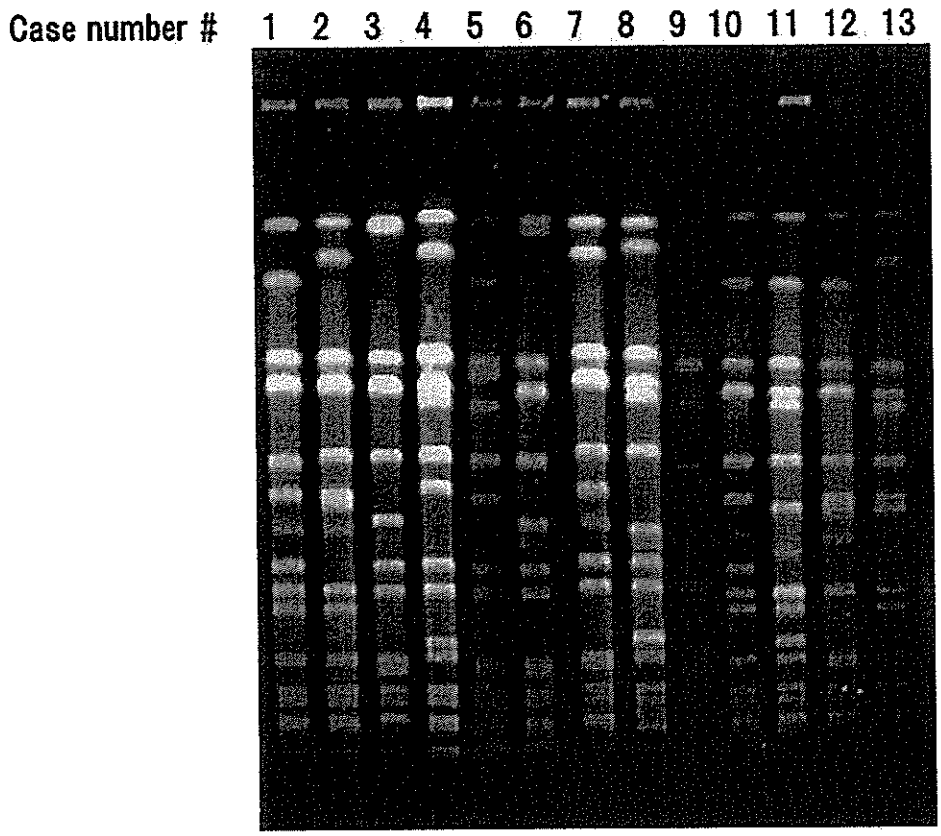

Fig. 3. PFGE analysis of isolated MRSA in the SCT unit. The PFGE pattern showed that there were no detectable differences in bands between cases 3 and 6, but more than two bands were identified in the other four cases (cases 1, 2, 4 and 5). Additionally, two strains that had been previously isolated in the SCT ward (cases 7 and 8) were distinguishable, and the five epidemiologically different isolates (cases 9 to 13) from the University of Tokyo Hospital (1,150 beds) were also distinguishable, with differences in more than two bands.

infection," while those without symptoms were considered "MRSA colonization."

RESULTS

Clinical Course of MRSA Outbreak

The clinical characteristics of six patients in whom MRSA was isolated are presented in Table I. The first patient (case 1) was admitted to the SCT ward because of severe intestinal symptoms induced by gut GVHD, chronic diarrhea, and continuous gastrointestinal bleeding, which occurred at 107 days after SCT. The patient received corticosteroid and intravenous antimicrobial therapy. For 4 weeks prior to his admission, there had been no case of MRSA infection or colonization in the ward. At 13 days after admission, the first isolation of MRSA in his stool was recorded (Table I). Subsequently, five other patients newly developed MRSA events over the next 4 weeks (Figure 1), while the incidence of MRSA detection of SCT ward had remained at one or two cases per month (mean 0.8 /month, range 0–2 /month, SD 0.61, Figure 2). Among these five cases, three (cases 4, 5, and 6) had been admitted to the SCT ward directly from the outpatient clinic without a past history of MRSA infection. The other two cases (cases 2 and 3) were transferred from other wards after the admission of case 1, and MRSA was isolated prior to transfer to the SCT ward (Figure 1). Since, in these two cases, MRSA was identified again in different site in SCT with different drug-sensitivity profile (data not shown) from a previous strain, we included these two cases in the analysis. There were no other patients who were previously identified with MRSA infection or colonization.

Tracing Procedure

The transmission, if any, appeared to take a random pattern, as illustrated in Figure 1. To better evaluate whether the transmission pattern was direct or indirect, we identified the layout of the patients' bed assignments. This revealed that there were nei-

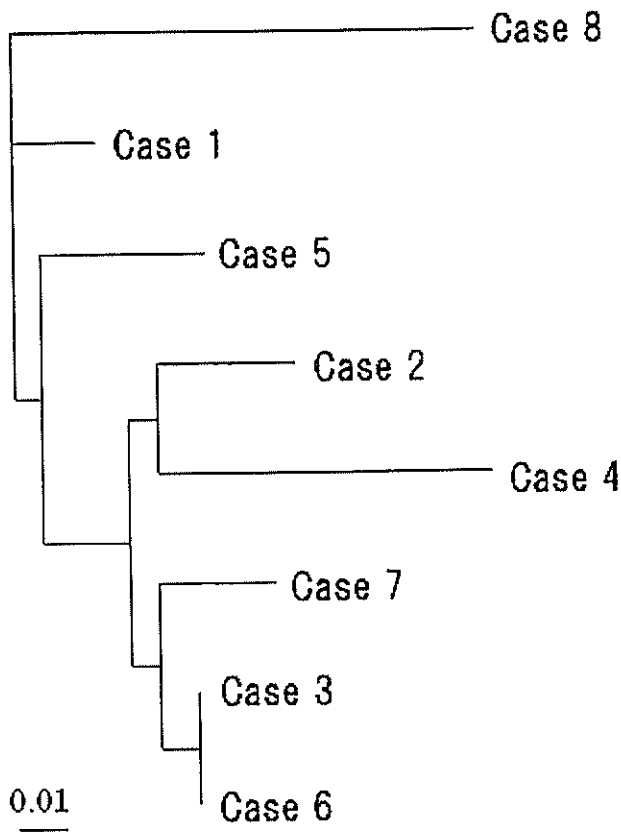

Fig. 4. AFLP pattern of isolated MRSA. AFLP analysis was performed for the same six isolates (case 1 to 6) described in Figure 4. Gene polymorphism showed same result of similarity as PFGE pattern had already indicated, i.e., cases 3 and 6 had the same polymorphism pattern and the others were different strains. The mutual relation of gene polymorphism is presented in the dendrogram and relatedness is indicated by the length of line. The scale bar drawn in the lower part indicated 1.0 % relatedness.

ther overlaps nor coexistence with preceding patients, except that cases 1 and 3 used the same room on different days without an overlap.

PFGE and AFLP Assays of MRSA Isolates

PFGE analysis of the six MRSA strains isolated (Figure 3) showed that two strains (cases 3 and 6) were indistinguishable and therefore considered to be derived from the same isolate, while the remaining four cases (cases 1, 2, 4, and 5) were considered to have different strains. Seven epidemiologically different isolates, i.e., two strains isolated from another ward at different times (cases 7 and 8) and five strains isolated from another hospital (cases 9 to 13) were used as in-hospital and extra-hospital controls, respectively. The results were confirmed by AFLP analyses as a dendrogram shown in Figure 4.

DISCUSSION

The spread of MRSA in highly protected care units, including ICU [19] and neonatal ICU [20], is a well-known major complication in compromised patients. Although few reports have been published on the outbreak of MRSA in a SCT unit, a continuous rise in the incidence of hospital-acquired MRSA infection [21] should influence the incidence of MRSA infection in SCT recipients [22]. Collin et al. reported that the incidence of multidrug resistant *S. aureus* was 15% in isolates from BMT patients with blood stream infection in 1991–1997 [23]. Prolonged neutropenia has been found to be a risk factor for the development of infectious complications in SCT recipients [24]. Since the outbreak of MRSA among immunocompromised patients can greatly affect their mortality, appropriate methods for infection control are strongly warranted. The Consensus Panel's guidelines for preventing the spread of MRSA recommend contact precautions and the isolation of infected or colonized patients in a single room or cohort, i.e., grouping them geographically with designated staff [18]. Also, since MRSA colonization precedes infection because of inpatient circumstances and rather strong treatments [25,26], a local control is very important for controlling MRSA outbreak in selected circumstances such as SCT ward in which many immunocompromised patients are taken care of.

