day 6 (initial differentiation). In this period, a colony begins forming a rosary-like morphology as it differentiates. The pictures were automatically taken every 8 minute by Biostation IM (Nikon Instruments, Tokyo, Japan).
(MOV)

Movie S2 Time-lapse microscopic movie showing the morphological change in a single colony from day 6 to day 25 (hematopoietic differentiation). After adding hematopoietic cytokines on day 6, hematopoietic cells first emerge from the areas near the edge of stratified zone. The pictures were automatically taken every 8 minute by Biostation IM (Nikon Instruments, Tokyo, Japan).
(MOV)

Movie S3 Close-up time-lapse microscopic movie showing hematopoietic cells moving about and generating colonies in surrounding cell layers. The pictures were automatically taken every 8 minute by Biostation IM (Nikon Instruments, Tokyo, Japan).
(MOV)

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Author Contributions

Conceived and designed the experiments: AN TH KU TN MKS. Performed the experiments: AN H. Sakai. Analyzed the data: AN TH KU KO IK H. Sakai. TN MKS. Contributed reagents/materials/analysis tools: H. Suemori H. Sakai. Wrote the manuscript: AN TN MKS.

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Neutrophil Differentiation From Human-Induced Pluripotent Stem Cells

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Induced pluripotent stem (iPS) cells are of potential value not only for regenerative medicine, but also for disease investigation. The present study describes the development of a neutrophil differentiation system from human iPS cells (hiPSCs) and the analysis of neutrophil function and differentiation. The culture system used consisted of the transfer of hiPSCs onto OP9 cells and their culture with vascular endothelial growth factor (VEGF). After 10 days, TRA 1-85^{+}CD34^{+}VEGF receptor-2 (VEGFR-2)^{high} cells were sorted and co-cultured with OP9 cells in the presence of hematopoietic cytokines for 30 days. Floating cells were collected and subjected to morphological and functional analysis. These hiPSC-derived neutrophils were similar to peripheral blood mature neutrophils in morphology, contained functional neutrophil specific granules, and were equipped with the basic functions such as phagocytosis, superoxide production, and chemotaxis. In the process of differentiation, myeloid cells appeared sequentially from immature myeloblasts to mature segmented neutrophils. Expression patterns of surface antigen, transcription factors, and granule proteins during differentiation were also similar to those of granulopoiesis in normal bone marrow. In conclusion, differentiation of mature neutrophils from hiPSCs was successfully induced in a similar process to normal granulopoiesis using an OP9 co-culture system. This system may be applied to elucidate the pathogenesis of various hematological diseases that affect neutrophils.

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Neutrophils and/or myeloid differentiation are most commonly affected in various hematological diseases including inherited bone marrow failure syndromes and neutrophil function disorders. Responsible genes have been identified in most of these syndromes or diseases, but the association between the gene mutation and the specific phenotype is not always clear. Moreover, often patients who present with a specific syndrome lack mutations in the known genes (Alter, 2007). Understanding the pathophysiology of these syndromes has been challenging despite the information provided by recent molecular findings, and in many of these syndromes, experimental models have not yet been generated.

Murine models of human congenital and acquired diseases are invaluable for disease investigation, but they provide a limited representation of human pathophysiology because they often do not faithfully mimic human diseases. The differences between murine and human physiologies make human cell culture an essential complement to research with animal models of disease.

Induced pluripotent stem (iPS) cells are reprogrammed somatic cells with embryonic stem (ES) cell-like characteristics generated by the introduction of combinations of specific transcription factors (Takahashi and Yamanaka, 2006; Meissner et al., 2007; Okita et al., 2007; Takahashi et al., 2007; Yu et al., 2007; Park et al., 2008b). Given the robustness of the approach, direct reprogramming promises to be a facile source of patient-derived cell lines. Such lines would be immediately valuable not only for regenerative medicine, but for disease investigation and drug screening as well.

The pluripotency and self-renewal potential of ES cells contributes to their value in various fields of science (Evans and Kaufman, 1981). Previous studies using normal or gene-manipulated ES cells have helped elucidate the process of normal embryogenesis and the genetic mechanisms of certain diseases (Lensch and Daley, 2006; Tulpule et al., 2010). Use of human embryos, however, faces ethical controversies that hinder the applications of human ES cells (hESCs). In addition, it is difficult to generate patient- or disease-specific ES cells, which are required for their effective application. The use of iPS cells would avoid the controversies surrounding human embryonic stem cell research.

Patient-specific iPS cells can be used for the generation of disease-corrected, patient-specific cells for cell therapy applications. Disease-specific pluripotent cells capable of differentiation into the various tissues affected in each condition can also provide new insights into disease pathophysiology by permitting analysis in a human system, under controlled conditions in vitro. Recent studies reported the generation of disease-specific iPS cell lines from patients with a variety of diseases (Park et al., 2008a; Raya et al., 2009; Agarwal et al., 2010). Therefore, disease-specific iPS cells are expected to be good models for the investigation of different diseases, and

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effective neutrophil differentiation systems are required to investigate the pathogenesis of various hematological conditions that affect neutrophils using human iPS cells (hiPSCs).

Recent reports describe in vitro culture systems for neutrophil differentiation from hESCs (Choi et al., 2009; Saeki et al., 2009; Yokoyama et al., 2009); however, neutrophil differentiation from hiPSCs has not yet been reported in detail. One of these studies demonstrated that myeloid differentiation could be induced from hiPSCs using the same methodology employed for their differentiation from hESCs (Choi et al., 2009), but the differentiation process and the functions of hiPSC-derived neutrophils were not shown in detail. A system for erythroid differentiation from primate ES and murine iPS cells by co-culture with OP9 stromal cells was developed in previous studies (Umeda et al., 2004; Umeda et al., 2006; Shinoda et al., 2007; Niwa et al., 2009). In the present study, a neutrophil differentiation system from hiPSCs was established by modifying the erythroid differentiation system, and the functions of the hiPSC-derived neutrophils and their differentiation process were analyzed in detail. This system may contribute to the elucidation of the pathogenesis of various blood diseases and the development of novel therapeutic approaches.

Materials and Methods

Maintenance of cells

The human iPS cell lines 201B6, 253G1 and 253G4 were a kind gift from Dr. Yamanaka (Kyoto University, Kyoto), and were generated from human dermal fibroblasts by retrovirus-mediated transfection of four (201B6) or three (253G1 and 253G4) transcription factors (Oct3/4, Sox2, and Klf4, with or without c-Myc) (Takahashi et al., 2007; Nakagawa et al., 2008). The human iPS cell lines and the human ES cell line KhES3-EGFPneo (KhES-3G) were maintained on mitomycin-C (Kyowa Hakko Kirin, Tokyo, Japan) -treated mouse embryonic fibroblasts (MEFs) in DMEM/F12 (Sigma-Aldrich, St. Louis, MO) supplemented with 20% Knockout™ Serum Replacement (Invitrogen, Carlsbad, CA), 5 ng/ml basic fibroblast growth factor (bFGF; R&D Systems, Minneapolis, MN), 1% non-essential amino acids solution (Invitrogen), 5 mM sodium hydroxide solution, 100 μM 2-mercaptethanol, and 2 mM L-glutamine. The culture medium was replaced daily with fresh medium. Colonies were passaged onto new MEFs every 3 or 4 days. The human ES cell line was used in conformity with The Guidelines for Derivation and Utilization of Human Embryonic Stem Cells of the Ministry of Education, Culture, Sports, Science, and Technology, Japan. OP9 stromal cells, which were a kind gift from Dr. Kodama (Osaka University, Osaka), were maintained in α-MEM (Invitrogen) supplemented with 20% fetal calf serum (FCS; Biological Industries, Bet Haemek, Israel).

Antibodies

The antibodies used for flow cytometric analysis included fluorescein isothiocyanate (FITC)-conjugated anti-human TRA 1-85 (R&D Systems), CD45 (Becton-Dickinson, Franklin Lakes, NJ) antibodies, phycoerythrin (PE)-conjugated anti-human CD11b, CD34 (Beckman Coulter, Fullerton, CA), CD13, CD16, CD33 (Becton-Dickinson) antibodies, and allophycocyanin (APC)-conjugated anti-human vascular endothelial growth factor receptor-2 (VEGFR-2) (eBioscience, San Diego, CA) antibody. The primary antibodies used for immunocytochemical analysis included goat anti-human lactoferrin (Santa Cruz Biotechnology, Santa Cruz, CA) and rabbit anti-human MMP9 (Abcam, Cambridge, UK). Biotinylated horse anti-goat or anti-rabbit antibodies (Vector Laboratories, Burlingame, CA) were used as secondary antibodies.

Differentiation of iPS cells

Methods used for the initial differentiation of iPS cells and cell sorting were based on earlier reports (Umeda et al., 2004, 2006). Briefly, trypsin-treated undifferentiated iPS cells were transferred onto OP9 cells and cultured with 20 ng/ml vascular endothelial growth factor (VEGF) (R&D Systems). After 10 days, the induced cells were harvested with cell dissociation buffer (Invitrogen), and sorted TRA $1\text{-}85^{+}CD34^{+}VEGFR\text{-}2^{high}$ cells were transferred onto fresh OP9 cells in six-well plates at a concentration of 3×10^3 cells per well. Sorted cells were cultured in α-MEM (Invitrogen) containing 10% FCS (Sigma, St Louis, MO), 50 μM 2-mercaptoethanol, 20 ng/ml interleukin (IL)-3, 100 ng/ml stem cell factor (SCF) (R&D Systems), and 10 ng/ml thrombopoietin (TPO) for 20 days. On day 20 after cell sorting, cytokines were changed into 20 ng/ml IL-3 and 10 ng/ml granulocyte colony-stimulating factor (G-CSF). IL-3, TPO and G-CSF were kindly provided by Kyowa Hakko Kirin.

Flow cytometric analysis and cell sorting

Cells were trypsinized and stained with antibodies. Dead cells were excluded by 4',6-diamidino-2-phenylindole (DAPI) staining. Samples were analyzed using an LSR flow cytometer and Cell Quest software (Becton Dickinson). Cell sorting was performed using a FACSVantage SE flow cytometer (Becton Dickinson).

