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The dynamics of active human cytomegalovirus (HCMV) infection was monitored by competitive nucleic acid sequence-based amplification (NASBA) assays for quantification of IE1 (UL123) and pp67 (UL65) mRNA expression levels in the blood of patients after lung transplantation. RNA was isolated from 339 samples of 13 lung transplant recipients and analyzed by the quantitative IE1 and pp67 NASBA in parallel with pp65 antigenemia and serology. Rapid increases in IE1 RNA exceeding 10^4 copies per 100 μl of blood were associated with active infection, whereas lower levels were suggestive for abortive, subclinical viral activity. Any positive value for pp67 RNA was indicative for active infection, and quantification of pp67 mRNA did not give additional diagnostic information. The onset of IE1-positive NASBA preceded pp67 NASBA and was earlier than the pp65 antigenemia assay, confirming previous studies with qualitative NASBA. Effective antiviral treatment was reflected by a rapid disappearance of pp67 mRNA, whereas IE1 mRNA remained detectable for longer periods. Quantification of IE1 might be relevant to monitor progression of HCMV infection but should be validated in prospective studies.

Human cytomegalovirus (HCMV) is ubiquitous in humans, and primary infection generally occurs without clinical symptoms. However, in AIDS patients, newborns, transplant recipients, and other immunocompromised individuals, HCMV can cause severe disease (5). In order to prevent development of HCMV-related disease in these patients, well-timed preemptive initiation of antiviral therapy is of importance, guided by an early and accurate diagnosis. Especially in transplant recipients, frequent monitoring for HCMV infection is essential for appropriate patient management, since symptoms of infection and rejection of the transplanted organ may be similar, whereas the therapeutic approaches are opposite (12, 23, 25). The development of accurate diagnostic approaches has been ongoing for many years, aiming to solve several problems: early detection of aberrant virus activity and discrimination between abortive, subclinical infection and clinically relevant viral activity leading to HCMV disease. Currently, antigenemia monitoring is increasingly used to initiate antiviral therapy (22, 25, 26) and may be confirmed by shell-vial culture (13), whereas nucleic acid (DNA and RNA) diagnostics are still being validated for their diagnostic relevance in many institutes (3).

For the specific detection of HCMV RNA transcripts in patient materials, nucleic acid sequence-based amplification (NASBA) was developed (1). In contrast to HCMV DNA, which may be present in circulating leukocytes as a stable and inert molecule (17), the presence of HCMV-specific mRNA directly reflects viral biological activity. Systemic spread of HCMV via productively infected circulating blood leukocytes is a hallmark of disseminating infection, closely linked to development of HCMV disease, and should be limited at an early stage (24). Studies using reverse transcription-PCR for detection of mRNA have indicated that late viral transcripts reflect active HCMV replication in contrast to immediate-early transcripts, which lack specificity for prediction of HCMV disease (11, 16, 18, 20). However, reverse transcription-PCR detecting late mRNA as pp150 (18) and UL18 (14) was only positive in the peak of infection. The low sensitivity may be overcome by using an abundantly expressed mRNA such as pp67 (6).

In recent studies, qualitative NASBA for the detection of late-stage pp67 (UL65) RNA, encoding a structural tegument protein, has proved to be a sensitive and specific assay for monitoring active systemic HCMV infection in solid transplant recipients (1, 8). From the study of Blok et al. (1) it was concluded that NASBA for late pp67 mRNA is more sensitive than the antigenemia assay for the detection of HCMV infection in renal allograft recipients. Furthermore, pp67 NASBA proved useful for monitoring progression of HCMV infection in heart, lung, and bone marrow patients and to determine the effect of antiviral therapy with results comparable to those of the antigenemia and DNA-emia assays (8). However, in high-risk bone marrow transplant recipients, the pp67 NASBA showed a mean delay of 2 days before becoming positive in comparison to antigenemia results.