In this report, we described an MRSA outbreak in the SCT ward during a limited period of 4 weeks. Initially, we suspected that all MRSA infections were caused by a single source, such as highly contaminated stool. However, unexpectedly, no direct contact was identified among patients and staff who were involved in their care. The transmission of MRSA mostly occurs through direct person-to-person contact, and transmission from the environment is extremely rare in places where strict precautions are taken and careful decontamination procedures are used. Hence, we undertook a molecular epidemiological analysis to critically examine the suspected break in our procedure. We found that four of the six isolates were genetically different, and our Infection Control Team concluded that horizontal transmission was unlikely. Nevertheless, the interest raised with this event resulted in further enforcement of essential precautions against droplets and contact,and the elimination of new MRSA cases for subsequent months.

Although our observation was well anticipated, in that molecular typing techniques are effective in the diagnosis and tracking of MRSA, the results are still unique, since they highlight the value of these methods over clinical judgment in a critical care situation

with highly immunocompromised patients. Since the molecular typing properties of MRSA are very similar in Japan, especially in the local areas [27], we focused on the genetic event detected by molecular typing and diagnosed those differences as different strain from outbreak. Thus, this report should be helpful for evaluating whether the routine application of these measures should be critically considered in the assessment of outbreak.

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Nutritional Support for Patients Suffering From Intestinal Graft-versus-Host Disease After Allogeneic Hematopoietic Stem Cell Transplantation

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Background: Patients who exhibit gastrointestinal (GI) involvement due to graft-versus-host disease (GVHD) after allogeneic hematopoietic stem cell transplantation (SCT) are often recommended to withhold oral intake (NPO) to avoid further damage to the GI mucosa. However, it is possible that continuing oral intake could be beneficial in many patients compared to total parenteral nutrition (TPN).

Objective: The primary objective of this prospective study was to evaluate whether programmed step-ladder oral dieting (enteral nutrition; EN) is feasible and beneficial for these patients.

Methods: A total of 18 patients who exhibited GI-acute GVHD (stage I to III gut GVHD) after SCT received an EN dieting program, and changes in clinical and laboratory parameters were compared to those in a control cohort of 17 patients who were placed on NPO with TPN. Patients with GVHD were included prospectively and those with intestinal bleeding/obstruction, severe pancreatitis, and cytomegalovirus enterocolitis were excluded.

Results: None of the patients in the EN group experienced significant adverse events, including exacerbation of GI symptoms. Although there was no statistically significant difference in the volume or frequency of diarrhea or the time to complete dietary recovery, parameters including body weight and serum levels of total protein and albumin tended to improve faster in the EN group.

Conclusion: The EN diet is safely applicable to patients suffering from GI involvement by GVHD. Am. J. Hematol. 81:747–752, 2006. © 2006 Wiley-Liss, Inc.

Key words: graft-versus-host disease (GVHD); enteral nutrition; immunonutrition

INTRODUCTION

Graft-versus-host disease (GVHD) is a major complication of allogeneic hematopoietic stem cell transplantation (SCT) that influences the ultimate prognosis of patients [1]. Gut involvement due to GVHD particularly impairs the host nutritional status and QOL due to long-lasting diarrhea and anorexia. Hence, effective supportive care of patients suffering from GVHD should include attention to intense nutritional support and bone mineral retention, since many receive concomitant steroid therapy. Additionally, normal intestinal architecture and functions are required to prevent biliary stasis, retarded bowel movement, bacterial translocation, and resultant systemic infection [2,3]. With the development of gut GVHD, patients are often recommended to withhold oral intake (NPO, "bowel rest") to avoid further damage to the gastrointestinal (GI) mucosa. However, this raises a serious concern since NPO care can induce atrophic deficit of the GI mucosa and resultant dysfunction

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TABLE I. Grade of Programmed EN Dieting

Step	Staple food (form of rice)	Side dishes (approved foods and cuisines)	Nutritive value
0	Liquid	Juice (without grain, without oranges), electrolytic supplement solution	500–2000 ml
1	Liquid	Water gruel, starch gruel, clear soup, consomme, juice, miso soup	Calories 300–350 kcal Protein 5–7 g Fat 15–2 g Dietary fiber 15 g
2	Mush	Potato, vegetables, canned fruits, vegetable juices, noodles, tofu, whitefish	Calories 600–650 kcal Protein 20–25 g Fat 5–8 g Dietary fiber 1.5–8 g
3	Rice gruel	Eggs, breads, banana, apple	Calories 900–1000 kcal Protein 30–35 g Fat 10–13 g Dietary fiber 8–9 g
4	Boiled rice	Blue-skinned fish, oil (~3 g/day)	Calories 1200–1300 kcal Protein 40–45 g Fat 15–20 g Dietary fiber 9–10 g
5	Boiled rice	Chicken (low fat), yogurt, oil (~8 g/day)	Calories 1500–1600 kcal Protein 60–65 g Fat 30–35 g Dietary fiber 12–13 g

Note: A patient-oriented stepped-up dieting program was gradually applied over six steps that varied with regard to the solidity, intensity, and acceptability by the patient.

of the GI system. Moreover, it has recently been reported that enteral nutrition (EN) was more effective than parenteral nutrition for the nutritional support of patients with an injured intestine due to trauma or an invasive operation [4,5]. Taken together, these findings suggest that the current patient management procedure that includes the interruption of oral feeding to enforce "bowel rest" in SCT patients suffering from GVHD should be critically reevaluated. Furthermore, EN, if tolerable, may be a preferred route for maintaining digestive and absorptive function as intact as possible.

In those suffering from GI involvement of GVHD, such evaluation becomes more complex since diarrhea is very often multifactorial and includes secretory dysfunction, osmotic factors, and rapid passage. Hence, the establishment of a standard care procedure remains very difficult. To address these concerns, we conducted a controlled cohort study to evaluate the benefit of different nutritional support measures for patients suffering from acute gut GVHD after SCT. Our clinical hypothesis was that a programmed and controlled scheduled oral nutritional support with EN is beneficial for patients who have mild to moderately progressing acute symptoms of gut GVHD.

PATIENTS AND METHODS

Patients

Seventy patients who were treated at the National Cancer Center Hospital from January 2001 to December 2003 and who developed GI symptoms by GVHD were involved in this prospective study. Forty among those eligible patients met the following inclusion criteria: (i) pathologically diagnosed GVHD with biopsied specimens, (ii) presented symptoms within 100 days after SCT, and (iii) clinically diagnosed as stage I to III gut GVHD and grade II to III acute GVHD according to the clinical grading criteria [6,7]. Patients who had intestinal tract bleeding, intestinal obstruction, or severe pancreatitis were excluded from this analysis, since these pathophysiologies are considered contraindications for EN. Additionally, patients with pathologically diagnosed cytomegalovirus enterocolitis were also excluded, and thus a total of 35 patients were left for this study.

Methods

In the study periods, two different nutritional intervention procedures were applied; patients who developed gut GVHD before July 2002 ($n = 17$) were treated with NPO and total parenteral nutrition (TPN) (C group), while the remaining patients who developed gut GVHD after July 2002 ($n = 18$) were treated by programmed GVHD dieting intervention (EN group). The patients were consecutively registered to our database at National Cancer Center Hospital, and this prospective study was approved by the IRB. The programmed EN dieting consisted of six steps with regard to solidity, intensity, and acceptability for intestinal digestion, as shown in Table I. Each food and nutrient was made more solid and dense

in a step-up manner, after the confirmation of stable symptoms that lasted for a minimum of 3 days. Each step of programmed EN dieting was suitably stepped down when intolerance or exacerbation of gut GVHD symptoms developed. Patients were made NPO with the appearance of significant abdominal symptoms (nausea, vomiting, and abdominal pain). Patients in the EN group only received oral intake without enteral tube feeding. On the other hand, the patients in group C were adequately allowed to eat according to their symptoms with TPN.

We evaluated "time to complete dietary recovery," which was defined as the duration from the start of nutritional management (stopping oral intake or start of programmed EN dieting) to the restoration of a normal diet with the recovery of nutritional parameters. Nutritional parameters evaluated in this study included (1) clinical symptoms, including volume and frequency of diarrhea, and body weight and (2) laboratory data, including total serum protein and albumin. Body mass index (BMI) was calculated as BMI = {height (m)}2/body wt (kg).

