Cytomegalovirus DNA in Semen and Blood Is Associated With Higher Levels of Proviral HIV DNA

Sara Gianella,1 Christy M. Anderson,1 Milenka V. Vargas,1 Douglas D. Richman,2 Susan J. Little,1 Sheldon R. Morris,1 and Davey M. Smith1,2
1University of California–San Diego, La Jolla, and 2Veterans Affairs San Diego Healthcare System, San Diego, California

Over three-fourths of human immunodeficiency virus (HIV)–infected men who have sex with men (MSM) have at least one herpesvirus detected in their semen, and cytomegalovirus (CMV) is the most prevalent. While the presence of CMV is associated with higher T-cell immune activation and with HIV disease progression in treated and untreated individuals. In this study of 113 antiretroviral (ART)–naive HIV-infected MSM, we found that CMV replication in blood and semen was associated with higher levels of HIV DNA in peripheral blood mononuclear cells. These observations suggest that interventions aimed to reduce CMV replication and, thus, systemic immune activation could decrease the size of the latent HIV reservoir.

Keywords. cytomegalovirus; HIV DNA; latent reservoir; immune activation; early HIV infection.

Over three-fourths of human immunodeficiency virus (HIV)–infected men who have sex with men (MSM) have at least one actively replicating herpesvirus detected in their semen, and cytomegalovirus (CMV) is the most prevalent. While the interactions between herpesviruses and HIV are relevant to HIV transmission [1], the role of herpesviruses in HIV pathogenesis may be equally important. Presence of CMV is associated with HIV disease progression and higher T-cell immune activation [1, 2]. Such immune activation can blunt CD4+ T-cell recovery during antiretroviral therapy (ART) and lead to premature mortality [2]. Moreover, immune activation in response to CMV may be responsible for accelerated immunosenescence in HIV-infected and HIV-uninfected individuals [2]. Since activated T cells undergo extensive cell division and differentiation [3], we hypothesized that bystander proliferation of HIV-infected CD4+ T cells could be an important factor in determining the size of the HIV proviral reservoir [4].

The latent HIV reservoir is established during primary HIV infection [5], but the mechanisms that maintain this reservoir are unclear. It is therefore particularly important to understand which factors contribute to increase the immune activation and which mechanisms drive and modulate the establishment of the viral reservoir during the earliest phase of HIV infection. Here, we investigated the relationships between CMV replication in semen and paired peripheral blood mononuclear cells (PBMCs) and estimated the duration of infection, the HIV DNA level in PBMCs, the HIV RNA load in blood plasma, and CD4+ T-cell numbers.

MATERIALS AND METHODS

Participants, Samples, and Clinical Laboratory Tests

A total of 229 semen samples from 113 participants in the San Diego Primary Infection Cohort [1] were included. All subjects had recently acquired HIV infection, were naive to ART, and were CMV seropositive. Semen and blood were collected as described previously [1]. In blood, the CD4+ T-lymphocyte count was measured by flow cytometry (LabCorp), and the plasma HIV RNA load was quantified by the Amplicor HIV Monitor Test (Roche Molecular Systems). Demographic characteristics and standard laboratory values were collected, and screening for sexually transmitted infections (STIs; Neisseria gonorrhoeae infection, Chlamydia trachomatis infection, and syphilis) was performed at baseline for a subset of 95 participants. The estimated duration of infection was calculated using an established algorithm [6], and HIV subtype was determined from HIV pol sequence data (ViromeQ 2.0; Applied Biosystems), using SCUORL-2 [7]. The study was conducted with written consent, as approved by Human Research Protections Program at University of California–San Diego.

Quantification of HIV DNA and CMV DNA

DNA was extracted from 5 million PBMCs and 200 μL of seminal plasma from each participant (QIAamp DNA Mini Kit, Qiagen, CA). Total HIV DNA was quantified by real-time polymerase chain reaction (PCR) from extracted DNA, using primers as described elsewhere [1]. Because of the large genetic variability of HIV, accurate quantification by real-time
PCR may require primers and probes specific for each viral variant. This study used the conserved probe mf348 [8], which matches 81% of HIV subtype B pol sequences downloaded from the Los Alamos HIV Sequence Database (available at: http://www.hiv.lanl.gov; accessed March 2009). Since fluorescent PCR probes are particularly sensitive to mismatches [9], for each participant we determined whether the mf348 probe would match the sequence of each patient’s HIV RNA population, as determined by the population-based HIV pol sequence.