In order to identify active HCMV infection at an earlier stage, an NASBA assay was developed for qualitative detection.
of mRNA encoded by the immediate-early gene UL123 (IE1) (2, 9). IE1 NASBA proved to be highly sensitive, detecting the onset of both primary and secondary cytomegalovirus infection significantly earlier than cell culture, antigenemia, and pp67 NASBA in renal, liver, heart, and lung transplant recipients (2, 21). Also in bone marrow transplant patients, IE1 NASBA was significantly earlier than pp67 NASBA, pp65 antigenemia and DNA-emia (9). The IE1 NASBA results indicated that IE1 mRNA detection might provide a useful parameter for starting preemptive antiviral treatment in high-risk patients. However, following antiviral therapy, HCMV IE1 mRNA may still be expressed, since current antiviral drugs selectively inhibit viral DNA replication and thereby late RNA synthesis, but may leave earlier stages of viral gene expression relatively unaffected. Therefore, the merely qualitative IE1 NASBA may not be ideal for monitoring HCMV activity. The high sensitivity and associated lower specificity for predicting symptomatic HCMV infection of qualitative IE1 mRNA monitoring was further indicated in previous studies using reverse transcription-PCR (16, 18, 20). This was confirmed by a study of Oldenburg evaluating IE1, β2.7 (early mRNA), and pp67 gene expression by NASBA in thoracic organ transplant recipients (21). In this study, IE1 mRNA was detected in a significant number of cases with subclinical HCMV infection that did not require antiviral treatment. The early detection of IE1 mRNA in certain samples might be related to HCMV-positive blood transfusion. A quantitative NASBA for measuring IE1 RNA levels could be more informative for accurate monitoring of relevant HCMV activity potentially leading to disease. Currently no data are available on the quantity and kinetics of symptomatic and subclinical HCMV RNA expression in blood during active infection.

To analyze in more detail the in vivo dynamics of mRNA expression in the circulation of HCMV-infected patients and to determine their relevance for predicting the progression of subclinical infection to disease, quantitative versions of the HCMV-specific IE1 and pp67 NASBA assays were developed. Quantification was performed by incorporating a competitively amplified RNA construct with identical length and sequence as the wild-type (wt) RNA except for 20 randomized nucleic acids, allowing its specific detection. HCMV RNA expression levels were determined in weekly samples of unfractonated whole blood in control patients and in lung transplant recipients with primary and secondary HCMV infections by quantitative IE1 and pp67 NASBA and compared to pp65 antigenemia and serology in simultaneously obtained samples.

**MATERIALS AND METHODS**

**Clinical samples.** Heparinized whole-blood samples and serum specimens of patients transplanted between 1997 and 1998 were collected weekly following transplantation during admission and at each patient visit thereafter. One milliliter of blood was mixed with 9 ml of NASBA lysis buffer (5 M guanidine isothiocyanate, 0.1 M Tris [pH 6.4], 20 mM EDTA [pH 8.0], 1.2% [wt/vol]) and stored at −80°C. Serum samples were stored at −20°C.

**Patients.** In the period from 1997 to 1998, 17 patients received a lung transplant, of which 4 patients died within 3 months. Of the 13 lung transplant patients studied, 2 patients were HCMV seronegative and received a seronegative transplant, 3 patients were seronegative and received an organ from an HCMV-seropositive donor, and 8 patients were already seropositive, of which 6 transplanted, 3 patients were seronegative and received an organ from an HCMV-studied, 2 patients were HCMV seronegative and received a seronegative transplant, of which 4 patients died within 3 months. Of the 13 lung transplant patients stored at 100 μl of blood was mixed with 9 ml of NASBA lysis buffer (5 M guanidine isothiocyanate, 0.1 M Tris [pH 6.4], 20 mM EDTA [pH 8.0], 1.2% [wt/vol]) and stored at −80°C. Serum samples were stored at −20°C.

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and $b$ were estimated, which were used to calculate $\text{wt RNA}$ and $Q$ RNA concentrations according to the formula $\log \text{wt conc} = \frac{1}{a} \times (\log \text{wt ECL} - \log \text{QECL} + \log \text{Qconc}) - \frac{b}{a}$.