Statistical Analysis

Our clinical hypothesis was that a programmed and controlled schedule of nutritional support with oral intake (EN dieting) could be effective in the support of patients suffering from acute gut GVHD with mild to moderately progressing symptoms. We evaluated "the time to complete dietary recovery," which was defined as the duration from the start of nutritional management (stopping oral intake or start of EN dieting) to the recovery to normal diet, various enteral symptoms, and nutritional parameters. The time to complete dietary recovery is shown with a time–event cumulative curve, and the log-rank test was used to compare groups C and EN. Nutritional parameters are given as the mean of each group by time course, and the data in groups C and EN were compared by an analysis of variance (ANOVA). A P value of less than 0.05 was considered significant.

RESULTS

Patients' Characteristics

The patients' clinical backgrounds are summarized in Table II, which shows that there are no essential differences between groups C and EN. Older patients tended to receive a reduced-intensity regimen more often than a conventional regimen.

Safety of Programmed EN Dieting

Throughout the study, no severe adverse events associated with nutritional intervention were observed, indicating that our procedure with gradual stepped-up or -down dieting was safe. No severe infectious episodes were observed in each group. EN dieting had to be terminated early in 2 of 18 cases due to prolonged GI symptoms and exacerbation of an underlying malignant disorder. There were 4 censored cases in group C, mainly due to recurrence of the basic malignant disorder.

TABLE II. Patients' Characteristics

	EN group ($N = 18$)	C group ($N = 17$)
Age median (range)	53 (22–64)	53 (23–69)
Sex male/female	12/6	14/3
Disease		
AML	6	8
MDS	3	2
ALL	4	2
CML	3	1
NHL	1	2
ATL	1	1
Solid tumors	0	1
Transplantation source		
BM	1	3
PBSC	17	14
Transplantation regimen		
Conventional	5	7
Reduced intensity	13	10
Donor HLA typing		
Full match	14	14
1 locus mismatch	4	0
2 loci mismatch	0	3
GVHD prophylaxis		
CSP alone	10	8
CSP + MTX	6	4
CSP + ATG	2	2
Others	0	3
Gut GVHD stage		
1	5	9
2	7	3
3	6	5
GVHD grade		
II	6	8
III	12	9
Onset day of gut GVHD (mean of day)	74	68

Note: Patients who underwent SCT and developed gut GVHD were enrolled in this study. Patients who developed gut GVHD before July 2002 ($n = 17$) were treated with no oral intake (C group), while the EN group ($n = 18$) was treated by programmed GVHD dieting. AMI, acute myelogeneous leukemia; MDS, myelodysplastic syndrome; ALL, acute lymphoblastic leukemia; CML, chronic myelogeneous leukemia; NHL, non-Hodgkin lymphoma; ATL, adult T-cell leukemia; BM, bonemarrow; PBSC, peripheral blood stem cell; CSP, cyclosporine; MTX, methotrexate; ATG, anti-thymocyte globulin.

Efficacy of Programmed EN Dieting

Although there was a wide variation in each patient in diarrhea volume and frequency of diarrhea, we adapted ANOVA to evaluate whether there is a statistically significant difference between the two groups

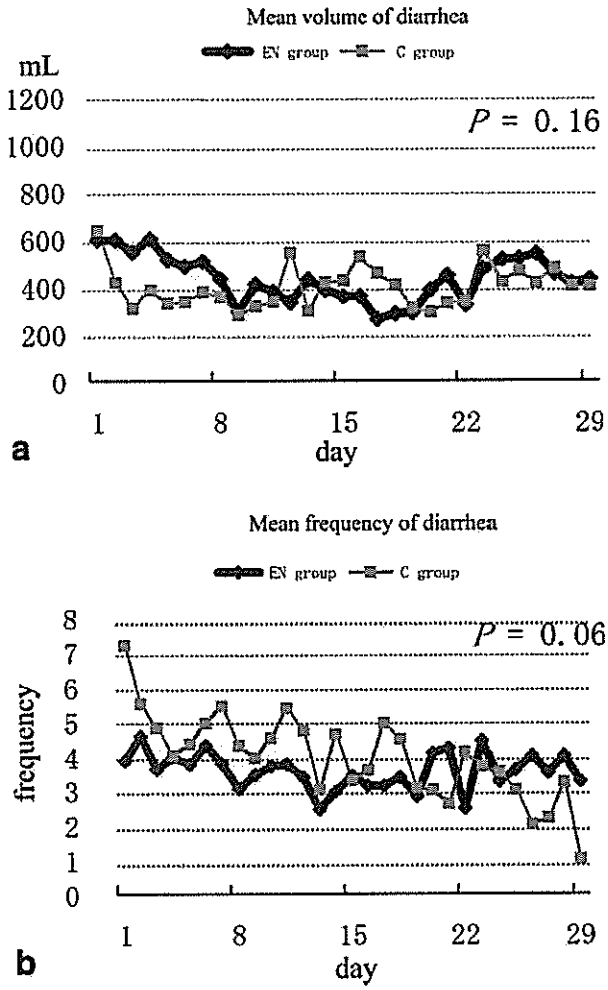

Fig. 1. Changes in mean volume and frequency of diarrhea. No difference was observed between the C and EN groups in the time-course of diarrhea as evaluated by volume ($P = 0.16$) (a) and frequency ($P = 0.06$) (b).

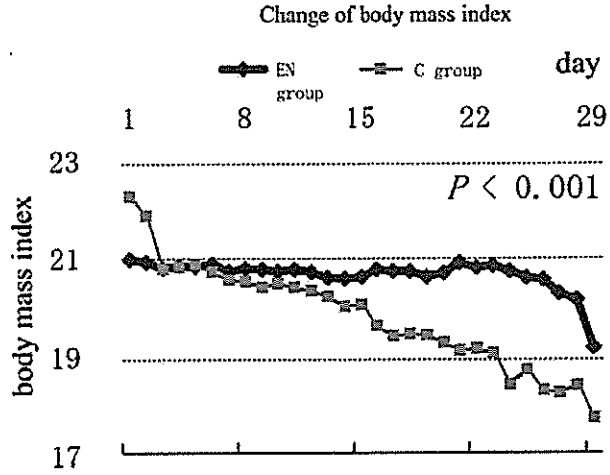

Fig. 2. Changes in BMI. The mean changes in BMI, with the first evaluation as a control, were compared between the two groups. A slower decrease in body weight tended to be observed in the EN group, while patients retained their BMI significantly better in the EN group than in the C group ($P < 0.001$). BMI was calculated as BMI = {height (m)}^{2}/body wt (kg).

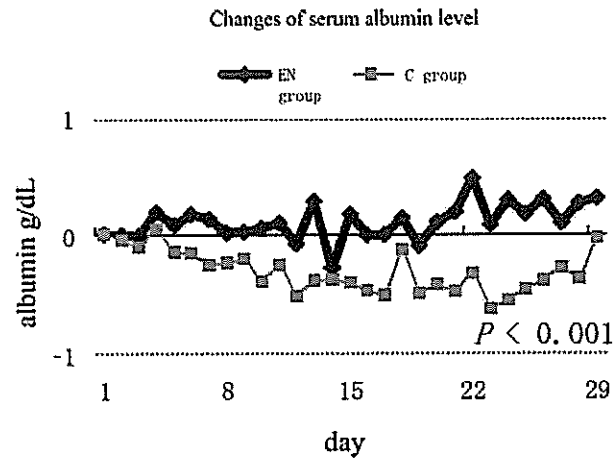

Fig. 3. Changes in albumin as nutritional parameter. One of the nutritional parameters, albumin (Alb), was evaluated between the C and EN groups. In the EN group, patients maintained significantly more stable levels of Alb ($P < 0.001$).

($P = 0.16$ and 0.06, respectively, Figure 1a and b). The mean body weight values in each group were compared by considering the absolute changes after adjusting by the value at the initial evaluation. In comparing the two groups, the decrease in body weight after the start of nutritional management was more obvious in group C than in group EN but this difference was not statistically significant ($P = 0.09$), since there was a wide interpatient variation. On the other hand, the change in BMI was significantly different between the two groups (Figure 2, $P < 0.001$).