Similarly, levels of CMV in DNA extracted from PBMCs and seminal plasma were measured by real-time PCR, as described previously [1]. Cellular input for both HIV and CMV DNA measurements in PBMCs was quantified by β-actin PCR, using the primers β-actin 959 F (CTGGCACCAGCA CAATG) and β-actin 1026 R (GCGGATCCACCGAGTA CT) and the detection probe β-actin 980 T (5’-TCAAGATCTTTGCTCCTCCTGAGCGC-q).

**Statistical Analysis**

A linear mixed-effects model for repeated measures was used to investigate the relationship between CMV and HIV DNA levels. Fixed effects included detectable CMV in PBMCs and semen, estimated duration of infection, HIV RNA blood plasma levels, CD4+ T-cell numbers, and status of probe match, and each subject was treated as the random effect. For 59 subjects with longitudinal data, a subanalysis was performed that included a binary variable that accounted for intermittent CMV seminal shedding. Because of the low numbers of subjects with longitudinal data and detectable CMV in PBMCs (n = 12), we were not able to assess the impact of intermittent CMV shedding in those subjects.

HIV and CMV DNA levels were normalized to cellular input (expressed in copies per 10^6 cell equivalents) with respect to β-actin levels, and both HIV DNA and RNA levels were transformed to their base-10 logarithm values. Univariate analysis was performed using all samples and using only those samples in which HIV DNA levels were obtained with a matched probe. Associations between STIs and HIV DNA levels were evaluated using the reduced data set of 95 subjects with available STI screening information. Multivariate analysis was performed using all samples and using only those samples with a complete match between HIV sequence and the detection probe (n = 159), de-
in PBMCs (Figure 1). The association between CMV in PBMCs and higher levels of HIV DNA in PBMCs remained significant in a multivariate analysis ($P = .05$) that included estimated duration of infection and presence of a mismatch between probe and target sequence as covariates. The presence of CMV in semen was not included in the multivariate analysis since it was highly correlated with the presence of CMV in PBMCs ($P < .0001$) and had weaker association with HIV DNA levels than CMV in PBMCs. Overall, subjects with detectable CMV in both semen and PBMCs were more likely to have higher HIV DNA levels in PBMCs than participants with undetectable CMV in both semen and PBMCs ($P = .02$ for the entire data set; $P = .008$ for the matched subset) and those with detectable CMV in only semen or PBMCs ($P = .07$ for the entire data set; $P = .05$ for the matched subset). After including a binary variable in the model that indicated intermittent CMV shedding, the associations between HIV DNA levels and seminal CMV remained unchanged, and the presence of intermittent shedding versus consistent shedding was not significantly different than 0 ($P = .47$).

Of note, detectable CMV in semen and/or PBMCs were not significantly associated with HIV RNA levels or with CD4$^+$ T-cell counts ($P > .5$).

**DISCUSSION**

The impact of low-level HIV replication on the replenishment and size of the latent reservoir is controversial [10, 11]. Recent studies have identified immune activation and homeostatic cell proliferation as a major mechanism to sustain the persistence of the HIV reservoir [4]. Since HIV DNA levels in blood predict the rate of CD4$^+$ T-cell loss, time to AIDS, virologic failure of ART, and dementia [12–14], reducing these proviral levels alone may have substantial clinical benefits.

This study demonstrated that presence of CMV in PBMCs and seminal plasma of HIV-infected ART-naive MSM was
associated with higher levels of proviral HIV DNA. It also found that simultaneous detection of CMV in semen and PBMCs was associated with the highest levels of HIV DNA in PBMCs. These findings were most robust when evaluating samples that harbored an HIV population whose sequences completely matched that of the real-time PCR detection probe. Interestingly, levels of HIV DNA in PBMCs and CMV replication were not associated with CD4+ T-cell numbers or HIV RNA levels. A significant association between HIV RNA and HIV DNA levels was found after excluding samples with low-level HIV DNA, suggesting that the HIV DNA reservoir had to be at a sufficient size to correlate with measured HIV RNA levels, independent of the estimated duration of infection.