**RESULTS**

Performance of the IE1 Qt and pp67 Qt NASBA. The analytical performance of the IE1 and pp67 Qt NASBA is described elsewhere (Greijer et al., submitted). The sensitivity of Qt NASBA was similar to the qualitative NASBA described earlier, which had a threshold level of 70 copies of IE1 RNA (9) and 100 copies of pp67 RNA. For analyzing the influence of whole blood on the quantification of HCMV RNA, HLF were infected with HCMV at 0.01 PFU per cell for 72 h followed by homogenization with NASBA lysis buffer. The homogenate was diluted to a range of 0.01 to 100 HCMV-infected cell equivalents per ml of lysis buffer or spiked at identical concentrations in whole blood from healthy individuals. The sensitivity of pp67 Qt NASBA in both lysis buffer and blood was 0.01 HCMV-infected cell equivalent per ml (Fig. 1). The IE1 NASBA is sensitive to 0.1 cell equivalent per ml due to the 10-fold-lower expression of IE1 mRNA in infected HLF cells (Greijer et al., submitted), confirming previous findings of Davis et al. (6). The quantification of cells spiked in both lysis buffer and blood was linear over a range of 0.1 to 100 cell equivalents, which is equivalent to a range of $10^3$ to $10^6$ RNA copies per ml (Greijer et al., submitted).

Detection of IE1 and pp67 mRNA in control groups. To determine the clinical relevance of IE1 and pp67 Qt NASBA assays, whole-blood samples from healthy individuals were analyzed. The IE1 Qt NASBA did not give any positive results for 144 healthy individuals tested. However, the pp67 Qt NASBA showed two weakly positive results among 144 healthy individuals. Since these results were obtained from seronegative individuals, these low positive values were considered to be due to contamination. From two HCMV-seronegative transplant recipients receiving an allograft from a seronegative donor, 25 and 28 subsequent samples were analyzed respectively, over a period of 36 and 60 weeks posttransplantation. Neither IE1 nor pp67 Qt NASBA showed any positive result.

Monitoring of IE1 and pp67 RNA during HCMV infection. For routine diagnosis of HCMV infection, the pp65 antigenemia assay was performed in a standardized method as described by The (25). Results of the pp65 antigenemia test were used as an indication to start and terminate antiviral therapy. The IE1 and pp67 Qt NASBA assays were performed retrospectively on samples collected simultaneously with routine pp65 antigenemia testing. Results of pp65 antigenemia, IE1, and pp67 Qt NASBA assays were compared (Table 1). Patients were grouped by primary and secondary infection. Of the 292 blood samples tested, 130 samples (45%) were pp65 antigenemia positive, whereas 188 (65.7%) were positive for IE1 Qt NASBA and 60 (21.0%) were positive for pp67 Qt NASBA. Most blood samples positive for pp65 antigenemia in patients with a primary or secondary HCMV infection had detectable levels of IE1 RNA (89.2%), whereas pp67 RNA was present less frequently (36.9%), especially in patients with a secondary