Nutritional status was also estimated by laboratory parameters, including serum levels of total protein and albumin (Alb), which were determined as absolute changes by adjusting by the value at the first evaluation at the starting point of nutritional management, and a significantly slower decrease was noted in the EN group ($P < 0.001$) (Figure 3). These nutritional parameters remained higher in group EN than in group C. During the study period, no patient actually met with stopping rules mentioned above and consequently, the total number of days for NPO was not evaluated. The time to complete dietary recovery was compared between the two groups. While 38 days were required for the

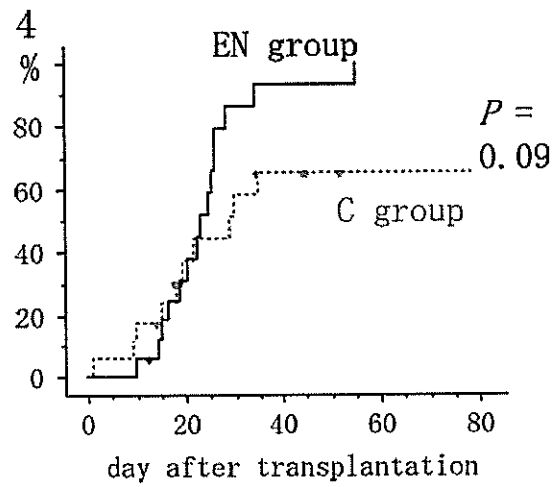

Fig. 4. Time to complete dietary recovery. The number of days required for return to a normal diet was 38 days in group C, while it was 31 days in group EN, with no statistically significant difference ($P = 0.09$).

recovery to a normal diet in group C, 31 days were required in group EN (Figure 4).

DISCUSSION

Since Weisdorf et al. reported that central venous parenteral nutritional support improved long-term survival in patients who underwent bone marrow transplantation (BMT) [8], intravenous TPN has been widely used in SCT. However, it has not yet been confirmed which procedure, enteral or parenteral nutrition, can provide more effective and safer nutritional support. In this study, we considered that the patients in the EN group may have preserved nutritional parameters better than the other group and ate sooner, although no differences were found in the time to complete dietary recovery. A clinical study group at Johns Hopkins University randomized BMT patients into two groups to receive different types of nutritional support, TPN or EN, and they did not observe any differences in nutritional parameters between the two groups [9]. In their study, patients who received TPN were allowed to eat anything they liked, while those with EN had few chances to receive TPN treatment. Moreover, those who had been receiving TPN were allowed to take oral intake and thus were not on strict NPO. Additionally, in our study, the two groups of patients were evaluated in different study periods, and there was a significant difference in the modality of the supportive measures. These points make a direct and strict comparison between the TPN and EN groups very difficult and unreliable. These biases, which are inherent to studies in this field, also existed in our study, which might explain why we failed to detect significant differences in clinical benefits.

We used to routinely advise patients to stop oral intake with the development of gut GVHD. Thereafter, they were encouraged to drink or eat gradually, since it has been suggested that inadequate nutritional support further deteriorates gut GVHD symptoms. To establish clearly defined subjective guidelines, we conducted this interventional cohort study. We found that both controlled and uncontrolled EN can be administered safely. Since the time to complete dietary recovery was almost comparable in the two groups, the results suggest that any EN program is acceptable and does not harm or degrade the QOL of patients suffering from GVHD. If this is confirmed, a restricted diet would not be necessary for those with moderately symptomatic gut GVHD. Nevertheless, the evaluation of nutritional parameters in this study suggested that controlled EN did a better job of maintaining body weight and serum nutritional status, compared to the results in the NPO group. The random administration of food intake may be inadequate compared to scheduled dieting, which attempts a gradual build-up of intestinal mucosa by the comprehensive supply of nutrients including glucose, protein, fat, fiber, etc. This may have a secondary advantage of keeping the mucosal barrier intact and preventing bacterial translocation through the GI tract.

Nevertheless, since the cause of diarrhea is multifactorial, it is inherently difficult to assess the effectiveness of and standardize nutritional intervention procedures. In the literature, four pathologies have been reported to be contraindications for EN since they cause undesirable bowel movement, i.e., presence of gastrointestinal bleeding, intestinal obstruction, severe pancreatitis, and intestinal perforation. The pathophysiology of diarrhea associated with gut GVHD includes osmotic and secretory diarrhea. Hypertonic EN is considered to further deteriorate symptoms of diarrhea. Hence, it is reasonable to suggest that dietary foods in EN adequately maintain an isotonic status as well as nutritional status to improve immunologic function. An intact GI system is vital for maintaining normal immune functions, and a novel concept of nutrition support, "immunonutrition," has been introduced, which focuses on the maintenance of the comprehensive biological protection system against external pathogens to maintain normal immune function [10]. Clinical benefits of immunonutrition, including improvement of nutritional parameters, decreased risk of infection, and shorter duration of hospitalization, have been reported in patients in the perioperation period and in those who required care in the ICU [11,12]. However, currently a precise evaluation

of the efficacy of each component of immunonutritional agents is difficult [13], and controversy still exists regarding the value of immunonutrition after SCT. This study did not evaluate this proposed immunonutrition, and to accomplish this in SCT practice, prospective monitoring of immune parameters would be required.

The serum level of albumin can be significantly affected by many variables including diarrhea associated with GVHD and, hence, would not be a very good marker for the evaluation of protein status in the HSCT population. However, in our experience, serum albumin decreased after SCT to suggest the possibility of the use in the estimation of patient's nutrition status at least for a short period of follow-up, when referring to the general description in the guideline by American Society for Parenteral and Enteral Nutrition, i.e., "low serum levels indicate which hospitalized patients are at increased risk of morbidity and mortality" [14].

In conclusion, the current study is hampered by preexisting biases including a small number of studied patients, a cohort analysis in different periods, and a lack of adequate measures for data evaluation. Nevertheless, it appears that patients supported by programmed EN experienced no exacerbation of gut GVHD symptoms, with a suggested benefit of enhanced maintenance of nutrition status. Further study is warranted to prospectively evaluate the value of various nutrients including arginine, o-3 fatty acid, and nucleic acid [13] and various clinical outcomes including the cost, complications, and QOL in an attempt to improve the nutritional and immune status of transplanted patients.

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Early Detection of Plasma Cytomegalovirus DNA by Real-Time PCR after Allogeneic Hematopoietic Stem Cell Transplantation

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[1]*Hematopoietic Stem Cell Transplantation Unit, and* [2]*Clinical Laboratory Division, National Cancer Center Hospital, Tokyo, Japan,*
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ONISHI, Y., MORI, S., HIGUCHI, A., KIM, S., FUKUDA, T., HEIKE, Y., TANOSAKI, R., MINEMATSU, T., TAKAUE, Y., SASAKI, T. and FURUTA, K. *Early Detection of Plasma Cytomegalovirus DNA by Real-Time PCR after Allogeneic Hematopoietic Stem Cell Transplantation.* Tohoku J. Exp. Med., 2006, **210** (2), 125-135 —— Cytomegalovirus (CMV) infection is an important cause of morbidity and mortality after allogeneic hematopoietic stem cell transplantation. Therefore, preemptive ganciclovir therapy based on early detection of CMV reactivation is widely used to prevent CMV disease. Real-time polymerase chain reaction (PCR) has been widely used for monitoring CMV reactivation as well as the antigenemia assay that detects CMV structural phosphoprotein with a molecular weight of 65,000 (pp65). We developed a real-time PCR assay system for CMV based on a double-stranded DNA-specific dye, SYBR Green I, and quantified DNA, which was extracted automatically from plasma. This real-time PCR assay and the pp65 antigenemia assay were compared in parallel with 357 blood samples obtained from 64 patients who underwent allogeneic hematopoietic stem cell transplantation (allo-HSCT). Real-time PCR assay results correlated with those of the pp65 antigenemia assay ($p < 0.0001$). It is noteworthy that the detection of CMV DNA by PCR preceded the first positive antigenemia by 14 days. In this study, 10 of 64 patients developed CMV disease. The antigenemia assay detected CMV reactivation earlier than the development of CMV disease only in four of 10 patients. In contrast, our real-time PCR detected CMV-DNA before the development of CMV diseases in eight of 10 patients. The real-time PCR with SYBR Green I as a detection signal is simple and readily performed, and may be a useful system for early detection of CMV reactivation after allo-HSCT. ——— cytomegalovirus; real-time PCR; SYBR Green I; allogeneic hematopoietic stem cell transplantation; ganciclovir

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Cytomegalovirus (CMV) continues to be a major cause of morbidity, and this occasionally leads to the death of patients after allogeneic hematopoietic stem cell transplantation (allo-HSCT) (Boeckh et al. 2003). Although ganciclovir is an effective agent for CMV infection and disease, the administration of ganciclovir causes various adverse effects, including myelosuppression and nephrotoxicity. Therefore, it is important to discriminate high-risk patients from others to avoid over-treatment. Approaches that ganciclovir is used only in high-risk patients based on monitoring of CMV reactivation are called preemptive therapies. Preemptive therapies based on the antigenemia assay which detects CMV structural phosphoprotein with molecular weight of 65,000 (pp65) as a guide for starting ganciclovir have been widely used in clinical settings (Boeckh et al. 1996; Kanda et al. 2002a, b). However, this assay requires processing within 8 hrs of sampling, is time-consuming and suffers from a lack of standardization (Boeckh et al. 1994). Moreover, it lacks the sensitivity needed to predict the occurrence of CMV gastroenteritis (Boeckh et al. 1996; Mori et al. 2004), and can not be used when the leukocyte count is very low (Boeckh et al. 1997).