Cytostaining

Floating cells were centrifuged onto glass slides using a Shandon Cytospin® 4 Cytocentrifuge (Thermo, Pittsburgh, PA), and analyzed by microscopy after May–Giemsa, myeloperoxidase (MPO), or alkaline-phosphatase staining. Sequential morphological analysis was performed as follows: all adherent cells including OP9 cells were trypsinized, harvested, and incubated in a new tissue-culture dish (Becton-Dickinson) for 1 h to eliminate adherent OP9 cells (Suwabe et al., 1998). Floating cells were then collected, centrifuged onto glass slides, and analyzed by microscopy after May–Giemsa staining. For immunocytochemical analysis, cells were fixed with 4% paraformaldehyde (PFA), immersed in citrate buffer, and autoclaved for 5 min at 121°C for antigen retrieval (Toda et al., 1999). The slides were then incubated with primary antibodies followed by application of the streptavidinbiotin complex immunoperoxidase technique with diaminobenzidine as chromogen, and nuclei were counterstained with hematoxylin.

Electron microscopy

Cells were fixed in 2% glutaraldehyde in 0.1 M phosphate buffer (PB) for at least 2 h, and then postfixed in 1% osmium tetroxide in 0.1 M PB for 1.5 h. After fixation, samples were dehydrated in a graded ethanol series, cleared with propylene oxide, and embedded in Epon. Thin sections of cured samples were stained with uranyl acetate and Reynolds lead citrate. The sections were inspected using a transmission electron microscope, H7650 (Hitachi, Tokyo, Japan).

Chemotaxis assay

Chemotactic ability was determined using a modified Boyden chamber method (Boyden, 1962; Harvath et al., 1980). Briefly, 500 μl of the reaction medium (Hank's Balanced Salt Solution (HBSS) containing 2.5% FCS) with or without 10 nM formyl-Met-Leu-Phe (fMLP; Sigma-Aldrich) was placed into each well of a 24-well plate, and the cell culture insert (3.0-μm pores; Becton Dickinson) was gently placed into each well to divide the well into upper and lower sections. Floating cells were suspended in the reaction medium at 7.0×10^4/ml, and a 500-μl cell suspension was added to the upper well, allowing the cells to migrate from the upper to the lower side of the membrane for 4 h at 37°C. After incubation, cells in the lower chamber were collected and counted using an LSR flow cytometer. Cells were counted by flow cytometry as follows:

equivalent amounts of counting beads were added to each sample and counted until the bead count reached 10,000.

MPO activity assay

The EnzChek Myeloperoxidase (MPO) Activity Assay Kit (Molecular Probes, Leiden, The Netherlands) was used for rapid and sensitive determination of MPO chlorination activity in cell lysates. The procedure was performed following the manufacturer's instructions. Cell lysate samples were prepared from 1×10^4 floating cells by freeze-thaw cycles. Fluorescence was measured with a fluorescence microplate reader (Wallac 1420 ARVO sx; PerkinElmer, Waltham, MA) using fluorescence excitation and emission at 485 and 530 nm, respectively. The background fluorescence measured for each zero-MPO control reaction was subtracted from each fluorescence measurement before plotting.

DHR assay

Neutrophil production of reactive oxygen species was detected by flow cytometry using dihydrorhodamine123 (DHR) as described previously (Vowells et al., 1995). Briefly, 3.5×10^4 floating cells were suspended in 100 μl of the reaction buffer (HBSS containing 0.1% FCS and 5 mM glucose) per tube, and two tubes were prepared for each sample. Catalase (Sigma-Aldrich) at a final concentration of 1000 U/ml and DHR at a final concentration of 1.0×10^5 nM were added and incubated for 5 min in a 37°C shaking water bath. After incubation, phorbol myristate acetate (PMA; Sigma-Aldrich) at a final concentration of 400 ng/ml was added to one of the two tubes and tubes were returned to the water bath for an additional 15 min. Following incubation, rhodamine fluorescence from the oxidized DHR was detected using an LSR flow cytometer.

Phagocytosis and detection of reactive oxygen species

Phagocytosis and neutrophil production of reactive oxygen species was detected by chemiluminescent microspheres (luminol-binding carboxyl hydrophilic microspheres; TORAY, Tokyo, Japan) as described previously (Uchida et al., 1985). Briefly, 2×10^4 floating cells were suspended in 50 μl of the reaction buffer (HBSS containing 20 mM N-2-hydroxyethylpiperazine-N′-2-ethanesulfonic acid (HEPES)) per tube. To activate the system, 5 μl of chemiluminescent microspheres was added, and light emission was recorded continuously. During the measurement, samples were kept at 37°C. To inhibit the phagocytosis, 1.75 μg of cytochalasin B (Sigma-Aldrich) was added to the sample. Chemiluminescence from the microspheres was detected using a luminometer (TD-20/20; Turner Designs, Sunnyvale, CA).

RNA extraction and RT-PCR analysis

RNA samples were prepared using silica gel membrane-based spin-columns (RNeasy Mini-Kit™, Qiagen, Valencia, CA) and subjected to reverse transcription (RT) with the Ominscript-RT Kit™ (Qiagen). All procedures were performed following the manufacturer's instructions. For reverse transcriptase-polymerase chain reaction (RT-PCR), yields were adjusted by dilution to produce equal amounts of the human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) amplicon. The complementary DNA (cDNA) templates were initially denatured at 94°C for 5 min, followed by 30–40 amplification reactions consisting of 94°C for 15–30 sec (denaturing), 55–63°C for 15–30 sec (annealing), and 72°C for 30–60 sec (extension), with a final extension at 72°C for 7 min. The oligonucleotide primers were as follows: NANOG, 5′-CAG CCC TGA TTC TTC CAC CAG TCC C-3′ and 5′-TGG AAG GTT CCC AGT CGG GTT CAC C-3′ (Takahashi et al., 2007); human GAPDH, 5′-CAC CAG GGC TGC TTT TAA CTC TG-3′ and 5′-ATG GTT CAC ACC CAT GAC GAA C-3′ (Umeda et al., 2006); PU.1, 5′-CTG CAT TGG CCC CCA CCG AG-3′ and 5′-AGG TCT TCT GAT GGC TGA GGG GG-3′; C/EBPα, 5′-TAA CCT TGT GCC TTG GAA ATG CAA AC-3′ and 5′- ATG TTT CCA CCC CTT TCT AAG GAC A-3′ (Duan and Horwitz, 2003); C/EBPε, 5′- AGT CTG GGG AAG AGC AGC TTC-3′ and 5′- ACA GTG TGC CAC TTG GTA CTG-3′ (Mori et al., 2009); MPO, 5′-TGA GGA CGG CTT CTC TCT TC-3′ and 5′-CCC GGT AAG TGA TGA TCT GG-3′; Lactoferrin, 5′-AGC TGG CAG ACT TTG CGC T-3′ and 5′-TTC AGA TTA GTA ATG CCT GCG ACA TAC-3′ (Kholodnyuk et al., 2006); Gelatinase (MMP-9), 5′-GCC TCC AAC CAC CAC CAC AC-3′ and 5′-GCC CAG CCC ACC TCC ACT C-3′ (Sugimoto et al., 2001); mouse GAPDH, 5′-ACG GCC GCA TCT TCT TGT GCA-3′ and 5′-CAC CCT TCA AGT GGG CCC CG-3′. PCR amplification reaction cycles were performed in the linear range for each primer by carrying out primer titrations. The number of reaction cycles per sample were: NANOG, 35 cycles; human GAPDH, 30 cycles; PU.1, 40 cycles; C/EBPα, 40 cycles; C/EBPε, 40 cycles; MPO, 35 cycles; Lactoferrin, 35 cycles; Gelatinase (MMP-9), 40 cycles; mouse GAPDH, 30 cycles.

Statistics

Statistical analyses were conducted using the Student's *t*-test. Statistical significance was defined as $P < 0.05$.

Results

Neutrophil differentiation from hiPSCs in co-culture with OP9 stromal cells

A culture system for the induction of erythroid cell differentiation from primate ES and murine iPS cells by co-culture with OP9 stromal cells (Umeda et al., 2004; Umeda et al., 2006; Shinoda et al., 2007; Niwa et al., 2009) was established, and this system was applied for neutrophil differentiation from hiPSCs. Prior data in primate ES cells suggested that the VEGFR-2^{high} fraction of differentiated cells contained hemangioblasts and VEGFR-2^{high}CD34^{+} cells had more hematopoietic potential (Umeda et al., 2006). Therefore, the expression of VEGFR-2 and CD34 was examined using three human iPS cell lines (201B6, 253G1, 253G4) and one ES cell line (KhES-3G). After 10 days of co-culture with OP9 in the presence of 20 ng/ml VEGF, VEGFR-2^{high}CD34^{+} cells appeared from all hiPSC lines in a similar manner to the ES cell line (Fig. 1A). Among these three human iPS cell lines, the highest percentage of VEGFR-2^{high}CD34^{+} cells was detected in 253G4 (Fig. 1B), and the data on this cell line is therefore presented below.

The VEGFR-2^{high}CD34^{+} cell fraction was sorted (Fig. 1C) and 1.1×10^4 (range; $0.6–2.2 \times 10^4$ in 14 independent cultures) VEGFR-2^{high}CD34^{+} cells were grown in one 10-cm dish containing hiPSCs. They were then transferred onto fresh OP9 cells and cultured in the presence of hematopoietic cytokines. Around 10 days after cell sorting (day10 + 10), small, round cell colonies appeared (Fig. 1D), and these colonies gradually grew in both size and number (Fig. 1E). At the same time, floating cells also appeared, and the average number of floating cells from 1×10^4 sorted VEGFR-2^{high}CD34^{+} cells at 30 days after cell sorting (day10 + 30) was 4.1×10^4 (range; $0.2–9.9 \times 10^4$ in 11 independent cultures).

May–Giemsa staining of the floating cells on day 10 + 30 revealed that 38.0 ± 1.6% of the cells were stab and segmented neutrophils (Fig. 1F), which were positive for MPO (Fig. 1G) and neutrophil alkaline-phosphatase (Fig. 1H). The rest were mainly immature myeloid cells and a small number of macrophages, and cells of other lineages, such as erythroid or lymphoid cells, were not observed. The frequency of MPO- and neutrophil alkaline-phosphatase-positive cells is shown in Table 1. The results were consistent with the morphological features revealed by May–Giemsa staining.

Surface marker analysis revealed that these floating cells were positive for CD45 and CD11b, and partially positive for CD13, CD33, and CD16 (Fig. 1I). The expression pattern of these surface markers was similar to that of neutrophils or immature myeloid cells in healthy bone marrow (van Lochem et al., 2004), although the CD16 expression level was lower.