<table>
<thead>
<tr>
<th>Infection</th>
<th>Antigenemia assay</th>
<th>No. of samples</th>
<th>IE1 Qt NASBA</th>
<th>pp67 Qt NASBA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positive</td>
<td>51</td>
<td>47 (92.2)</td>
<td>31 (60.8)</td>
</tr>
<tr>
<td></td>
<td>Negative</td>
<td>26</td>
<td>18 (69.2)</td>
<td>6 (23.1)</td>
</tr>
<tr>
<td></td>
<td>No result</td>
<td>11</td>
<td>2 (18.2)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Primary</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Secondary</td>
<td>Positive</td>
<td>79</td>
<td>69 (87.3)</td>
<td>17 (21.5)</td>
</tr>
<tr>
<td></td>
<td>$&gt;10^6$</td>
<td>11</td>
<td>11 (100)</td>
<td>6 (54.5)</td>
</tr>
<tr>
<td></td>
<td>Negative</td>
<td>53</td>
<td>23 (43.4)</td>
<td>1 (1.89)</td>
</tr>
<tr>
<td></td>
<td>No result</td>
<td>66</td>
<td>29 (43.9)</td>
<td>5 (7.58)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Positive</th>
<th>Negative</th>
<th>Positive</th>
<th>Negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary</td>
<td></td>
<td></td>
<td>4 (7.80)</td>
<td>20 (39.2)</td>
</tr>
<tr>
<td>Secondary</td>
<td></td>
<td>8 (44.4)</td>
<td>6 (23.1)</td>
<td>20 (76.9)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>9 (81.8)</td>
<td>0 (0)</td>
<td>11 (100)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>10 (12.7)</td>
<td>62 (78.5)</td>
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<td></td>
<td></td>
<td>0 (0)</td>
<td>6 (54.5)</td>
<td>5 (45.5)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>30 (56.6)</td>
<td>1 (1.89)</td>
<td>52 (65.8)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>37 (56.1)</td>
<td>5 (7.58)</td>
<td>61 (92.4)</td>
</tr>
</tbody>
</table>

*Notes:*

- Samples with “no result” for antigenemia are derived from patients who had two successive negative antigenemia results, after which antigenemia was not determined again.
- Clinically significant threshold value.
HCMV infection (21.5%). However, when clinically relevant levels of pp65 antigenemia were detected (>10 pp65-positive cells per 50,000 tested), a higher number of patients with secondary HCMV were also positive for pp67 mRNA (54.5%). Of 80 blood samples with negative results for antigenemia, detectable levels of IE1 mRNA were found in 41 samples (51.9%) and of pp67 mRNA in 7 samples (8.9%). Positive pp67 Qt NASBA results with negative pp65 antigenemia were all located in periods after the first peak of infection, where pp65 antigenemia results fluctuated between low positive and negative. For further interpretation, the time to the first positive IE1 and pp67 Qt NASBA results after transplantation was analyzed in more detail.

**Time to detection of HCMV infection.** In lung transplant patients with a primary infection, the first repeated pp65 antigenemia positive result was used to initiate antiviral treatment. The timing of the first positive result by the IE1 and pp67 Qt NASBA assays was determined relative to the pp65 antigenemia assay during the early phase of infection. The results are given in Table 2. In patients with a primary HCMV infection, the onset of infection could be detected at the same time (3.4 weeks after transplantation) by pp65 antigenemia and IE1 Qt NASBA. Late pp67 mRNA was detected with a 5-day delay compared to pp65 antigenemia and IE1 Qt NASBA. In patients with a secondary HCMV infection, pp65 antigenemia became positive at a mean 3.6 weeks after transplantation. In two patients, IE1 mRNA was detected 7 and 10 days earlier than pp65 antigenemia, whereas in the other patients, both assays became positive simultaneously. pp67 RNA was detected with a delay of 1.5 weeks compared to pp65 antigenemia. In this comparison, pp65 antigenemia results of more than one positive cell were used, which is considerably below the clinical level relevant for secondary infection. A patient with a secondary infection received antiviral therapy only where there were more than 10 pp65-positive cells in the antigenemia assay or when clinical symptoms indicated active HCMV infection. Using the latter as the criterion for the eight patients with a secondary infection, three patients had a positive result for pp67 mRNA. These patients already had high levels of pp65 antigenemia at the first available sample, and both IE1 and pp67 Qt NASBA were positive at the first tested sample.