The direct detection of CMV DNA based on PCR has been investigated as an alternative measure for monitoring CMV infection, but qualitative PCR may not be able to discriminate between clinically significant and insignificant reactivation in immunocompromised individuals. On the other hand, studies using quantitative PCR have been shown to be useful for detecting patients at high risk of developing CMV disease (Gor et al. 1998). Real-time PCR, one modality of quantitative PCR, is a simple, reliable, cost-effective, and time-saving alternative strategy (Holland et al. 1991). Many institutes have developed real-time PCR assays for monitoring CMV, and have reported encouraging results (Gault et al. 2001; Cortez et al. 2003; Li et al. 2003; Nitsche et al. 2003; Ikewaki et al. 2005), where a dual-labeled fluorogenic hybridization probe or two single-labeled probes have been used to monitor PCR product formation.

Recently, a novel real-time PCR technique using a fluorescence dye, SYBR Green I, which upon binding to double-stranded DNA exhibits fluorescence enhancement, has been developed. This is the simplest real-time PCR technique based on the detection of PCR products by DNA-intercalating dye of SYBR Green I (Karsai et al. 2002). The use of SYBR Green I dye provides great flexibility and reduced cost because no target-specific probes are required. We have designed a new real-time CMV PCR assay that incorporates this system (Higuchi et al. 2002). Since cell separation from whole blood and DNA extraction could strongly affect the assay's reproducibility, we used plasma instead of peripheral blood mononuclear cells (PBMC), and a MagNA Pure automated DNA extraction instrument to automatically extract DNA from plasma. These changes made our real-time CMV PCR system much simpler than previously reported. In this study, we compared the laboratory and clinical feasibilities of this newly developed real-time CMV PCR using SYBR Green I with the existing pp65 antigenemia assay, which has been widely used as a guide for starting ganciclovir after allo-HSCT.

Materials and Methods

Patients and samples

We tested 357 blood samples obtained from 64 consecutive patients who underwent allo-HSCT and achieved sustained engraftment in our center between April 2003 and January 2004. The blood samples for the CMV antigenemia and real-time PCR were collected once a week from day 5 - 9 after transplantation until leaving our hospital. The study was approved by the National Cancer Center Institutional Review Board. All patients gave their written informed consent. The characteristics of these patients are shown in Table 1.

Stem cell transplantation procedure

Conditioning regimens and graft-versus-host disease (GVHD) prophylaxis are shown in Table 1. Fludarabine- or cladribine-based reduced intensity regimens were used in 47 patients and conventional myeloablative regimens were used in 16. Another patient did not receive any conditioning treatment before transplantation because he had severe bone marrow suppression and bacterial

TABLE 1. Characteristics of 64 patients.

Sex (Male/Female)	38/26
Median age in years (range)	47 (17 - 68)
Underlying disease	
Acute nonlymphoblastic leukemia	16
Acute lymphoblastic leukemia	8
Myelodysplastic syndrome	7
Malignant lymphoma	26
Agnogenic myeloid metaplasia	1
Plasma cell neoplasm	2
Solid tumor	4
Conditioning regimen	
Cyclophosphamide/TBI 12 Gy	6
Busulfan/Cyclophosphamide	10
Fludarabine/Busulfan	15
Fludarabine/Busulfan/TBI 4 Gy	18
Fludarabine/Busulfan/ATG	1
Fludarabine/Melphalan/TBI 4 Gy	1
Cladribine/Busulfan	8
Cladribine/Busulfan/TBI 4 Gy	2
Cladribine/Busulfan/ATG	2
Other	1
Type of donor	
HLA-identical sibling	32
HLA-mismatched family	4
Unrelated donor	28
Type of graft	
Bone Marrow	18
Blood stem cells	34
Cord blood stem cells	12
GVHD prophylaxis	
Cyclosporin A	23
Cyclosporin A/Methotrexate	38
Tacrolimus	3
CMV serostatus (recipient/donor)	
+/+	40
+/-	9
+/ ND	10
-/+	3
-/-	2

*TBI, total body irradiation; ATG, anti-thymocyte globulin; GVHD, graft-versus-host disease; CMV, cytomegalovirus; ND, no data.

infection after reinduction chemotherapy with idarubicin and cytosine arabinoside. Cyclosporine A alone, Cyclosporine A with methotrexate or tacrolimus alone, orally or intravenously was given to prevent GVHD. Ciprofloxacin, fluconazole, and sulfamethoxazole/trimethoprim were given as prophylaxis for bacterial, fungal, and pneumocystis carinii infections. All patients were given acyclovir 750 mg/day orally from day -7 to the discontinuation of GVHD prophylaxis.

CMV antigenemia assay

CMV antigenemia assay was performed by the method described previously (van der Bij et al. 1988; Gondo et al. 1994). In brief, 150,000 peripheral blood leukocytes were cytocentrifuged on a slide and fixed with acetone within 6 hours after specimen collection. The cells were incubated with monoclonal antibody horseradish peroxidase-C7 (Teijin, Tokyo) raised against the pp65 antigen of CMV, and stained by the direct immunoperoxydase method. Under light microscopy, CMV antigen-positive cells were enumerated. The degree of antigenemia was expressed as the number of positively stained cells per 50,000 leukocytes.

Amplification and detection of viral DNA

DNA was extracted from 200 μl of blood plasma with a MagNA Pure instrument (Roche Molecular Biochemicals, Mannheim, Germany). A MagNA Pure LC DNA Isolation Kit I was used according to the manufacturer's instructions. In the initial 42 samples, DNA was extracted manually using a QIAmp Blood mini-kit (Qiagen, Valencia, CA, USA).

We selected and designed the sequences of primers in the UL75 region of CMV. The forward and reverse primers of UL75 were 5′-CCT TGC GTG TCG TCG TAT TCT AGC-3′, and 5′-GCC TCA TCA TCA CCC AAA CGG ACA G-3′, respectively. PCR amplification was performed in a total volume of 20 μl in the presence of 2 μl of DNA sample, 4.4 μl of PCR master mix (Takara Ex Taq R-PCR Version, Takara, Shiga), 10 pmol of each of the primers, 2 mmol of $MgCl_2$, 2 μl (1:15,000 dilution) of Syber Green I (SYBR Green I Nucleic Acid Gel Stains, Takara), and distilled water.

PCR was performed with a LightCycler instrument using the SYBR Green I system (Roche Diagnostics, Tokyo) under the following conditions: 95°C for 30 sec and 35 cycles at 95°C for 0 sec (i.e., an instrument setting of zero seconds), 57°C for 5 sec, and 72°C for 10 sec. Crossing points were determined by the operator dependent fit points method. Melting curve analysis was performed on all of the positive results. The melting temperature range used to determine that a specimen yielding a crossing point was a true positive was 86.5 to 87.5°C.