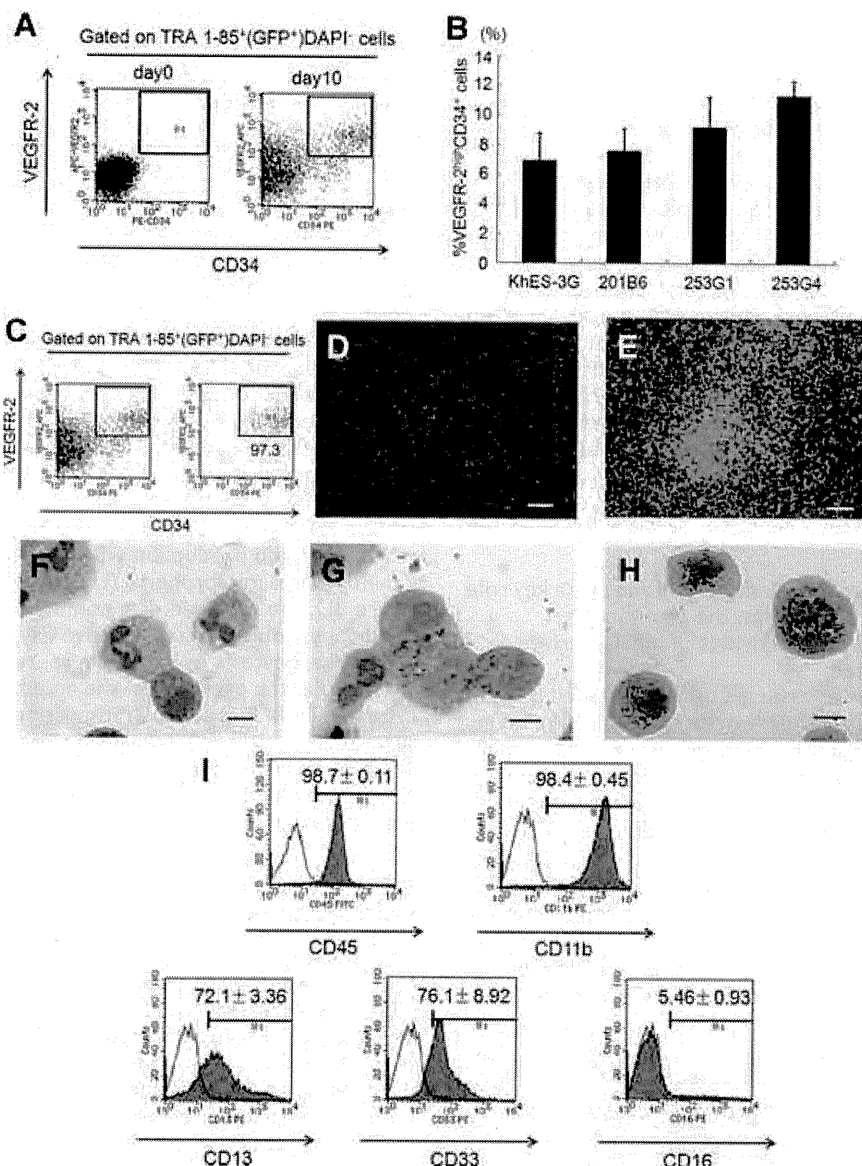

Fig. 1. Neutrophil differentiation from hiPSCs in co-culture with OP9 stromal cells. (A–B) Flow cytometric analysis of VEGFR-2 and CD34 during differentiation induction. TRA 1-85^{+} (GFP^{+}) DAPI^{-} cells were gated as human iPS (ES) cell-derived viable cells. Undifferentiated iPS (ES) cells and 10-day culture cells were stained with antibodies specific for VEGFR-2 and CD34. Representative results from one of three independent experiments (A) and percentages of VEGFR-2^{high}CD34^{+} cells on day 10 (B) are shown (n = 3; bars represent SDs). (C) VEGFR-2^{high}CD34^{+} cells were sorted on day 10. Representative dot plots and percentages of gated cells are shown. Purities of viable VEGFR-2^{high}CD34^{+} cells were calculated at 95.5 ± 1.9% from 14 independent experiments. (D–E) Micrographs of adherent hematopoietic cell clusters generated on day 10 (D) and day 30 (E) after cell sorting. Scale bars: 200 μm. (F–H) May–Giemsa staining (F), myeloperoxidase staining (G), and neutrophil alkaline-phosphatase staining (H) of floating cells on day 10 + 30. Scale bars: 10 μm. (I) Flow cytometric analysis of floating cells on day 10 + 30 were stained with antibodies specific for CD45, CD11b, CD13, CD33, or CD16. Plots show the negative control profile (open bars) versus the specific antibody staining profiles (shaded bars). Representative results from one of three independent experiments are shown. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

TABLE 1. Frequency of staining-positive cells for neutrophil specific granules

Staining	Frequency of positive cells (%)
Myeloperoxidase	93.7 ± 1.7
Neutrophil alkaline-phosphatase	39.0 ± 2.2
Lactoferrin	79.0 ± 1.4
Gelatinase	59.0 ± 3.7

Data are shown as mean ± SD (n = 3 independent experiments).

This lower CD16 expression level was similar to that of neutrophils derived in vitro from bone marrow CD34^{+} cells by stimulation with G-CSF (Kerst et al., 1993b) and to the effect in vivo when G-CSF is administered to healthy volunteers (Kerst et al., 1993a). These results indicated that the modified OP9 co-culture system could differentiate mature neutrophils from immature hiPSCs.

hiPSC-derived neutrophils contain neutrophil specific granules

Mature neutrophils in vivo have intracellular granules that are important for their bactericidal function. The granules can be

classified into three types based on their size, morphology, or electron density, or with reference to a given protein: primary (azurophilic) granules contain MPO, secondary granules contain lactoferrin, and tertiary granules contain gelatinase (Borregaard and Cowland, 1997).

To assess the presence of these granules in hiPSC-derived neutrophils, they were imaged using transmission electron microscopy, which showed that the hiPSC-derived mature neutrophils contained peroxidase-positive and negative granules, as was observed in peripheral blood neutrophils (Fig. 2A–B). Immunocytochemical analysis revealed that hiPSC-derived mature neutrophils were also positive for lactoferrin and gelatinase (Fig. 2C–D). The frequencies of cells that were positive for neutrophil specific granules, as observed by transmission electron microscopy (Table 2) and immunocytochemical analysis (Table 1), were more than 90% for primary granules, about 80% for secondary granules, and approximately 60% for tertiary granules. These results indicated that hiPSC-derived neutrophils contained neutrophils-specific granules.

hiPSC-derived neutrophils exhibit biological bactericidal activities

Because neutrophils patrol circulating blood and play a key role in early phase defense mechanisms, the chemotactic, phagocytotic, and bactericidal activities of hiPSC-derived neutrophils were analyzed.

Chemotactic activity was assessed using a modified Boyden chamber method (Boyden, 1962; Harvath et al., 1980). After incubation with or without fMLP in the lower well, neutrophils had migrated from the upper side to the lower side of the membrane. Incubation with fMLP caused an increase in the number of migrated cells of more than three times compared to cells without fMLP, suggesting that hiPSC-derived neutrophils had chemotactic activity in response to a chemoattractant similar to natural neutrophils derived from bone marrow (Fig. 3A).

The MPO-dependent chlorination activity and reactive oxygen production of hiPSC-derived neutrophils, which are

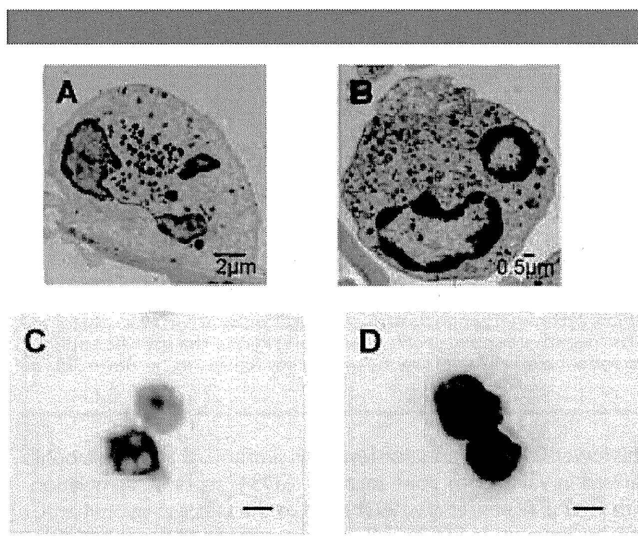

Fig. 2. Neutrophil-specific granules in hiPSC-derived neutrophils. (A–B) Floating cells on day10 + 30 (A) and peripheral blood neutrophils (B) were analyzed by transmission electron microscope. (C–D) Immunocytochemical analysis. Floating cells on day10 + 30 were stained for lactoferrin (C) and MMP9 (gelatinase) (D). Scale bars: 10 μm. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

TABLE 2. Frequency of positive cells for neutrophil specific granules under transmission electron microscopy

Granules	Frequency of positive cells (%)
Peroxidase-positive granules	95.1 (135/142)
Peroxidase-negative granules	86.6 (123/142)

both essential for their bactericidal function, were determined next. MPO reacts with hydrogen peroxide (H_2O_2) to form the active redox and enzyme intermediate compound MPO-I, which oxidizes chloride (Cl^-) to HOCl (Winterbourn, 2002). As shown in Figure 3B, hiPSC-derived neutrophils showed MPO-dependent chlorination activity. To evaluate reactive oxygen production, the ability to convert DHR to rhodamine was assessed using flow cytometry (Vowells et al., 1995) and the results revealed that hiPSC-derived neutrophils characteristically produced superoxide in response to PMA (Fig. 3C).

Finally, phagocytotic activity and phagosome-dependent reactive oxygen production were measured using luminol-bound microspheres (Uchida et al., 1985). As shown in Figure 3D, the captured data confirmed that hiPSC-derived neutrophils could produce reactive oxygen species in response to the phagocytosis of microspheres, which was completely abolished in the presence of the antiphagocytic agent cytochalasin B. Moreover, transmission electron microscopy successfully captured a screenshot of a neutrophil phagocytosing the microbeads (Fig. 3E). The above results clearly show that neutrophils derived from hiPSC using the present culture system maintain their functional status.

Step-wise neutrophil differentiation from hiPSCs is similar to normal granulopoiesis

Disorders of neutrophil differentiation are observed in various hematological diseases, among them the maturation arrest of neutrophil precursors in the bone marrow at the promyelocyte stage in severe congenital neutropenia. Thus, in clinical applications for disease investigation, the sequential analysis of the differentiation process from hiPSC to mature neutrophils in this culture system is required.