**Quantification of HCMV IE1 and pp67 mRNA levels in transplant recipients.** In order to define the clinical relevance of HCMV RNA quantification, the levels of mRNA encoded by the IE1 and UL65 gene were compared to the level of pp65 antigenemia. For this purpose, pp65 antigenemia results were divided into negative and positive pp65 antigenemia and clinically relevant numbers of pp65-positive cells (Table 3). The mean level of expression of IE1 was log 5.3 RNA copies per 100 μl of blood. In patients with a primary infection, mean IE1 expression levels rose 19-fold to log 6.6 RNA copies per 100 μl of blood, paralleled by antigenemia levels exceeding 10 cells per 50,000 polymorphonuclear leukocytes, whereas in patients with a secondary infection IE1 RNA levels did not exceed log 5.8 copies of IE1 RNA per 100 μl of blood. Quantification of pp67 RNA shows an increase in the number of RNA copies with the number of pp65-positive cells. The overall mean level of pp67 RNA molecules was log 4.5, and the maximum number of RNA copies was log 5.6 per 100 μl of blood. The comparison of IE1 and pp67 RNA quantification relative to the number of pp65-positive cells in the antigenemia assay of the individual blood samples is shown in Fig. 2. The level of IE1 RNA expression correlated with the level of the antigenemia (Fig. 2A), with 0 to 10^3 RNA copies per 100 μl of blood being associated with negative antigenemia results. The level of pp67 RNA also showed correlation with increasing antigenemia levels, although much less stringent (Fig. 2B).

**Kinetics of IE1 and pp67 mRNA levels in blood of patients with HCMV infection.** In the current routine diagnostic approach, the course of HCMV infection in lung transplant recipients is reflected by the number of pp65-positive cells in the antigenemia assay. In order to acquire additional information on the progression of HCMV infection, the kinetics of IE1 and pp67 mRNA expression in blood were analyzed. The antigenemia, IE1, and pp67 mRNA levels of four representative patients are presented in Fig. 3. For evaluation of the immune response, the levels of HCMV-specific IgM and IgG antibodies are presented as well. Figures 3A and B represent two lung transplant recipients with a primary infection. Figures 3C and D represent two patients with a secondary HCMV infection. Patient 1 was seronegative and received a positive lung transplant. In order to prevent acute rejection, the patient was treated four times with methylprednisolone. The onset of HCMV infection was detected by antigenemia at 12 days after transplantation. At the same moment, IE1 Qt NASBA became positive, whereas the pp67 Qt NASBA became positive at 19 days. Three periods of active infection were seen. During the

<table>
<thead>
<tr>
<th>Infection</th>
<th>HCMV assay</th>
<th>No. of patients</th>
<th>Mean time postransplantation (wk) of first HCMV appearance (first result–last result)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary</td>
<td>Antigenemia</td>
<td>3</td>
<td>3.4 (1.7–4.4)</td>
</tr>
<tr>
<td></td>
<td>IE1 Qt NASBA</td>
<td>3</td>
<td>3.4 (1.7–4.4)</td>
</tr>
<tr>
<td></td>
<td>pp67 Qt NASBA</td>
<td>3</td>
<td>4.1 (2.7–5.4)</td>
</tr>
<tr>
<td>Secondary</td>
<td>Antigenemia</td>
<td>5</td>
<td>3.6 (2.1–6.0)</td>
</tr>
<tr>
<td></td>
<td>IE1 Qt NASBA</td>
<td>7</td>
<td>3.3 (1.6–6.0)</td>
</tr>
<tr>
<td></td>
<td>pp67 Qt NASBA</td>
<td>5</td>
<td>5.8 (3.3–8.0)</td>
</tr>
</tbody>
</table>

**TABLE 3.** Comparison of RNA levels with antigenemia results in 11 transplant recipients (153 samples) with a primary and secondary HCMV infection