Positive control and negative control

Positive PCR product DNA from a clinical sample was confirmed based on its positivity in electrophoresis and selected as the PCR standard. A direct sequence analysis was performed on this PCR product, which was confirmed to show a 100% match with GenBank data (NC_001347, similar as AD169 strain). The DNA from this sample was then subjected to molecular cloning by being inserted into the pCR4-TOPO vector (TOPO cloning kit, Invitrogen, Carlsbad, CA, USA). This plasmid was used as the CMV standard in this study. CMV was quantified using serially diluted CMV standards within the range of 1.41×10 to 1.41×10^8 copies per μl, and the numbers of CMV copies were calculated. The specificity of the CMV PCR was assessed by testing murine CMV (Smith strain) and herpes simplex viruses (HSV) (HSV-1; KOS strain and HSV-2; Savage strain) as negative controls. The CMV PCR assay with 35 cycles was negative for these samples.

Preemptive therapy for prevention of CMV disease

The decision to start preemptive therapy was based on the detection of 10 or more positive cells per 50,000 cells by the antigenemia assay, or by the clinical diagnosis of CMV disease with apparent or infection-related symptoms. In this study, PCR results were not used in the decision-making process regarding preemptive therapy. Intravenous ganciclovir was started at 5 mg/kg/day three times per week, and was continued until the positive cell count had decreased to less than 10 per 50,000 cells. If the number of positive cells increased or CMV-related symptoms worsened, the dose of ganciclovir was increased.

Statistical analysis and definition of CMV infection

Correlations between the number of CMV DNA and CMV antigen-positive cells were analyzed by calculating Spearman ranked correlation coefficient. Differences between two groups were assessed by the Mann-Whitney's U-test. ROC (Receiver Operating Characteristic) analysis was performed using ROCKIT 0.9B (Dorfman et al. 1992). The diagnostic power of UL75-PCR was assessed by calculating of the Area

under the ROC Curve (AUC). We accessed several cut-off values for positive cells, 1, 5, 10, or 50 per 50,000 examined cells, in the antigenemia assay to reflect "positive for CMV infection" on the ROC analysis. *P* values less than 0.05 were considered statistically significant.

Results

Clinical sample amplification

Threshold cycle values of the serially diluted standard were plotted (Fig. 1A), and showed good linearity (Fig. 1B). The amplification results of

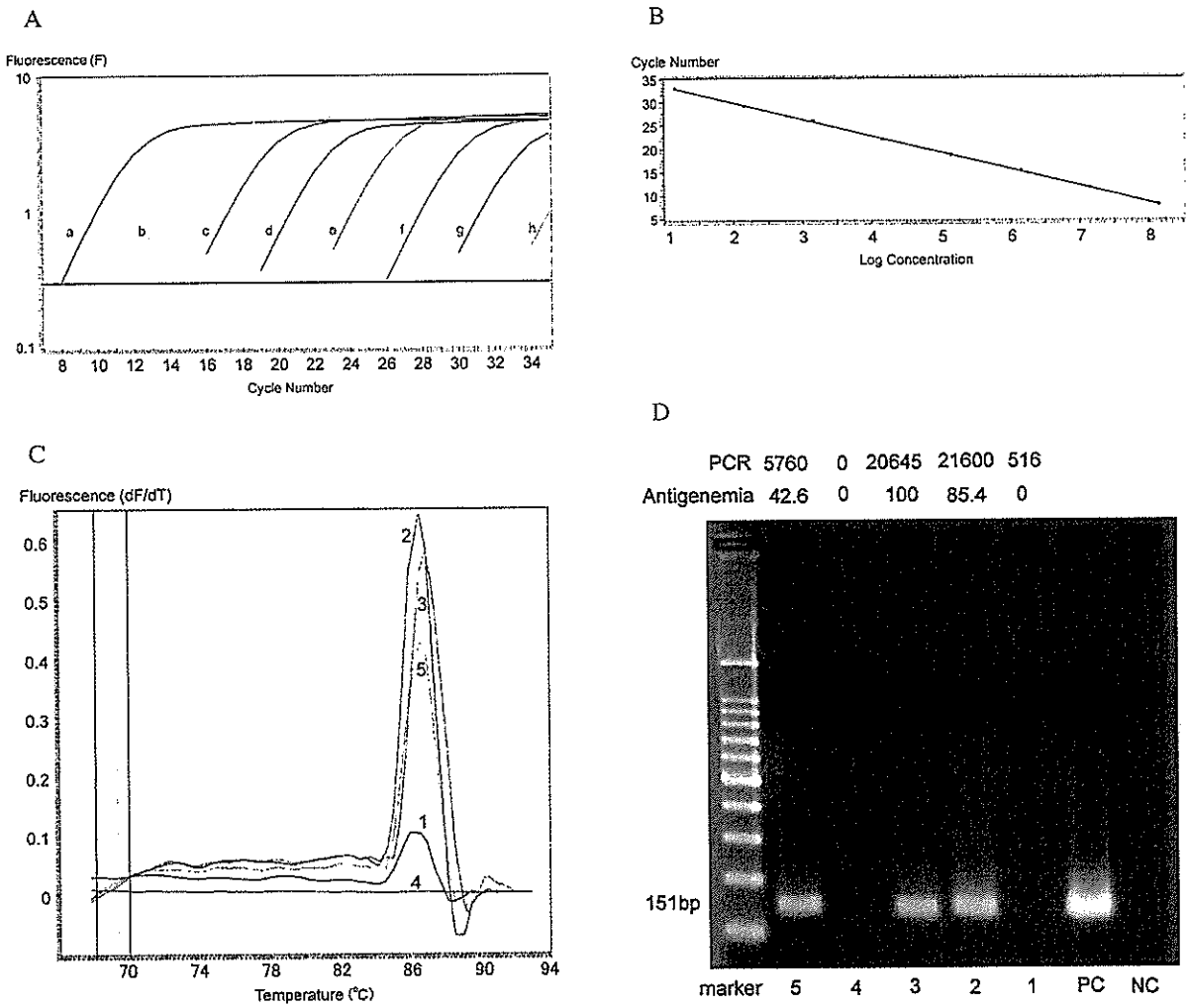

Fig. 1. Real-time PCR for CMV.
(A) Amplification plots obtained with the control plasmid for CMV. Serial 10-fold dilutions with 1.41×10^8 (a) to 1.41×10 (h) copies per reaction were amplified for 35 cycles. The horizontal line represents threshold of fluorescence signal. (B) Crossing points (cycle number) plotted against the log of copy number to obtain a calibration curve. The assay was linear from 1.41×10 to 1.41×10^8 copies per μl. (C) Melting curves for PCR products of five randomly selected clinical samples are shown. No extra peak was observed. (D) Amplification of PCR was confirmed by 2% agarose gel electrophoresis, which showed tight single bands, except in lanes 1 and 4. The numbers in upper line above the gel indicate the copy numbers per ml in cases 1, 2, 3, 4 and 5. The numbers in lower line above the gel indicate the corresponding results of the antigenemia test per 50,000 examined cells. Panels (C) and (D) share the same case numbers. The expected size of the PCR product is 151 bp. PC, positive control; NC, negative control.

five randomly selected clinical samples are shown as representative data. To confirm the purity of amplification, melting curves for PCR products after amplification were examined and the presence of an extra peak was neglected (Fig. 1C). Furthermore, amplification was confirmed by 2% agarose gel electrophoresis. Three of five samples showed a tight single 151 base-pair band in each lane, except lanes 1 and 4 (Fig. 1D), indicating that only one product was amplified. As a reference, the calculated copy numbers and the results of the antigenemia test for these samples are shown in Fig. 1D.

Comparison of the pp65 antigenemia assay with CMV real-time PCR

A total of 357 weekly samples were obtained from 64 patients and analyzed by both real-time PCR and antigenemia assays. As a result, a total of 158 samples obtained from 40 patients were positive for antigenemia assay, 220 samples from 55 patients were positive for real-time PCR which were confirmed by electrophoresis and melting curve analysis, 113 samples were negative for both assays, and 134 were positive for both assays (Kappa = 0.53). Eighty-six samples were positive by real-time PCR and negative by the antigenemia assay, while 24 samples were negative by real-time PCR and positive by the antigenemia assay (Table 2). The median number of pp65-positive cells in these 24 samples was 2 (range, 1.4 – 10.3) per 50,000 leukocytes.

