



HAL
open science

Interpretation of Real-Time PCR Results for Hepatitis C Virus RNA When Viral Load Is Below Quantification Limits

Syria Laperche, Françoise Bouchardeau, Vincent Thibault, Anne-Marie Roque-Afonso, Pascale Trimoulet, Ronald Colimon, Gilles Duverlie, Hélène Leguillou-Guillemette, Françoise Lunel, Magali Bouvier-Alias, et al.

► **To cite this version:**

Syria Laperche, Françoise Bouchardeau, Vincent Thibault, Anne-Marie Roque-Afonso, Pascale Trimoulet, et al.. Interpretation of Real-Time PCR Results for Hepatitis C Virus RNA When Viral Load Is Below Quantification Limits. *Journal of Clinical Microbiology*, 2011, 49 (3), pp.1113-1115. 10.1128/JCM.01511-10 . hal-02014377

HAL Id: hal-02014377

<https://hal.science/hal-02014377>

Submitted on 1 Feb 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Copyright

Interpretation of Real-Time PCR Results for Hepatitis C Virus RNA When Viral Load Is Below Quantification Limits[▽]

Syria Laperche,¹ Françoise Bouchardeau,¹ Elisabeth André-Garnier,² Vincent Thibault,³ Anne-Marie Roque-Afonso,⁴ Pascale Trimoulet,⁵ Ronald Colimon,⁶ Gilles Duverlie,⁷ Hélène Leguillou-Guillemette,⁸ Françoise Lunel,⁸ Magali Bouvier-Alias,⁹ Jean-Michel Pawlotsky,⁹ Cécile Henquell,¹⁰ Evelyn Schvoerer,¹¹ Françoise Stoll-Keller,¹¹ Marie-Laure Chaix,¹² Michel Branger,¹³ Catherine Gaudy-Graffin,¹⁴ Arielle R. Rosenberg,¹⁵ Bruno Pozzetto,¹⁶ Sophie Vallet,¹⁷ Yazid Baazia,¹⁸ Jacques Izopet,¹⁹ and Jean-Jacques Lefrère^{20,21*}

*Centre National de Référence pour les Hépatites B et C en Transfusion, Département des Agents Transmissibles par le Sang, Institut National de la Transfusion Sanguine, Paris, France*¹; *Institut de Biologie, Hôtel Dieu, Nantes, France*²; *Laboratoire de Virologie, Centre Hospitalo-Universitaire Pitié-Salpêtrière, Paris, France*³; *Laboratoire de Virologie, Centre Hospitalier Paul Brousse, Villejuif, France*⁴; *Laboratoire de Virologie, Centre Hospitalo-Universitaire, Bordeaux, France*⁵; *Laboratoire de Virologie, Centre Hospitalo-Universitaire, Rennes, France*⁶; *Laboratoire de Virologie, Centre Hospitalo-Universitaire, Amiens, France*⁷; *Laboratoire de Virologie-Bactériologie, Centre Hospitalo-Universitaire Angers, France*⁸; *Laboratoire de Virologie-Bactériologie, Centre Hospitalo-Universitaire Henri-Mondor, Créteil, France*⁹; *Laboratoire de Virologie, Centre Hospitalo-Universitaire, Clermont-Ferrand, France*¹⁰; *Laboratoire de Virologie, Centre Hospitalier-Universitaire, Strasbourg, France*¹¹; *Laboratoire de Virologie, Centre Hospitalo-Universitaire Necker, Paris, France*¹²; *Laboratoire de Virologie, Centre Hospitalo-Universitaire Bichat, Paris, France*¹³; *Université François Rabelais, Inserm ERI19, Centre Hospitalier Universitaire, Tours, France*¹⁴; *Université René Descartes, Faculté de Médecine, and AP-HP, Groupe Hospitalier Cochin, Paris, France*¹⁵; *Laboratoire de Virologie-Bactériologie, Centre Hospitalo-Universitaire, Saint-Etienne, France*¹⁶; *Laboratoire de Microbiologie, Centre Hospitalo-Universitaire, Brest, France*¹⁷; *Laboratoire de Virologie-Bactériologie Associé au CNR des Hépatites B et C, Centre Hospitalo-Universitaire Avicenne, Bobigny, France*¹⁸; *Laboratoire de Virologie, Centre Hospitalo-Universitaire, Toulouse, France*¹⁹; *Laboratoire d'Hématologie, Centre Hospitalo-Universitaire, Amiens, France*²⁰; and *Département des Agents Transmissibles par le Sang, Institut National de la Transfusion Sanguine, Paris, France*²¹