<table>
<thead>
<tr>
<th>Infection</th>
<th>Antigenemia (no. of positive cells)</th>
<th>IE1 Qt NASBA (No. positive RNA copies (log))</th>
<th>pp67 Qt NASBA (No. positive RNA copies (log))</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary</td>
<td>0</td>
<td>18 3.9</td>
<td>6 4.1</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>9 4.0</td>
<td>2 2.9</td>
</tr>
<tr>
<td></td>
<td>2–10</td>
<td>13 4.8</td>
<td>7 4.2</td>
</tr>
<tr>
<td></td>
<td>&gt;10</td>
<td>23 6.0</td>
<td>22 4.7</td>
</tr>
<tr>
<td>Secondary</td>
<td>0</td>
<td>24 3.6</td>
<td>1 0.7</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>20 4.2</td>
<td>3 3.3</td>
</tr>
<tr>
<td></td>
<td>2–10</td>
<td>35 4.6</td>
<td>8 4.0</td>
</tr>
<tr>
<td></td>
<td>&gt;10</td>
<td>11 4.7</td>
<td>6 4.6</td>
</tr>
</tbody>
</table>
second and third peak of infection, the number of positive cells in the antigenemia assay increased considerably, to a maximum of 640 positive cells. Therapy with ganciclovir was successful at first but proved ineffective in the second period and was therefore replaced by foscarnet. Sequencing of the viral DNA isolated from samples at weeks 24 and 25 revealed a C→T (Ala→Val) mutation at codon 594 of the UL97 gene, known to cause ganciclovir resistance. Due to adverse side effects, foscarnet treatment was ended 15 weeks after transplantation, and ganciclovir in combination with Megalotect was given until the antigenemia levels had decreased significantly. Figure 3A clearly shows that at the initial phases of viral activity, the dynamics of IE1 and pp67 RNA expression were similar to the antigenemia. However, IE1 RNA levels remained positive during the period of foscarnet therapy, while antigenemia and pp67 Qt NASBA were negative. The pp67 Qt NASBA detected HCMV infection in all three periods of active infection 1 week later than IE1 NASBA. During therapy with foscarnet, pp67 RNA and antigenemia were negative. Significantly decreased pp67 RNA levels indicated the final success of therapy at 14 weeks, which was before antigenemia and IE1 RNA.

Patient 2 had a primary HCMV infection and subsequently developed a primary Epstein-Barr virus (EBV) infection. Antirejection therapy was given six times. The acyclovir treatment for EBV is also shown in Fig. 3B. After 4.4 weeks, increasing antigenemia showed the first signs of HCMV infection. In contrast to patient 1, the levels of IE1 RNA expression were substantially lower. The acyclovir treatment for EBV was given during IE1 RNA levels were positive, and IE1 RNA levels corresponded with the antigenemia levels. pp67 RNA was detected with a delay of 7 days and was 3 weeks later in the second peak of infection. In contrast to patient 1, the levels of IE1 RNA expression were substantially lower. Furthermore, IE1 RNA reappeared each time a rejection treatment was given, while the antigenemia and the pp67 Qt NASBA assay remained negative. The sole presence of IE1 RNA indicated restricted activity of the HCMV infection, since clinical symptoms of HCMV infection were absent (subclinical infection).

An example of the kinetics of IE1 and pp67 RNA expression in an HCMV-seropositive transplant patient is shown in Fig. 3C. Patient 3 had seven rejection treatments and four periods of HCMV activity, with short antiviral treatments with ganciclovir. Although antigenemia did not exceed 20 pp65-positive cells, ganciclovir was given in order to prevent progression of the infection during antirejection therapies. The onset of HCMV infection was defined at 18 days after transplantation. Prior to this period, samples were not available for analysis of IE1 and pp67 mRNA. In the second peak of infection, antigenemia and IE1 Qt NASBA were positive simultaneously at 6 weeks, whereas pp67 Qt NASBA was positive with a 2-week delay. Levels of IE1 RNA remained elevated during periods of positive antigenemia, and when antigenemia and pp67 became negative, IE1 RNA was still detectable, although at lower levels. The pp67 Qt NASBA showed positive results only in the highest peaks of infection.