Observation of the sequential changes in cell morphology was done using May–Giemsa staining. Visualization of the morphology of day10 + 10 cells revealed that the cells were mainly myeloblasts and promyelocytes (Fig. 4A). On day10 + 20, myelocytes and metamyelocytes became predominant (Fig. 4B), and on day 10 + 30, stab and segmented neutrophils became predominant (Fig. 4C).

Surface antigen expression at each differentiation stage of hiPSC-derived cells was analyzed by flow cytometry (Fig. 4D). CD34, cell surface marker on normal immature hematopoietic cells, was detected in about 20% of the cells on day 10 + 10, but disappeared gradually thereafter. From day 10 + 10 to 10 + 30, the common myeloid antigens CD11b and CD33 were expressed in almost all the cells. Interestingly, expression of CD13, also a common myeloid antigen, was observed in less than 20% of cells at day 10 + 10 and did not subsequently increase. The expression level of CD16, which is a representative marker of matured neutrophils (van de Winkel and Anderson, 1991), doubled from day 10 + 10 to day 10 + 20, although the increase in expression was not statistically significant. These expression patterns were consistent with the patterns observed during normal neutrophil differentiation in healthy bone marrow (van Lochem et al., 2004).

The gene expression patterns of the pluripotency marker, transcription factors and granule proteins during neutrophil

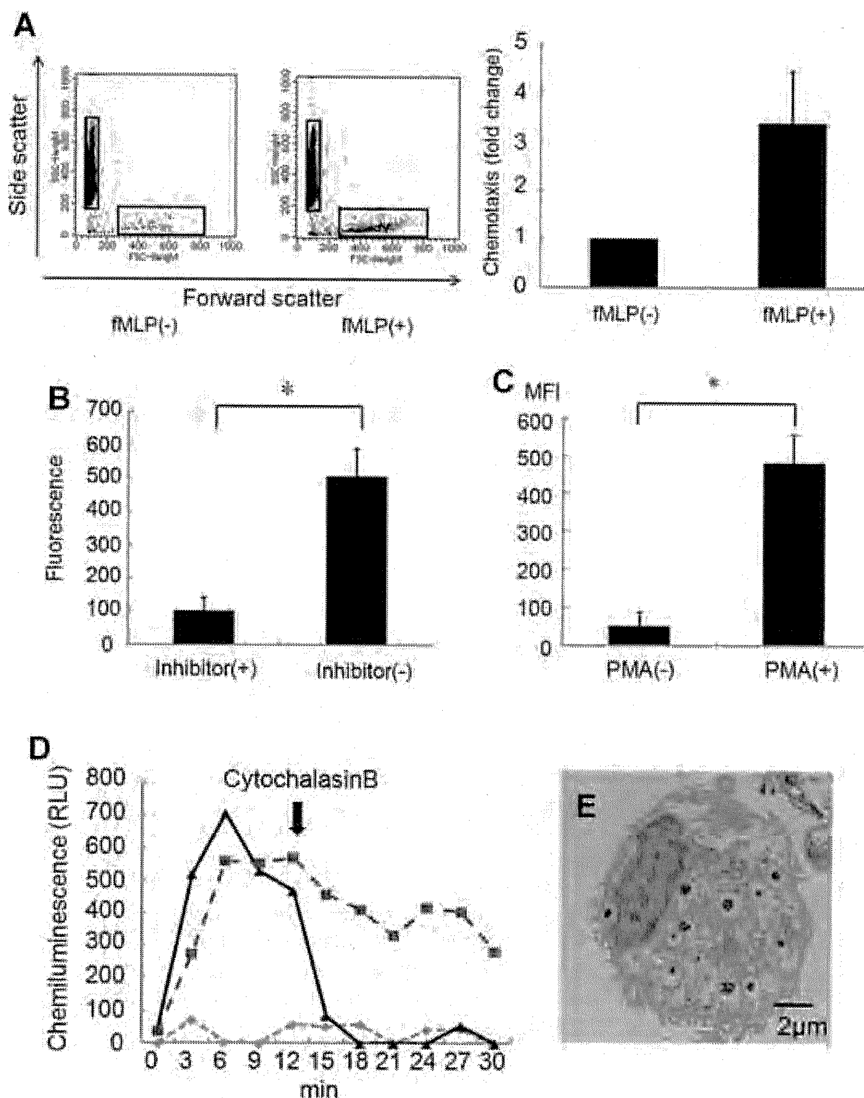

Fig. 3. Functional analysis of hiPSC-derived neutrophils. (A) Chemotactic activity of floating cells on day10 + 30 in response to fMLP was determined as described in Materials and Methods section. After a 4-h culture, the transwell inserts were removed, and the cells in the lower chamber were counted by an LSR flow cytometer (n = 3; bars represent SDs). (B) MPO chlorination activity in cell lysates from floating cells on day10 + 30 was analyzed by EnzChek Myeloperoxidase (MPO) Activity Assay Kit as described in the Materials and Methods section. The chlorination activity in neutrophil cell lysates was almost completely abolished by the addition of a chlorination inhibitor (n = 3; bars represent SDs; *$P < 0.05$.). (C) Floating cells on day10 + 30 were subjected to DHR assay. DHR was reacted with neutrophils with or without PMA, and the resultant rhodamine fluorescence was detected by flow cytometry. The addition of PMA increased the levels of fluorescence. Results are expressed as mean fluorescence intensity (MFI) (n = 3; bars represent SDs; *$P < 0.05$.). (D) Floating cells on day10 + 30 were subjected to the assay for phagocytosis-induced respiratory burst activity using chemiluminescent microspheres (luminol-binding microspheres). Gradual increase in chemiluminescence indicates the respiratory burst triggered by the phagocytosis of luminol-binding microspheres (squares). The increase in chemiluminescence was almost completely abolished by the addition of cytochalasin B (diamonds) and inhibited by its later addition (triangles). The figures are representative of three independent experiments. Abbreviation: RLU, relative light units. (E) hiPSC-derived neutrophils phagocytosing the microbeads were analyzed by transmission electron microscopy.

differentiation in this culture system were investigated by RT-PCR (Fig. 4E–F). NANOG, a pluripotency marker, was expressed in undifferentiated iPS cells but disappeared in sorted VEGFR2^{high}CD34^{+} cells after 10 days differentiation. PU.1 and C/EBPα, essential transcription factors for commitment and differentiation of the granulocytic lineage (Borregaard et al., 2001; Friedman, 2007) were first detected on day 10 + 10 and persisted thereafter. C/EBPε, which had a critical role for the later stages of neutrophil development and transcription of key granule proteins (Borregaard et al., 2001; Friedman, 2007) were first detected faintly on day 10 + 10 and upregulated thereafter. MPO and lactoferrin, which were expressed at the highest levels in myeloblasts/promyelocytes and myelocytes/metamyelocytes, respectively (Cowland and Borregaard, 1999; Borregaard et al., 2001), were detected on day 10 + 10. Gelatinase, which was expressed at the highest level in band and segmented neutrophilic cells (Cowland and Borregaard, 1999; Borregaard et al., 2001), was first detected on day 10 + 20 and upregulated thereafter. Altogether, these results suggested that the neutrophil differentiation in this co-culture system might recapitulate the orderly differentiation process in bone marrow.

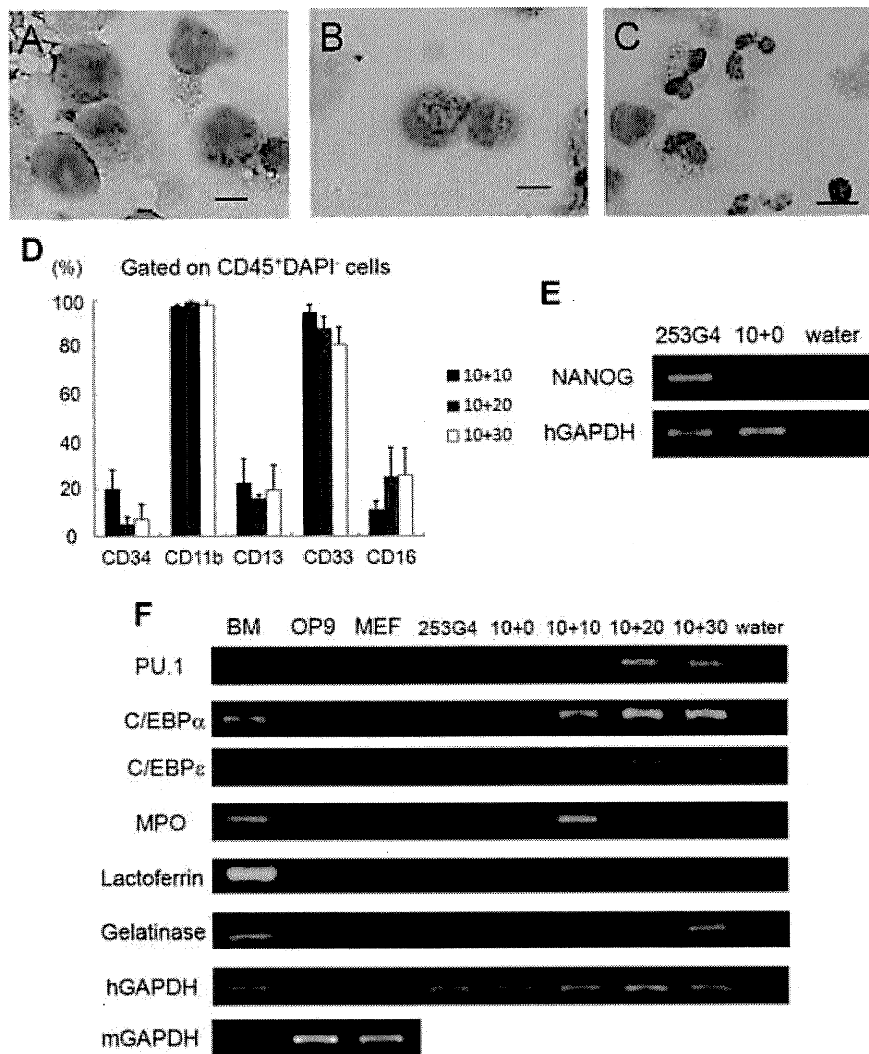

Fig. 4. Sequential analysis of neutrophil differentiation from hiPSCs. (A–C) Sequential morphological analysis of day10 + 10 (A), day10 + 20 (B) and day10 + 30 (C). Scale bars: 10 μm. (D) Surface antigen expression at each level of differentiation of hiPSC-derived cells was analyzed by flow cytometry. All adherent cells including OP9 cells were harvested and stained with antibodies. Human CD45$^+$DAPI$^-$ cells were gated as hiPSC-derived viable leukocytes (n = 3; bars represent SDs). (E–F) Sequential RT-PCR analysis of a pluripotency marker (E), genes associated with neutrophil development and neutrophils-specific granules (F) during differentiation. Human GAPDH was used as a loading control. Abbreviations: BM, human bone marrow cells; 253G4, undifferentiated 253G4 cells; 10 + 0, sorted VEGFR2^{high}CD34$^+$ cells after 10 days differentiation; 10 + 10, 20, 30, all cells after 10, 20, 30 days differentiation after cell sorting; hGAPDH, human GAPDH; mGAPDH, mouse GAPDH. The figures are representative of three independent experiments. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Discussion

The analysis of the differentiation process of neutrophils can provide helpful information for the elucidation of the pathogenesis of hematopoietic diseases that affect neutrophils and/or myeloid differentiation, including inherited bone marrow failure syndromes and neutrophil function disorders. Traditionally, HL-60, an acute promyelocytic cell line, has been used as a neutrophil differentiation model (Collins et al., 1978; Newburger et al., 1979). Although this cell line grows well and differentiates easily into neutrophils, the neutrophil differentiation model is not suitable for the analysis of neutrophil-affected disorders because of its leukemic cell-origin. Development of a neutrophil differentiation system based on iPS cells would provide a better model for the analysis of such diseases, because iPS cells can be generated from the somatic cells of patients suffering from these diseases.