There was a correlation between the CMV DNA copy number and the pp65-positive cell count (R = 0.738, $p < 0.0001$ by the Spearman test) (Fig. 2). Samples from patients were classified into four groups according to the results of the antigenemia assay (Fig. 3). Group 1 ($n = 199$) was negative by the antigenemia assay, group 2 ($n = 75$) was positive at 1 to 9 cells, group 3 ($n = 42$) was positive at 10 to 49 cells, and group 4 ($n = 41$) was positive at > 50 cells. The median CMV DNA load was 0 copies/ml (range, 0 to 39,345) in group 1, 344 (2.5 $\log_{10}$) copies/ml (0 to 172, 750) in group 2, 4,910 (3.7 $\log_{10}$) copies/ml (0 to 141,650) in group 3, and 22,200 (4.3 $\log_{10}$) copies/ml (2,285 to 464,750) in group 4. The CMV DNA load was significantly different in each group, as shown in Fig. 3 ($p < 0.0001$ by the Kuruskal-Wallis test). The specimens negative by real-time PCR or the antigenemia test are not depicted on the graphs in Fig. 2 and 3.

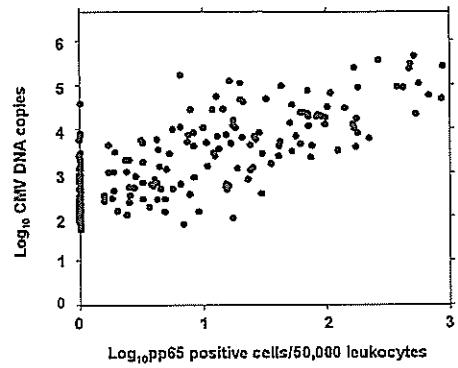

Fig. 2. Correlation between CMV DNA copy number in plasma and CMV pp65-positive cells. The CMV copy number was plotted on a logarithmic graph against the number of pp65-positive cells. The correlation between the two tests was examined (R = 0.738, $p < 0.0001$ by the Spearman test). The specimens negative by real-time PCR or the antigenemia test are not depicted. Minimum value by real-time PCR was 52 copies/ml.

TABLE 2. Results of real-time CMV PCR and CMV pp65 antigenemia of blood plasma for 357 samples.

CMV pp65 antigenemia	CMV PCR in blood plasma		Total
	Positive	Negative	
Positive	134	24	158
Negative	86	113	199
Total	220	137	357

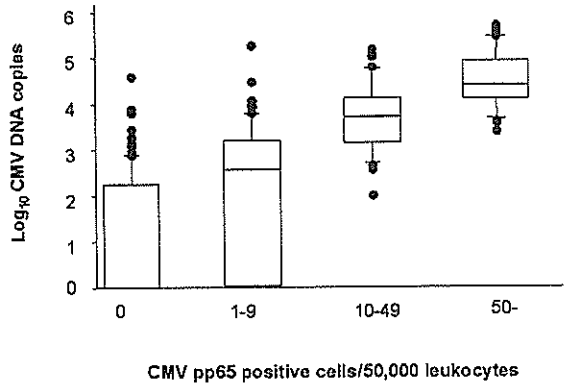

Fig. 3. CMV DNA loads in plasma based on the number of CMV pp65-positive cells per 50,000 leukocytes. Samples were classified into four groups: group 1 (n = 199), negative by the antigenemia assay; group 2 (n = 75), 1 to 9 positive cells; group 3 (n = 42), 10 to 49; and group 4 (n = 41), 50 and more. The median CMV DNA levels in samples were 0 copies/ml (range, 0 to 39,345), 344 (2.5 $\log_{10}$) copies/ml (range, 0 to 172,750), 4910 (3.7 $\log_{10}$) copies/ml (0 to 141,650), and 22,200 (4.3 $\log_{10}$) copies/ml (2,285 to 464,750), respectively. The CMV DNA load was significantly different among the four groups ($p < 0.0001$ by the Kuruskal-Wallis test). The box-and-whisker plots show 10th, 25th, 50th, 75th, 90th percentile values. The specimens negative by real-time PCR are not depicted. Outliers are indicated by dots.

Longitudinal analysis of the first detection of CMV DNA and CMV antigenemia cells

The CMV PCR and CMV antigenemia assays became positive simultaneously in 13 of 64 patients. The first positive PCR test preceded the first positive antigenemia by 14 days (7 to 35) in 20 patients, while the first positive antigenemia preceded the first positive PCR by 7 days in 4 patients. CMV PCR alone was positive in 18 patients, and CMV antigenemia alone was positive in 3 patients. Neither CMV PCR nor CMV antigenemia was positive in 6 patients. The median number of days for the first development of positive antigenemia and PCR results after transplantation was 34 days (12 to 141) and 20 days (12 to 97), respectively. Therefore, CMV PCR was positive significantly earlier than the CMV antigenemia assay ($p < 0.0001$ by the Mann Whitney's U-test). The WBC count at the first development of positive PCR was significantly lower, with a median of 2,700/μl (range, 100 to 27,400) than at the first positive antigenemia, with a median of 4,700/μl (700 to 40,900, $p = 0.027$ by Mann Whitney's U-test). In 23 of 64 patients, preemptive ganciclovir therapy was started upon the detection of 10 or more positive cells per 50,000 cells by the antigenemia assay at a median of day 39 (range, 18 to 122) after transplantation. Despite the preemptive therapy, five of 23 patients developed CMV disease at a median of day 50 (38 to 123) after transplantation. In five of 64 patients, ganciclovir was started based on the clinical diagnosis of CMV disease with apparent or infection-related symptoms at a median of day 38 (34 to 42).

Incidence of CMV disease

Ten of the 64 patients developed CMV disease. The time pattern of PCR and antigenemia detection relative to the onset of CMV disease in the 10 patients is shown in Fig. 4. Eight patients had CMV colitis, one had CMV retinitis (patient no. 8 in Fig. 4), and one had CMV pneumonia (patient no. 3). In these 10 cases, cord blood transplants were performed in three cases, transplants from an HLA-mismatched unrelated donor were performed in two, transplant from an HLA-matched unrelated was performed in one, transplant from an HLA-mismatched sibling was performed in one, and transplants from an HLA-identical sibling were performed in three. The median number of days to the onset of CMV disease was 42 days after transplant (33 to 123 days). CMV reactivation was detected 3 days or more before the development of CMV disease in 8 of 10 patients by real-time PCR. However, CMV antigenemia detected CMV reactivation earlier than the development of CMV disease only in 4 of 10 patients (Fig. 4). Five patients with CMV disease were successfully treated with ganciclovir and are currently alive, but the other five patients with CMV disease died from causes other than CMV disease. None of the patients in this series died of causes directly related to CMV disease.

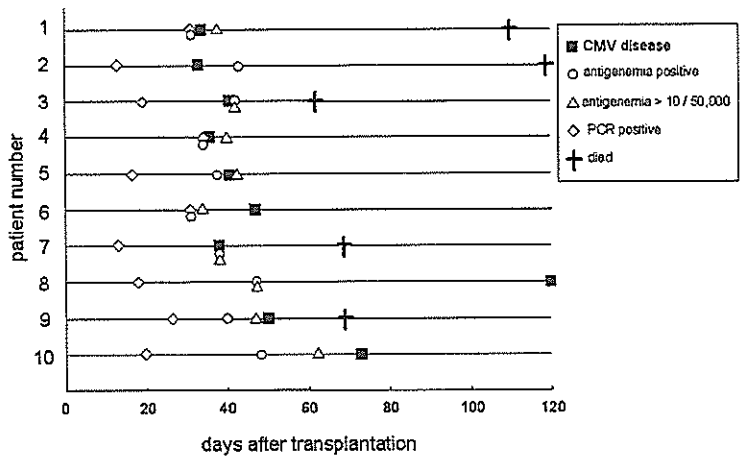

Fig. 4. Clinical course of individual patients with CMV disease. Solid squares, onset of CMV disease; open circles, first positive antigenemia; open triangles, first detection of > 10 positive cells per 50,000 cells by the antigenemia assay; open diamonds, first positive real-time PCR; cross, date of death.

The five deaths were caused by acute GVHD in one, disease progression in one, fungal infection in one, and bacterial infection in two. The peak CMV DNA load was significantly higher in patients with CMV disease, with a median of 82,250 copies/ml (range, 1,468 to 464,750) than in those without CMV disease, with a median of 628 copies/ml (0 to 374,150, $p = 0.005$, by Wilcoxon test).