Patient 4 was seropositive and received an HCMV-positive organ. A secondary infection was diagnosed 12 days after transplantation, and antigenemia was detectable for 1 week (Fig. 3D). The first positive result by antigenemia could not be tested by NASBA, but the second sample was positive for both antigenemia and IE1 Qt NASBA. The pp67 Qt NASBA did not show any positive results in the period of elevated IE1 RNA level. The low positive antigenemia did not necessitate antiviral therapy, but in combination with rejection therapy, ganciclovir was given prophylactically.

**DISCUSSION**

Active HCMV infection remains a significant problem in the transplantation population. Control of HCMV activity in solid organ transplant recipients is of importance for preventing HCMV disease and improving overall clinical performance. The main implication of our study is that quantification of pp67 RNA does not provide additional information compared to the previously described qualitative pp67 RNA detection, whereas quantification of IE1 RNA more directly reflects the dynamics of HCMV infection. Furthermore, the rapid increases to high levels of IE1 RNA are associated with progres-
A  patient 1  
primary infection

Rejection treatment
GCV
PFA
Megalotect

Serology and pp65 antigenemia

Number of positive cells
Time after transplantation (weeks)

1000
100
10
1
0.1
0

IE1 and pp67 RNA copies per 100 μl blood

RNA copies (log)
Time after transplantation (weeks)

10^0
10^2
10^4
10^6
10^8

B  patient 2  
primary infection

Rejection treatment
GCV
ACV

Serology and pp65 antigenemia

Number of positive cells
Time after transplantation (weeks)

1000
800
600
400
200
0

IE1 and pp67 RNA copies per 100 μl blood

RNA copies (log)
Time after transplantation (weeks)

10^0
10^2
10^4
10^6
10^8
NT
FIG. 3. Course of HCMV infection in four representative patients by serology, pp65 antigenemia, and IE1 and pp67 Qt NASBA assays. (A and B) Patients with primary HCMV infection. (C and D) Patients with secondary HCMV infection. GCV, ganciclovir; PFA, foscarnet; ACV, aciclovir. Arrows, rejection treatment.
sion to disease. Previous studies have shown that qualitative monitoring for the presence of HCMV RNA by either reverse transcription-PCR or NASBA could provide a useful diagnostic approach directly reflecting active viral gene expression in circulating HCMV-infected cells (11, 16, 18, 20). In recent years, monitoring for the presence of pp67 and IE1 mRNA by NASBA was introduced to provide a new approach for early detection of systemic active infection. The pp67 NASBA has a relatively limited sensitivity, since it detects only the late productive stage of infection. However, pp67 mRNA monitoring may provide timely diagnosis for initiation of preemptive therapy (1, 8, 21). IE1 NASBA, although providing very early positive results, may lack specificity for predicting disease (2, 9, 21).

In order to monitor patients more closely and analyze the kinetics of expression of IE1 and pp67 in more detail, quantitative competitive pp67 and IE1 NASBA assays were developed. In healthy control blood donors and HCMV-seronegative patients receiving an HCMV-negative organ, IE1 and pp67 mRNA could not be detected by the Qt NASBA assays at any time during follow-up. Of the lung transplant recipients tested, three primary infected patients had active, symptomatic HCMV infection, whereas of the eight seropositive transplant recipients, five had an active and partly subclinical infection. The two seropositive patients receiving a negative organ did not develop HCMV infection, suggesting that the infections in the former may be derived from the donor organ and therefore were defined as secondary infection. Local cytokine responses related to early rejection episodes might be responsible for triggering HCMV reactivation in the transplanted organ (19).