The current study aimed to investigate two issues in hiPSC-derived neutrophil differentiation: tracking the step-wise maturation in vitro and evaluating the wide spectrum of neutrophil functions. Through the use of a modified OP9 co-culture system, the directed and step-wise differentiation from hiPSCs to mature neutrophils containing neutrophil specific granules was first accomplished. The expression of surface antigens, transcription factors and granule proteins during differentiation exhibited the characteristic pattern of normal granulopoiesis. The biological functions of hiPSC-derived neutrophils were demonstrated through the quantitative assessment of granule enzyme activities and biological bactericidal activities such as chemotaxis and phagocytosis.

Defects in the maturation and function of neutrophils are associated with certain blood diseases including inherited bone marrow failure syndromes and neutrophil function disorders.

Among bone marrow failure syndromes, certain conditions affect a specific maturation stage, such as the maturation arrest at the plomyelocyte/myelocyte stage seen in severe congenital neutropenia. Neutrophil function disorders can affect specific bactericidal activities, such as the absence of MPO activity characteristic of MPO deficiency disorders. The use of hiPSCs for the investigation of these diseases requires sequential analyses that can identify each neutrophil maturation stage and include a functional analysis to evaluate each bactericidal activity separately on disease-specific, iPSC-derived neutrophils. Although previous studies have reported neutrophil differentiation models from hESCs (Choi et al., 2009; Saeki et al., 2009; Yokoyama et al., 2009) and hiPSC-derived neutrophils have been shown before (Choi et al., 2009), evidence showing that hiPSCs, which are artificially reprogrammed somatic cells, can follow the normal developmental pathway into fully functional mature neutrophils is of great significance, and the description of methods for identifying each neutrophil maturation step and analyzing each bactericidal pathway separately is important for clinical applications.

Although flow-cytometric analysis combined with RT-PCR identified the neutrophil maturation step relatively successfully, discrepancies between the neutrophil differentiation system in this study and normal granulopoiesis were noted such as the lower expression of CD16 than that shown by previous reports on hESC-derived neutrophils (Choi et al., 2009; Saeki et al., 2009; Yokoyama et al., 2009). As CD16 is a mature neutrophil marker in peripheral blood, two reasons could explain this phenomenon. First, residual precursors could have been more significant contaminants in the present system than in previously reported methods due to the function of cytokines and stroma supporting immature hematopoietic cells. Another possible reason is the shift of protein types between membrane-bound and soluble forms. Calluri previously reported that G-CSF is not only a myeloid cell growth factor, but also a modulator of neutrophil behavior (Carulli, 1997), and its stimulation decreases the membrane bound CD16 and increases its soluble form. Low CD16 expression has been documented in neutrophils derived in vitro from bone marrow $CD34^{+}$ cells by stimulation with G-CSF (Kerst et al., 1993b), and it has been observed in vivo when G-CSF is administered to healthy volunteers (Kerst et al., 1993a). This phenomenon, which is also documented in a report of hESC-derived neutrophils (Yokoyama et al., 2009), is unavoidable in differentiation culture systems using recombinant cytokines. The combination of flow cytometric and PCR analyses enables a more accurate staging of progenitors that could be of importance in the investigation of maturation arrest in future studies.

The culture system presented in this study is considered ineligible for clinical applications due to the use of xenogeneic factors such as OP9 cells and FCS. To overcome this problem, a xeno-free hematopoietic differentiation system from pluripotent cells is currently being established.

In conclusion, the present study shows the establishment of a fully functional mature neutrophil differentiation system from hiPSCs and the detailed analysis of their function and differentiation process. This system could become a useful tool for the investigation of various hematological diseases with defects in maturation and function of neutrophils.

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Outcome of unrelated umbilical cord blood transplantation in 88 patients with primary immunodeficiency in Japan

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Summary

We report the results of umbilical cord blood transplantation (UCBT) performed in 88 patients with primary immunodeficiency (PID) between 1998 and 2008 in Japan; severe combined immunodeficiency (SCID, $n = 40$), Wiskott–Aldrich syndrome (WAS, $n = 23$), chronic granulomatous disease ($n = 7$), severe congenital neutropaenia (SCN, $n = 5$) and other immunodeficiencies ($n = 13$). Five-year overall survival (5-year OS) for all patients was 69% [95% confidence interval (CI), 57–78%], and was 71% and 82% for SCID and WAS, respectively. The main cause of death before day 100 was infection (17/19), while that after day 100 was graft-versus-host disease (GVHD) (5/7). Using multivariate analyses, pre-transplant infection, no conditioning, ≥2 human leucocyte antigen (HLA) mismatches or diagnosis other than SCID, SCN or WAS were all associated with poor prognosis. Reduced-intensity conditioning was associated with decreased overall mortality compared with myeloablative therapy. The cumulative incidence of grade 2–4 acute GVHD at day 100 was 28% (95% CI, 19–38%), and that of chronic GVHD at day 180 was 13% (95% CI, 7–23%). We conclude that UCBT should be considered for PID patients without an HLA-matched sibling. The control of pre-transplant infection and selection of HLA-matched donors will lead to a better outcome.

Keywords: primary immunodeficiency, severe combined immunodeficiency, Wiskott-Aldrich syndrome, cord blood transplantation, reduced-intensity conditioning.

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Allogeneic haematopoietic stem cell transplantation (HSCT) has been successfully used as a curative therapy for most severe forms of primary immunodeficiency (PID) (Zeidler et al, 2000; Antoine et al, 2003; Sakata et al, 2004; Rao et al, 2005; Kobayashi et al, 2006; Mazzolari et al, 2007; Dvorak & Cowan, 2008; Griffith et al, 2008; Cuvelier et al, 2009). Stem cell transplantation from a human leucocyte antigen (HLA)-identical family donor provides better prognosis than bone marrow transplantation from an unrelated donor (Antoine et al, 2003). Survival with this type of transplantation from a matched unrelated donor has improved significantly over the years in patients with severe combined immunodeficiency (SCID), whereas no improvement in survival has been observed with this transplantation in non-SCID patients (Antoine et al, 2003). The optimal stem cell source for PID patients with no HLA-identical sibling remains to be determined (Dvorak & Cowan, 2008; Griffith et al, 2008; Cuvelier et al, 2009).

Umbilical cord blood grafts from unrelated donors have been successfully used, primarily in children and subsequently in adults (Kurtzberg et al, 1996; Wagner et al, 1996; Gluckman et al, 1997; Rubinstein et al, 1998; Rocha et al, 2000, 2004; Laughlin et al, 2004). Theoretically, unrelated cord blood transplantation (UCBT) has the following distinct advantages in PID patients: (i) the cord blood product is rapidly accessible in most cases; (ii) the incidence and severity of graft-versus-host disease (GVHD) is not excessive, even in mismatched transplantation and (iii) the risk of latent viral transmission is low. The disadvantages of UCBT include slower haematopoietic/immunological reconstitution and graft failure, which have been observed with UCBT for malignant disorders, and naivety of lymphocytes to pathogens (Brown et al, 2008; Griffith et al, 2008; Szabolcs et al, 2008). Rapid immune reconstitution is particularly important in PID patients with ongoing infection who undergo UCBT.

The limited data available show that UCBT can be a curative measure in patients with SCID, Wiskott–Aldrich syndrome (WAS), chronic granulomatous disease (CGD) and severe congenital neutropaenia (SCN) (Knutsen & Wall, 2000; Bhattacharya et al, 2003, 2005; Fagioli et al, 2003; Knutsen et al, 2003; Kobayashi et al, 2006). Most of the available data have come from a single centre, and thus, detailed information on the outcome and problems associated with UCBT in PID patients is still lacking. In this study, we report the results of UCBT performed in 88 PID patients between 1998 and 2008 in Japan.

Methods

Collection of data

All UCBTs carried out for PIDs through the Japan Cord Blood Bank Network (JCBBN) between August 1998 and January 2008 was enrolled in this study. Eighty-eight patients with PID underwent UCBT during this period. All data were provided by JCBBN, which collects recipients' clinical information at day 100 after transplantation. Recipients' data on survival, disease status and long-term complications are renewed annually by administering follow-up questionnaires. Latest data acquisition was performed in November 2009. The present study was approved by the institutional ethical and data management committees of JCBBN.

Patients

A summary of patients enrolled in this study is shown in Table I. Forty patients had SCID (45%) and 48 (55%) had non-SCID. Patients with familial haemophagocytic syndrome were not included in this study. The median age at the time of transplantation was 10 months (range, 0–248 months).

Procedures

Cryopreserved, unrelated cord blood cells were used as the source of haematopoietic stem cells. The type of conditioning used and median cell dose infused are shown in Table I.

In most cases, HLA matching was performed by both serological and DNA typing for HLA-A, HLA-B and HLA-DRB1. In this study, HLA mismatch was defined according to serological or low-resolution molecular typing for HLA-A and HLA-B and high-resolution molecular typing for HLA-DRB1. Of the UCB donors, 29 (33%) were HLA fully compatible. Of the mismatched donors, 40 (45%) were 1-antigen mismatched, 15 (17%) were 2-antigen mismatched and four (5%) were 3-antigen mismatched (Table I). In 48 patients in whom high-resolution genotypical typing was performed for HLA-A, HLA-B and HLA-DRB1, 11 were fully matched, 13 were 1-antigen mismatched, 16 were 2-antigen mismatched, five were 3-antigen mismatched and three were 4-antigen mismatched.