This study has several limitations. First, it was conducted on ART-naive individuals, so the measured HIV DNA levels included both integrated and unintegrated viral forms and might represent the extent of HIV replication, in addition to the size of the stable HIV reservoir. Since the latent viral reservoir includes only integrated HIV DNA, our total HIV DNA levels cannot represent solely the latent reservoir, although other studies found that >90% of HIV-infected cells in both untreated and treated HIV-infected individuals have a latent viral transcription pattern [15]. Future studies should evaluate the relationships between continuous and intermittent CMV reactivation and HIV DNA levels in the setting of ART and suppressed HIV RNA (which is representative of the latent reservoir).

Second, although we used a conserved set of primers and probe to quantify HIV DNA [8], we observed that samples with mismatches in the probe-binding site in their major HIV population presented significantly lower HIV DNA levels. We evaluated this by introducing a “mismatch variable” in our statistical model. We recognize that accounting for the mismatches as a binary variable is not ideal, since each primer mismatch could affect the efficiency of the PCR in a different way. Future studies should account for this potential technological artifact by perhaps using newer techniques, like digital droplet PCR, which may be less sensitive to single-base mismatches in primer and probe sequences. Moreover screening for STIs was performed only on a subset of participants at baseline, and unrecognized STIs might have confounded our findings. Last, because this was a retrospective, observational study, we cannot establish a causal relationship between CMV reactivation and HIV DNA levels, and the extent of immune activation during untreated HIV infection could be a determinant of CMV shedding and HIV DNA levels. Alternatively, subjects with larger HIV reservoirs might be more immunosuppressed and thus have more CMV reactivation. Despite those limitations, this study provides important insights in regard to one possible mechanism contributing to the establishment of the viral reservoir during early HIV infection. Future studies should determine whether persistent CMV replication could be targeted as a strategy to reduce the size of the latent HIV reservoir.

### Supplementary Data

**Supplementary materials** are available at The Journal of Infectious Diseases online (http://jid.oxfordjournals.org). Supplementary materials consist of data provided by the author that are published to benefit the reader. The posted materials are not copyedited. The contents of all supplementary data are the sole responsibility of the authors. Questions or messages regarding errors should be addressed to the author.

### Notes

**Acknowledgments.** We are grateful to all of the participants in the San Diego Primary Infection Cohort; the CFAR Genomic and Translational Virology Cores; and Nadir Weibel, for his support and inspiring discussions. We also thank and commemorate our dear friend and outstanding research colleague, Marek Fischer, for all his contributions and support to our research over many years. The HIV RNA quantification standard was obtained through the NIH AIDS Research and Reference Reagent Program, DAIDS, NIAID. The HIV VQA RNA quantification standard was obtained from the DAIDS Virology Quality Assurance Program. Primer and probe for quantification of herpesviruses, as well as the plasmids and quantification standards, were kindly provided by Fred Lakeman.

S. G. participated in the study design, performed the laboratory experiments, participated in the data analyses for this study, and wrote the primary version of the manuscript; C. M. A. performed the statistical analysis and wrote the primary version of the manuscript; S. R. M. participated in the data analyses and revised the manuscript; M. V. V. performed the laboratory experiments; S. J. L and D. M. S. enrolled participants; D. D. R., S. J. L., and D. M. S. designed the present study, participated in data analysis, and revised the manuscript; and all authors read and approved the final manuscript.

**Disclaimer.** The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Financial support.** This work was supported by the Department of Veterans Affairs, the James Pendleton Charitable Trust, the National Institutes of Health (awards AI0024, AI043638, MH62512, MH083552, DA034987, AI077304, AI36214 [Center for AIDS Research (CFAR)], AI077475, AI14621, GM093993, and AI080353, and AI06214 [CFAR]), the Swiss National Science Foundation (grant PASMP3_136983), the California HIV Research Program (grant RN07-SD-702), and the National Institute of General Medical Sciences (grant GM093939).

**Potential conflicts of interest.** D. D. R has served as a consultant for Bristol-Myers Squibb, Gilead Sciences, Merck, Monogram Biosciences, Biota, Chimerix, Tobira, and Gen-Probe. D. M. S. has received grant support from ViIV Pharmaceuticals and consultant fees from Gen-Probe. All other authors report no potential conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

### References