The time of first detection of IE1 and pp67 RNA by Qt NASBA in the lung transplant recipients is comparable to the qualitative findings by Blok et al. (2) and Gerna et al. (9), as expected, since both qualitative and quantitative NASBA assays showed comparable levels of sensitivity for in vitro RNA (9; Greijer et al., submitted). The mean time to detect a positive result for IE1 Qt NASBA in lung transplant recipients was 3.4 weeks, compared to 3.7 weeks in kidney transplants (2) and 5.4 weeks in bone marrow transplant recipients (9). The mean time to the first detection of pp67 RNA was 4.1 weeks post-transplantation in primary infected patients and 5.8 weeks in transplant recipients with secondary infection, compared to 5.1 weeks in kidney transplant recipients and 6.2 weeks in bone marrow patients. The primary infections were detected at an earlier stage compared to patients with a secondary infection. The peak levels of RNA in 100 μl of blood of lung transplant recipients were log 6.6 molecules of IE1 RNA and log 5.6 molecules of pp67 RNA. In the blood of patients with an active HCMV infection, pp67 RNA levels were lower than IE1 RNA levels, which contrasts to the observation in infected HLF cells in vitro (log 4.7 copies of IE1 RNA and log 5.3 copies of pp67 RNA per infected cell) (Greijer et al., submitted). However, in vivo the HCMV RNA expression levels in circulating cells may be different from cultured cells and may differ for different cell types as well. Therefore it is important to note that levels in whole blood represent an averaged value of HCMV RNA expression. In addition, the higher levels of IE1 RNA may be explained by high numbers of cells with a restricted or abortive infection, expressing only immediate-early RNA without pp67 RNA expression, or by a difference in the mRNA expression ratios in blood leukocytes compared to HLF cells (10).

When monitoring patients with antigenemia and IE1 and pp67 Qt NASBA, pp67 RNA was detected only in the highest peak of infection, during the period in which the antigenemia assay shows medium and high levels of positive cells. Immediate-early RNA was often present at levels of up to 104 copies before positive antigenemia results are seen. After treatment with ganciclovir or foscamet, pp67 levels decreased rapidly, whereas IE1 RNA remained detectable for longer periods. The prolonged detection of IE1 RNA reflects the limitation of current antiviral therapy, which interferes only with the late phase of the viral replication cycle, leaving the expression of IE1 unaffected. The final disappearance of IE1 RNA may indicate full immunological recovery and may suggest long-term control over HCMV infection. This, however, remains to be determined in subsequent studies.

Our results suggest that the dynamics of the IE1 RNA level are useful for monitoring disease progression. IE1 RNA levels of up to 106 were detected in patients with subclinical HCMV infection, and rapidly increasing levels equal to or above 104 were related to disease development. pp67 RNA is detectable at a productive infection, though not detectable in the early phases of viral replication, when clinical symptoms are still absent. The number of pp67 RNA molecules did not relate to the number of pp65-positive cells in the antigenemia assay. This perception indicates that the presence and not the level of pp67 RNA is of prognostic value for antiviral drug management. However, it should be realized that antiviral treatment guided by early pp65 antigenemia may have influenced the pp67 mRNA levels detected in this study. The simultaneous pp67 and IE1 mRNA levels determined by Qt NASBA could provide additional clinically relevant information on the biological activity and progression of HCMV infection in vivo.

Especially in primary infected transplant recipients, initiation of antiviral therapy at the first activation of the virus would improve the outcome of HCMV infection, since the host’s immune system might not be able to establish a rapid and appropriate response to HCMV. However, the early initiation of antiviral therapy may prevent appropriate antigen stimulation of the immune system, allowing relapse of HCMV replication upon cessation of treatment. On the other hand, the increase and decrease in IE1 RNA could give an indication of the extent to which the HCMV infection is controlled by the host’s immune system. Therefore, the pp67 NASBA, indicating active replicating HCMV, in combination with a quantitative IE1 mRNA result might be preferred for optimal patient management.

The results of this study indicate that combined testing for quantitative IE1 RNA and qualitative pp67 RNA can recognize ongoing subclinical HCMV infection, allowing fine-tuning of the period of antiviral therapy to prevent progression to clinically significant HCMV activity. It is now possible to study the effect of treatment intended to prevent all HCMV activity, which may improve long-term allograft outcome. Since antigenemia results were used for guiding antiviral therapy, the clinical relevance of patient monitoring by IE1 Qt NASBA and qualitative pp67 needs to be determined by prospective studies.
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