Immunosuppressive prophylaxis against GVHD after UCBT consisted of ciclosporin A (CyA)- and tacrolimus-based regimens in 48 and 35 patients, respectively. Five patients were not administered any immunosuppressive drug after UCBT.

Various techniques including karyotyping, HLA typing and fluorescence *in situ* hybridization for the XY chromosome and variable number of tandem repeats were used to confirm the engraftment of donor cells.

Definitions

Neutrophil recovery was defined by an absolute neutrophil count of at least $0{\cdot}5 \times 10^9$/l for three consecutive days. Platelet recovery was defined by a count of at least 20×10^9/l, unsupported by transfusion for 7 d. Reticulocyte recovery was defined by a count of at least 20‰.

Patients without conditioning or with only anti-thymocyte globulin (ATG) were categorized as receiving no conditioning. Patients administered busulfan (BU)/cyclophosphamide (CY) ± total body irradiation (TBI) or total lymphoid irradiation

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Table I. Age at the time of transplantation, type of conditioning and HLA disparity.

	Patients (*N*)	Median age at transplantation (months) (range)	Median cell dose ($\times 10^7$/kg) (range)	Second or third transplantation (*N*)	Conditioning			HLA disparity			
					No (*N*)	RIC (*N*)	MAT (*N*)	0 (*N*)	1 (*N*)	2 (*N*)	3 (*N*)
Total	88	9 (0–248)	8·60 (1·89–31·1)	8	14	31	43	29	40	15	4
SCID	40	6·5 (0–27)	11·4 (4·55–31·1)	1	12	18	10	17	15	5	3
WAS	23	14 (4–84)	6·49 (2·89–13·6)	1	0	2	21	7	10	6	0
CGD	7	63 (31–248)	6·00 (1·89–12·3)	5	1	4	2	2	4	1	0
SCN	5	10 (4–124)	5·99 (4·16–9·19)	0	0	1	4	1	4	0	0
Others	13	37 (6–194)	8·11 (3·01–19·8)	1	1	6	6	2	7	3	1

RIC, reduced-intensity conditioning; MAT, myeloablative therapy. Definition of conditioning regimens are described in *Methods* section. 'Others' include four CD40L deficiency, two common variable immunodeficiency and one of each of the following disorders: Major histocompatibility complex (MHC) class II deficiency, DiGeorge syndrome, X-linked lymphoproliferative disorder, NEMO (NF-κ-B essential modulator) deficiency, IPEX (immunodysregulation polyendocrinopathy enteropathy X-linked) syndrome, Idiopathic CD4 lymphopenia and Blau syndrome.

(TLI), BU/CY + ATG ± TLI, BU/CY + fludarabine (Flu) or CY/etoposide/high-dose cytarabine were categorized as receiving myeloablative therapies (MATs). CY dose ranged from 120 to 240 mg/kg (median, 200 mg/kg) in patients receiving MAT.

TBI < 4 Gy was classified as 'low-dose TBI'. Patients administered Flu/melphalan (L-PAM) ± low-dose TBI or TLI, Flu/BU ± TLI or Flu/CY (50–60 mg/kg) ± low-dose TBI/TLI, Flu + low-dose TBI or Flu + ATG were categorized as receiving reduced-intensity conditioning (RIC). L-PAM dose was $\leq$140 mg/m^2 in patients receiving RIC.

GVHD was graded according to the standard criteria (Przepiorka *et al*, 1995).

Statistical analyses

The probability of survival was estimated by the product-limit method, and the log-rank test was used for group comparisons. Cumulative incidence curves were used in a competing-risks setting to calculate the probability of neutrophil, platelet and reticulocyte recovery and that of acute and chronic GVHD. Death before recovery was the competing event for haematological recovery, and death without GVHD was the competing event for GVHD. Gray's test was used for group comparisons of cumulative incidence (Gray, 1988; Gooley *et al*, 1999). The Cox regression model was used to analyse data for the identification of prognostic factors. Factors found to be significant ($P < 0{\cdot}05$) or marginally significant ($P < 0{\cdot}1$) in univariate analysis were included in multivariate analysis. The variables considered were patient age at the time of transplantation, diagnosis, duration from diagnosis to transplantation, second or third transplantation, HLA disparity, presence of infection at the time of transplantation, conditioning regimen and cell dose infused. Variables with >2 categories were included in the final model using dichotomized dummy variables when at least one of the categories showed significant effect on survival. Continuous variables were dichotomized for the prognostic factor analyses. Variables were dichotomized as follows; patient age greater or <12 months at transplantation, dichotomized at a median nucleic cell dose of $<8{\cdot}2 \times 10^7$/kg vs. $\geq 8{\cdot}2 \times 10^7$/kg and CD34 cell dose of $<2{\cdot}1 \times 10^5$/kg and $\geq 2{\cdot}1 \times 10^5$/kg, shorter than or equal to or longer than 180 d for time to transplant. All *P*-values were two-sided.

Results

Engraftment

Sixty-seven patients (76%) achieved stable engraftment. The cumulative incidence of neutrophil, platelet and reticulocyte recovery at day 100 after transplantation was 77% [95% confidence interval (CI), 66–85%], 56% (95% CI, 45–65%) and 64% (95% CI, 53–73%) respectively (Fig 1A, B; data not shown). The median time for neutrophil, platelet and reticulocyte recovery was 19 d (range, 9–104 d), 40 d (range, 10–122 d) and 27 d (range, 12–98 d), respectively. The cumulative incidences of neutrophil recovery were not statistically different among the disease groups (SCID, 74%; WAS, 91% and others, 68% at day 100 after transplantation) (Fig 1C), although incidence was low in CGD patients ($N = 7$, 43%).

The time required for neutrophil recovery was similar in all disease groups, while that required for platelet recovery varied to some extent among the different disease groups. Platelet engraftment was slightly delayed in WAS patients, but the time required for engraftment in these patients was not significantly different from that required in other patients (Fig 1D).

Forty-three, 31 and 14 patients received MAT, RIC and no conditioning, respectively. No difference was observed in the incidence of neutrophil recovery between the MAT and RIC groups (84% vs. 87% at day 100). Similarly, no difference was observed in platelet recovery between these two groups (data not shown).

The cell dose infused ranged from $1{\cdot}89$ to $31{\cdot}1 \times 10^7$/kg, with a median of $8{\cdot}60 \times 10^7$/kg. No correlation was observed between the cell dose infused and engraftment.

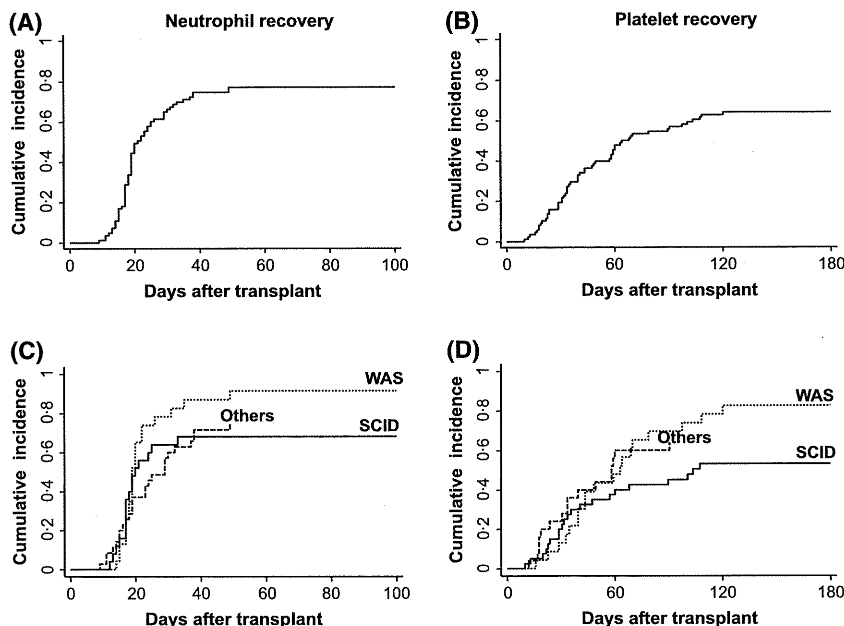

Fig 1. Cumulative incidence of neutrophil and platelet recovery after UCBT. (A) The cumulative incidence of neutrophil recovery 77% (95% CI, 66–85%). (B) The cumulative incidence of platelet recovery 56% (95% CI, 45–65%). The cumulative incidence of neutrophil (C) and platelet (D) recovery according to disease category is shown.

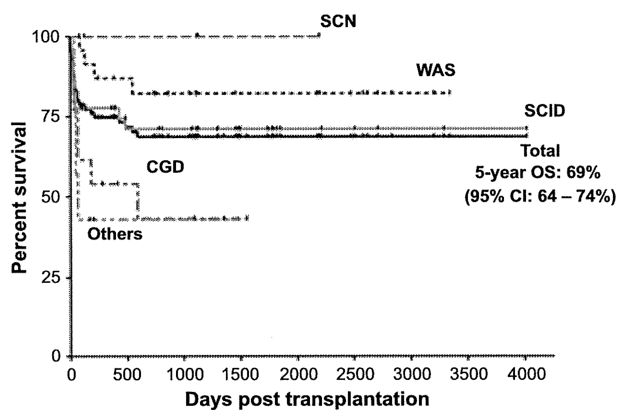

Fig 2. Kaplan–Meier estimates of overall survival after umbilical cord transplantation.

Five of 21 patients with engraftment failure received a second transplantation. Two WAS patients achieved successful engraftment in the second transplantation, while one SCID and two CGD patients did not survive the second transplantation. Only two of the remaining 16 patients who rejected the UCB graft remained alive at the latest data analysis.

Survival and causes of death

Of the 88 PID patients who underwent UCBT, 62 remained alive at the latest follow-up. Five-year OS for all patients was 69% (95% CI, 57–78%) (Fig 2), while that for SCID and WAS patients was 71% and 82%, respectively. All five SCN patients remained alive, although one patient had rejected the graft on day 79 after UCBT. Three of seven CGD patients survived UCBT; this low survival rate may be due to the fact that UCBT was selected in five patients after the first or second failed bone marrow transplantation (BMT). Seven of 14 patients categorized as 'other diseases' remained alive at the latest follow-up.