Receiver Operating Characteristic (ROC) curve analysis

The ROC curves for UL75 PCR are shown in Fig. 5, in which four cut-off points for positive antigenemia, 1, 5, 10, or 50 positive cells per 50,000, were used. The LightCycler assay was clearly better than the discrimination limit. The Area Under the ROC Curve (AUC) values were 0.8426, 0.9240, 0.9483, and 0.9564, respectively, when 1, 5, 10, and 50 positive cells was used as a cut-off point for positive antigenemia. The 95% confidence intervals were as follows: 0.7917 – 0.8846, 0.8831 – 0.9529, 0.9205 – 0.9677, and 0.9311 – 0.9736, respectively. When the cut-off point was based on 10 pp65-positive cells per 50,000 cells, there was a better correlation between the CMV antigenemia assay and CMV PCR than when the cut-off point was based on 1

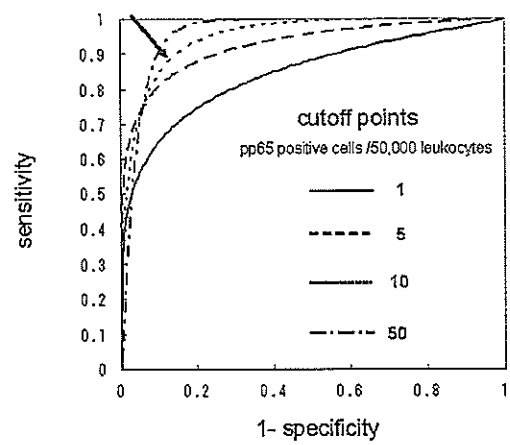

Fig. 5. ROC curves for UL75 PCR, with four cut-off points for the positivity for antigenemia: 1, 5, 10, or 50 cells per 50,000. The assay was far better than the discrimination limit. The AUC (Area Under the ROC Curve) values are 0.8426, 0.9240, 0.9483, and 0.9564, respectively. The 95% confidence intervals are as follows: 0.7917 – 0.8846, 0.8831 – 0.9529, 0.9205 – 0.9677, and 0.9311 – 0.9736, respectively. A tentative cut-off point at copy number 1,600 (arrow) gave a sensitivity of 87.2% and a specificity of 87.9% on the ROC curve in which 10 pp65-positive cells was used as the threshold for positive antigenemia.

pp65-positive cell. The cut-off points based on 5, 10, and 50 pp65-positive cells did not significantly differ from each other by the ROC analysis. A tentative cut-off point at copy number 1,600, as indicated by the arrow in Fig. 5, gave a sensitivity of 87.2% and specificity of 87.9% on the ROC curve, where 10 pp65-positive cells was used as the threshold for positive antigenemia.

Discussion

In our study, the CMV DNA copy number determined by real-time CMV PCR using SYBR Green I correlated with the number of pp65-positive cells, in agreement with the results of other studies using a TaqMan-based assay (Gault et al. 2001; Sanchez et al. 2001; Leruez-Ville et al. 2003; Li et al. 2003; Ikewaki et al. 2005). ROC analysis showed that this real-time CMV PCR exhibited adequate sensitivity and specificity, using the pp65 antigenemia assay as a reference standard. Corresponding to a pp65 antigenemia value of 10 positive cells per 50,000 leukocytes, which is used as the cutoff point for initiating preemptive therapy at our institute, a CMV DNA load of 1,600 copies/ml will be proposed as a cutoff point. However, we might have to start preemptive ganciclovir therapy at a cut off value of less than 1,600 copies/ml for high-risk patients. Our real-time PCR detected CMV-DNA earlier than the antigenemia assay detected CMV reactivation in the patients with CMV disease. Our real-time PCR makes it possible to adjust timing to start preemptive therapy more accurately according to the risk for CMV disease. The risks for CMV infection and/or disease have been increasing as new strategies have been introduced in allo-HSCT, including reduced-intensity stem cell transplantation, which enables older and/or heavily pretreated patients to undergo allo-HSCT, and HLA-mismatched transplantation with T-cell depletion or anti-T-cell agents (Kanda et al. 2001a; Nakai et al. 2002). Furthermore, Tomonari et al. (2003) suggested that the recovery of CMV-specific immunity after cord blood transplantation is delayed compared to that after BMT. Hence, in highly immunocompromised recipients, it may be advisable to set a lower cutoff point for the CMV DNA load to prevent CMV disease at the earliest stage. In this study, 47 patients underwent reduced-intensity stem cell transplantations (RIST) and 16 patients underwent conventional myeloablative stem cell transplantations (CST). The incidence of positive CMV antigenemia in the RIST group (33 of 47 patients, 70%) was higher than in the CST group (6 of 16 patients, 38%, $p = 0.019$). However, there was no significant difference in the incidence of positive PCR (85% and 88%) and CMV disease (17% and 13%) between the RIST group and the CST group. A higher incidence of CMV disease (10 of 64 patients, 16%) was observed and this might be attributed to our preemptive protocol consisting of a higher cutoff point and a lower initial dose of ganciclovir. It has been reported that preemptive therapy based on CMV antigenemia let to the more frequent development of CMV diseases other than pneumonitits, including gastrointestinal (GI) diseases, retinitis, and hepatitis (Boeckh et al. 1996; Kanda et al. 2001b). Mori et al. (2004) reported that among 19 and 14 patients who developed CMV-GI disease, only 4 (21%) and 7 patients (50%), respectively, became positive for antigenemia and plasma real-time PCR before the onset of CMV-GI disease. On the other hand, our plasma real-time PCR could detect CMV-DNA before the development of devastating CMV diseases in eight of 10 patients. The immediate initiation of antiviral therapy at low CMV DNA levels may become critical for highly immunocompromised recipients.

The detection of PCR products by the DNA-intercalating dye SYBR Green I system is simpler, cheaper, and probably more sensitive, since many fluorescent labels, rather than a single molecule, are incorporated into the amplified fragment (Karsai et al. 2002). However, this technique is not sequence-specific, and consequently nonspecifically amplified PCR products and primer dimers will also be detected. Nevertheless, we performed a melting curve analysis and electrophoresis to confirm that specific PCR products were formed, and these demonstrated specific and reproducible results.

We chose plasma as an assay material since

it still can be used during neutropenia (Boeckh et al. 1997). Plasma does not require labor-intensive processing such as isolation, counting, and adjustment of the number of peripheral blood leukocytes (PBL) before final analysis. It does not necessarily require normalization by a housekeeping gene, which is needed in real-time PCR using whole blood or PBL (Gault et al. 2001; Li et al. 2003). Despite these advantages of plasma as an assay material, it was long considered to be a poor source for PCR-driven assays because of its low sensitivity. Since the presence of CMV is strongly associated with cell components, it is considered that samples that incorporate whole blood or PBL provide a more sensitive detection of virus than plasma (Boeckh et al. 1997). However, recent improvements in plasma-based PCR assay have provided high sensitivity and clinical usefulness (Boeckh et al. 2004; Kalpoe et al. 2004; Schvoerer et al. 2005). Leruez-Ville et al. (2003) reported that a smaller PCR target (74bp) could provide better quantitative results because CMV DNA of plasma might be highly fragmented. In their study, the sensitivity of the PCR test was equivalent for plasma and whole blood. Although we did not compare the sensitivities with different components of blood, we demonstrated that our plasma real-time PCR was more sensitive than CMV antigenemia, perhaps due to the use of SYBR green I, i.e., the PCR target used in this study was 151 bp, which is not small enough to explain the improved sensitivity.

DNA extraction could strongly affect the assay's reproducibility (Gault et al. 2001). Mengelle et al. (2003) demonstrated that automated extraction and quantification of DNA from whole blood, instead of separated and counted PBL, provided acceptable results. They reported that 3.4 $\log_{10}$ genome copies in 200 μl of whole blood was equivalent to a threshold value of 50 pp65-positive cells per 200,000 cells. We applied the automated extraction of DNA in plasma and demonstrated that the plasma sample had an equivalent sensitivity for preemptive therapy for CMV. Hong et al. (2004) also reported that the combination of automated plasma DNA preparation and real-time PCR detection allowed for a sensitive assay of CMV viral load after bone marrow transplantation. It is evident that the standardization of plasma separation and storage methods should improve the reproducibility of plasma CMV DNA assays, which may further support the value of automated DNA extraction.

Our real-time PCR system for the measurement of CMV DNA in plasma using automated extraction and SYBR Green I dye appears to be a practical and simple system for obtaining reliable data and early detection of CMV reactivation, particularly for the purpose of prospectively guiding preemptive therapy for CMV disease after allo-HSCT.

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