Table II summarizes the survival and causes of death after UCBT. Of the 26 patients who died, 19 had died within day 100 (17 from infection) and seven (SCID, six and congenital CD4 lymphopenia, one) had died within day 28 after UCBT.

Causes of early death (≤28 d) were cytomegalovirus (CMV) disease (three patients), *Pneumocystis* pneumonia (one patient), interstitial pneumonia (one patient), bacterial infection (one patient) and veno-occlusive disease (VOD) (one patient). All those who died of CMV disease had CMV pneumonia before transplantation.

The cause of death between days 28 and 100 in the remaining 12 patients was bacterial infection (seven had concomitant fungal infection, one also had VOD and one had CMV disease), CMV disease (two patients), fungal infection (one patient), multiple organ failure (one patient) and VOD (one patient). Four of seven CGD patients died of bacterial or fungal infection without engraftment. Although detailed data on bacterial/fungal infections at the time of transplantation were not collected, all the CGD patients were administered both antimicrobial and antifungal agents at the time of transplantation.

The causes of death after day 100 were GVHD (five patients), Epstein–Barr virus (EBV)-associated post-transplant lymphoproliferative disorder (EBV-PTLD, one patient) and

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Table II. Survival and causes of death.

	Cases (*N*)	Alive (*N*)	Death (day) <28 (*N*)	Death (day) <100 (*N*)	Death (day) ≥100 (*N*)	Infection at CBT (*N*)	Cause of death (<day 100) Bac/Fung infection (*N*)	Cause of death (<day 100) Viral infection (*N*)	Cause of death (<day 100) Others (*N*)	Cause of death (≥day 100) GVHD (*N*)	Cause of death (≥day 100) Others (*N*)
Total	88	62	7	19	7	18	10	7	VOD 3 MOF1	5	PTLD 1 AI 1
SCID	40	29	6	9	2	11	2	6	1 (VOD)	1	1 (AI)
WAS	23	19	0	1	3	1	1	0	0	3	0
CGD	7	3	0	4	0	5	4	0	1 (VOD)	0	0
SCN	5	5	0	0	0	0	0	0	0	0	0
Others	13	6	1	5	2	1	3	1	1 (VOD) 1 (MOF)	1	1 (PTLD)

Bac/Fung infection, bacterial and/or fungal infection. VOD, veno-occlusive disease; MOF, multiple organ failure; AI, adrenal insufficiency; PTLD, post-transplant lymphoproliferative disorder. Cause of death total does not equal the number of deceased patients because one patient died of VOD and bacterial infection.

adrenal insufficiency (one patient). None of the other patients died of infection after day 100.

GVHD

All but five patients in the present study received either CyA- or tacrolimus-based immunosuppressant prophylaxis for GVHD. The cumulative incidence of grade 2–4 acute GVHD at day 100 was 28% (95% CI, 19–38%), and that of grade 3–4 GVHD was 8% (95% CI, 4–15%) (Fig 3A, D).

The incidence of grade 2–4 GVHD was higher in patients who underwent 2- or 3-antigen-mismatched UCBT compared with those who underwent HLA-matched or HLA-1-antigen–mismatched UCBT, but it was not statistically significant ($P = 0{\cdot}071$) (Fig 3B). On the other hand, no difference was observed in the incidence of grade 3–4 GVHD between <2-antigen-mismatched and >2-antigen-mismatched transplants (Fig 3E), although grade 3–4 GVHD was not observed by high-resolution DNA typing in patients who underwent genotypically HLA-matched transplantation.

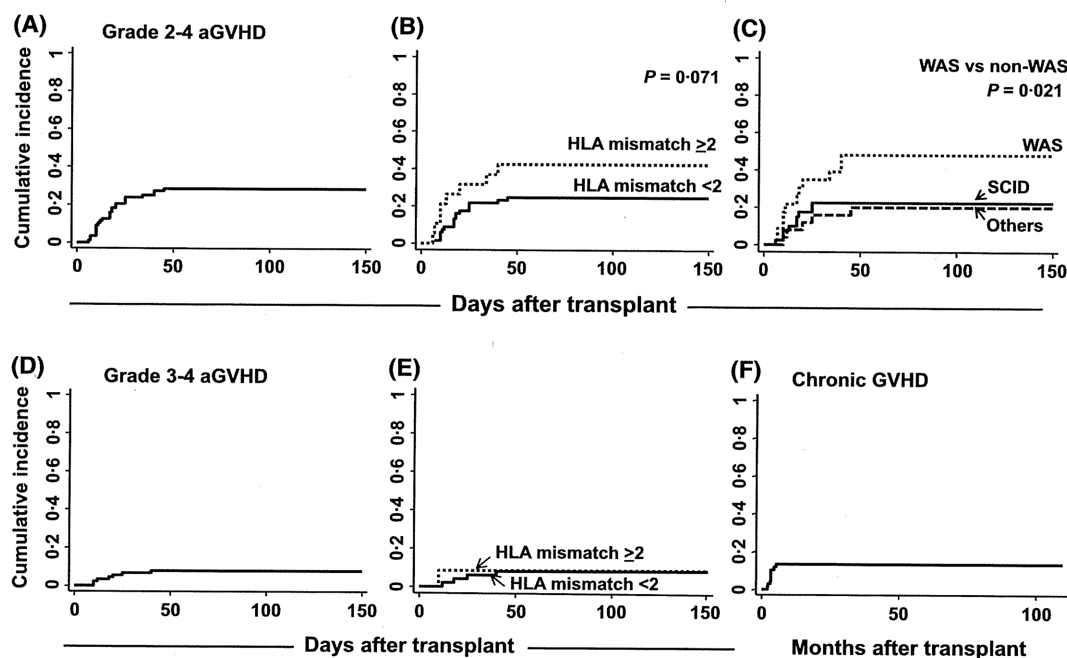

Fig 3. Cumulative probability of acute and chronic GVHD after UCBT. The cumulative incidence of grade 2–4 acute GVHD (aGVHD) at day 100 was 28% (95% CI, 19–38%) (A). The incidence was higher in transplantation mismatched for ≤2 antigens (B) and in that for WAS patients (C). The cumulative incidence of grade 3–4 acute GVHD at day 100 was 8% (95% CI, 4–15%) (D) and the incidence was not different between patients undergoing transplantation for ≥2-antigen mismatched transplant and those undergoing <2-antigen mismatched transplant (E). The cumulative incidence of chronic GVHD at day 180 was 13% (95% CI, 7–23%) (F).

When focusing on differences among the disease groups (Fig 3C), a significantly higher incidence of grade 2–4 GVHD was observed in WAS patients than in non-WAS patients, $P = 0.021$. In addition, three of five WAS patients who developed grade 3–4 GVHD died of either GVHD (two patients) or VOD (one patient).

Chronic GVHD was observed in nine patients, and its cumulative incidence at day 180 was 13% (95% CI, 7–23%) (Fig 3F).

Infections

Twenty-eight patients (SCID, 11; WAS, eight; CGD, three and other diseases, six) developed bacterial infection after UCBT. Sixteen of the 28 patients remained alive at the time of data collection.

Fungal infection mainly caused by *Aspergillus* species was observed in eight patients (CGD, three; SCID, two; WAS, two and X-linked hyperIgM syndrome, one). Three of the eight patients died of bacterial infection, bacterial/fungal infection or GVHD.

Twenty patients (SCID, eight; WAS, four; CGD, two; SCN, two and others, four) developed CMV disease after UCBT. CMV was detected before conditioning in all eight SCID patients of which four patients died of CMV disease after transplantation. Twelve of the 20 patients remained alive at the time of analysis.

Other notable virus-related complications were respiratory syncytial virus bronchiolitis accompanied by chronic GVHD in one SCID patient and EBV-PTLD in one patient with Blau syndrome; both infections led to a fatal outcome. One WAS patient had severe haemorrhagic colitis caused by Coxsackie virus B infection, which was treated successfully by infusion of expanded CD4 T cells prepared from the infusion residual of donor cord blood (Tomizawa *et al*, 2005). Another WAS patient had persistent norovirus infection. Interstitial pneumonia not due to CMV or *Pneumocystis* was noted in three patients of which one patient had parainfluenza/rhinovirus infection, while the causative agent for infection in the remaining two patients was not identifiable.

Risk factors for overall mortality

Lastly, we analysed the factors contributing to overall survival. Using univariate analyses, the following were found to be significant contributory factors to a poor prognosis: HLA mismatch of ≥2 antigens, time to transplant >180 d, second or third transplantation, ongoing infection at the time of transplantation, no conditioning for UCBT and diagnosis other than SCID, SCN or WAS (Table III). The dose of transfused nucleated cells or CD34-positive cells did not affect the 5-year OS.

Using multivariate regression analyses, the following were found to be significant contributory factors to patient death: infection at the time of transplantation, no conditioning, HLA mismatch of >2 antigens and diagnosis other than SCID, SCN or WAS (Table IV). RIC was determined to be the favourable factor for patient survival ($P = 0.01$) (Fig 4 and Table IV).

Table III. Univariate analyses of factors that contributed to 5-year OS.

Factors	Hazard ratio	95% CI	*P*-value
Age: ≥12 months	1·73	(0·78–3·83)	0·175
Diagnosis			
WAS and SCN	1·00		
SCID	2·34	(0·75–7·36)	0·145
Other diseases	5·39	(1·70–17·0)	0·004*
Nucleic cell dose: ≥8·2 × 10^7/kg	1·51	(0·69–3·29)	0·299
CD34 cell dose: ≥2·1 × 10^5/kg	0·86	(0·36–2·08)	0·744
HLA disparity			
6/6 matched	1·00		
5/6 matched	1·68	(0·58–4·83)	0·337
4/6 matched	3·78	(1·23–11·60)	0·020*
3/6 matched	3·24	(0·63–16·74)	0·160
4/6 or 3/6 matched	2·64	(1·20–5·83)	0·016*
Time to transplant: ≥180 d	1·89	(0·85–4·17)	0·117
Infection at transplant	6·24	(2·61–14·9)	<0·0001*
Second or third transplantation	3·37	(1·26–9·02)	0·016*
Conditioning			
MAT	1·00		
RIC	0·41	(0·13–1·23)	0·111
No conditioning	2·89	(1·21–6·93)	0·017*

*Significant contributory factors to the poor prognosis.

Discussion

This paper reports the outcome of UCBT for 88 PID patients, the largest cohort of PIDs to receive UCBT to date. The overall survival rate for PID patients undergoing UCBT was comparable to that previously reported for 46 Japanese PID patients undergoing BMT from either HLA-identical siblings or unrelated donors (Sakata *et al*, 2004), and also to that reported by the European Society of Immunodeficiency and other stem cell transplantation centres for PID patients receiving BMT from HLA-matched related donors, HLA-mismatched related donors or unrelated donors (Antoine *et al*, 2003; Rao *et al*, 2005; Dvorak & Cowan, 2008). The time for haematopoietic recovery was comparable to or better than the median recovery time observed in a large cohort of UCBT in children with haematopoietic disorders (Thomson *et al*, 2000; Michel *et al*, 2003) and in adults with leukaemia (Laughlin *et al*, 2004; Atsuta *et al*, 2009). The incidence of grade 2–4 GVHD (28%) in UCBT was lower compared with that reported in unrelated donor BMT in PID patients in Japan (47%) (Sakata *et al*, 2004), with that reported in BMT in 90 SCID patients (34%) (Neven *et al*, 2009) and with that observed in the studies of UCBT for childhood haematological malignancies (Thomson *et al*, 2000; Michel *et al*, 2003; Sawczyn *et al*, 2005). The incidence of chronic GVHD (13%) after UCBT was slightly

Table IV. Multivariate analyses of factors that contributed to 5-year OS.

Factors	HR	95% CI	*P*-value
Diagnosis			
WAS and SCN	1·00		
SCID	1·71	(0·39–7·38)	0·475
Other diseases	7·50	(2·06–27·19)	0·002*
HLA disparity			
6/6 matched	1·00		
5/6 matched	1·53	(0·50–4·66)	0·454
4/6 matched	5·64	(1·66–19·14)	0·006*
3/6 matched	1·04	(0·68–23·96)	0·124
4/6 or 3/6 matched	3·87	(1·63–9·19)	0·002*
Infection at transplant	4·61	(1·74–12·16)	0·002*
Conditioning			
MAT	1·00		
RIC	0·20	(0·06–0·69)	0·011†
No conditioning	4·87	(1·79–13·3)	0·002*

*Significant contributory factors to an unfavourable prognosis.
†Significant contributory factors to a favourable prognosis.

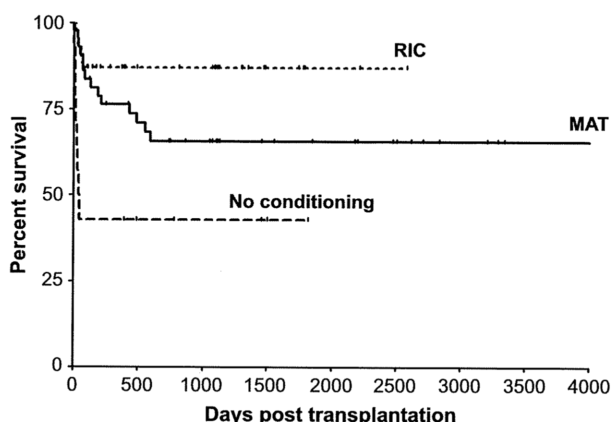

Fig 4. Kaplan–Meier estimates of overall survival after umbilical cord transplantation. Comparison of overall survival between reduced intensity conditioning (RIC), myeloablative therapy (MAT), and no conditioning is shown. For 5-year OS, MAT *versus* RIC, $P = 0·111$, MAT *versus* no conditioning, $P = 0·017$ in univariate analysis.

lower than that after URBMT in PID patients in Japan (20%) (Sakata *et al*, 2004), and was lower compared to that in UCBT studies for childhood leukaemia (Michel *et al*, 2003; Sawczyn *et al*, 2005). Thus, UCBT in PID patients in the present study was associated with a good survival rate, good engraftment rate, rapid haematological recovery and a lower incidence of acute and chronic GVHD.

Given that the 5-year OS for SCID patients (71%) was better than that for SCID patients receiving bone marrow from HLA-mismatched related donors in both Japan (5-year OS, 36%, Imai, Morio, Kamachi, Kumaki, Ariga, Nonoyama, Miyawaki, and Hara, unpublished observations) and Europe (5-year OS, 52%, Antoine *et al*, 2003), UCBT would be particularly beneficial for patients requiring rapid access to donor units yet lacking a matched related donor.

The present study found that several key risk factors were associated with overall mortality. First, infection was the major cause of mortality during the first 100 d after UCBT in PID patients, and the frequency was much higher than that observed in other disorders following UCBT (Rocha & Gluckman, 2006; Kurtzberg *et al*, 2008, Szabolcs *et al*, 2008). As predicted and reported in previous studies (Antoine *et al*, 2003; Cuvelier *et al*, 2009), infection at the time of transplantation was associated with poor survival ($P < 0·0001$), suggesting that the control of pre-existing infection at the time of UCBT is critically important.

Eight of 11 SCID patients who had active infection, mainly CMV pneumonia, died before day 50, while 26 of 28 patients without infection at the time of UCBT remained alive at the time of data collection. UCBT without conditioning was selected for 12 patients, of which seven had CMV infection and one had *Pneumocystis* pneumonia at the time of transplantation. Six out of the seven patients died of CMV infection; and one patient with *Pneumocystis* pneumonia did not survive UCBT.

UCBT in WAS patients achieved a good 5-year OS, as reported in a previous study of 15 cases (Kobayashi *et al*, 2006). One of the key factors would have been the time from diagnosis to transplantation. In our WAS patients, UCBT was performed at a median age of 14 months (range, 4–84 months), when most patients were thrombocytopenic, but did not yet have uncontrolled infection or autoimmunity.

Four CGD patients died of bacterial or fungal infection without engraftment. Although these patients were not categorized as those with active infection at the time of transplantation, they required intravenous administration of antimicrobial and antifungal agents before and after transplantation.

Second, HLA disparity was a risk factor associated with overall mortality. Lower survival was observed in UCB recipients transplanted with a ≥2 antigen-mismatched graft compared with those transplanted with a <2 antigen-mismatched graft [Hazard Ratio (HR) = 3·87, $P = 0·002$]. Although no difference was observed in 5-year OS between recipients of HLA-matched and those of HLA 1-antigen mismatched UCBT in the present study, we would need data from a larger number of patients with information on more extensive and sensitive HLA typing to discuss the impact of fully matched HLA on transplant outcome.

Finally, non-SCID/SCN/WAS patients showed a significantly lower survival rate (HR = 5·40, $P < 0·0001$ by multivariate analyses). Although a previous large-scale study showed that results of HSCT according to disease did not show obvious disease-specific findings (Antoine *et al*, 2003), it is not yet known if UCBT is suitable for all types of PIDs. This may indicate donor source other than UCB is preferable for certain types of PID. Although the success of UCBT noted for X-linked hyperIgM syndrome, bare lymphocyte syndrome and

X-linked recessive anhidrotic ectodermal dysplasia with immunodeficiency (Tono *et al*, 2007) is encouraging, optimization of transplantation procedures and determination of suitable timing for UCBT may be necessary for this group of patients. Alternatively, this may simply indicate an expansion of transplantation to less favourable clinical conditions or to less favourable transplantation conditions. Studies on a larger cohort are necessary for drawing any conclusion on whether diagnosis is significant overall.

Recent studies suggest improved survival after BMT for PID with the RIC regimen; however, to date, comparison of CBT using RIC *versus* MAT has not been made. In our study, 87% of patients on the RIC regimen and 66% on the MAT regimen remained alive at the latest follow-up. Multivariate analyses revealed that the RIC regimen is associated with a higher 5-year OS than the MAT regimen (HR = 0·20, P = 0·011). Although it is premature to conclude that RIC provides an equal or superior outcome to MAT for all PID patients, non-myeloablative treatment may be beneficial at least for certain types of PID. RIC was selected preferentially in SCID and CGD patients, with good survival rates: 17 of 18 SCID patients and three of four CGD patients remain alive. As a result of this, we are in the process of initiating a clinical trial of UCBT with RIC in SCID patients. On the other hand, only two of 23 WAS patients received RIC. Our previous data showed that a conditioning regimen other than BU/CY or BU/CY/ATG was the only independent factor associated with failure in HSCT for WAS patients (Kobayashi *et al*, 2006). However, whether this holds true for UCBT in younger WAS patients should be determined.

Notably, although the outcome of UCBT for WAS in this cohort was excellent compared with that from previously reported HSCT results using different donor sources (Kobayashi *et al*, 2006; Friedrich *et al*, 2009), UCBT in WAS patients was associated with a high rate of grade 2–4 acute GVHD (11 of 23 patients) and a post-transplant infectious episode (13 of 23 patients). Eight patients experienced bacteraemia/sepsis and six suffered a viral infection (CMV pneumonia, four; Coxsackie virus enterocolitis, one and persistent norovirus infection, one). The high rate of serious infections and GVHD in WAS patients after transplantation warrants further study in search of preventive measures that might include RIC for severe, transplantation-related toxicities.

Long-term follow-up of the clinical and immunological status is necessary when considering the lifespan of PID patients. Recent studies on the long-term outcome after HSCT for SCID revealed the presence of relatively late complications, such as chronic GVHD, autoimmune events, severe or recurrent infections, chronic human papilloma virus infection, nutritional problems and late rejection in 50% of patients (Mazzolari *et al*, 2007; Neven *et al*, 2009). Similarly, long-term follow-up of HSCT in WAS patients revealed that 20% of patients developed chronic GVHD-independent autoimmunity (Ozsahin *et al*, 2008). One possible measure that might be taken to avoid the chronic problems associated with CBT would be to select a HLA-matched UCB unit, as HLA disparity was a risk factor for both overall survival and the development of GVHD in our study. The advantage of RIC over MAT in preventing late complications needs careful assessment, together with data on mortality, engraftment and early post-transplant complications.

Finally, the issue of SCID patients who died before or without receiving SCT, most likely due to uncontrolled infection, still remains unresolved. This suggests that the early diagnosis of SCID and prevention of opportunistic infection within a protected environment and the administration of appropriate prophylactic drugs is critically important for the improvement of survival in SCID patients in general. To that end, neonatal screening with the employment of T cell receptor excision circles should be beneficial for an improved outcome in SCID patients (McGhee *et al*, 2005; Morinishi *et al*, 2009).

We report the results of UCBT for 88 PID patients in Japan. Despite the limitations of a retrospective, non-randomized study, our study suggests that unrelated umbilical cord blood can be considered as a promising stem cell source for children with congenital immunodeficiency when a HLA-matched related donor is not available.

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