Received 27 July 2010/Returned for modification 29 October 2010/Accepted 4 January 2011

Hepatitis C virus RNA quantification results obtained in 18 laboratories using real-time PCR methods with 10 negative samples and 22 sample dilutions (viral loads of 0.5 to 500 IU/ml) showed a score of correct results of up to 93.5%. However, 55.6% of the laboratories did not follow the recommendations for the interpretation of their results, leading to ambiguous conclusions.

The determination of hepatitis C virus (HCV) RNA levels has become an essential part of patient care, from early diagnosis of infection to treatment monitoring. Thus, the interpretation of HCV RNA quantification results should be done in accordance with precise and standardized diagnostic criteria. The use of molecular assays for HCV RNA quantification based on real-time PCR has become more widespread since they are able to detect levels of viral nucleic acids below 100 IU/ml (1–4). Moreover, these methods show high analytical sensitivity, making it possible to detect viral RNA below the lower limit of quantification (LoQ). Since the goal of antiviral treatment is full eradication of HCV from the blood (8) and since a diagnosis of acute infection may sometimes be based on the detection of very low viral loads (VLs) (5, 6), it is essential to distinguish the true absence of circulating viral RNA from a low and unquantifiable VL.

The Action Coordonnée 11 group of the Agence Nationale de Recherches pour le SIDA initiated, with 18 laboratories, a

study focused on the interpretation of the results of real-time PCR assays showing VLs below the threshold of the assay. The objective of this study was to point out the differences in the interpretation of such samples in order to allow virologists to give unambiguous results for low HCV RNA VLs to physicians.

A panel including 32 coded samples was sent to 18 participating laboratories. This panel was composed of three groups of samples. Group 1 included 10 HCV RNA-negative samples collected from blood donors who tested negative for hepatitis B surface antigen, HCV and human immunodeficiency virus antibodies (Prism; Abbott, Rungis, France) and for HCV RNA (COBAS *TaqMan* HCV; Roche, Meylan, France). The other two groups were made up of dilutions of two specimens. Specimen 1 was genotype 1a, with an HCV RNA VL of 150,000 IU/ml (COBAS *TaqMan* 48), and specimen 2 was genotype 2a with a VL of 5,200 IU/ml (COBAS *TaqMan* 48). Group 2 included 12 samples corresponding to three dilutions of specimens 1 and 2 with theoretical VLs of 0.5, 5, and 10 IU/ml present in duplicate. Group 3 included eight samples corresponding to three duplicated dilutions of the same specimens with VLs of 50 and 100 IU/ml, one dilution at 500 IU/ml for specimen 1 and one at 300 IU/ml for specimen 2.

* Corresponding author. Mailing address: Institut National de la Transfusion Sanguine, 6 rue Alexandre-Cabanel, 75015 Paris, France. Phone: 01 44 49 30 51. Fax: 01 44 49 30 59. E-mail: slaperche@ints.fr.

[▽] Published ahead of print on 12 January 2011.

TABLE 1. Results obtained with CAP/CTM and ART for the 32 samples in the panel

Test	No. of labs	No. of samples/total (%)				Score (%), range ^e
		Group 1 ^a	Group 2 ^b	Group 3 ^c	Total ^d	
CAP/CTM	6	59/59 (100) ^f	72/72 (100)	55/60 (91.7)	186/191	97.4, 93.7–100
ART	12	117/118 (99.1) ^g	135/144 (93.7)	120/120 (100)	372/382	97.4, 93.5–100
Both ^e	18	176/177 (99.4)	207/216 (95.8)	175/180 (97.2)	558/573	97.4, 93.5–100

^a Negative, 10 samples.

^b VLs, 0.5 to 10 IU/ml, 12 samples.

^c VLs, >50 IU/ml, 10 samples.

^d Thirty-two samples.

^e The score is the percentage of correct results among the expected results. The expected results were negative for group 1, negative or positive but under the LoQ for group 2, and positive with a VL in the range of quantification for group 3. The range of scores according to laboratory is shown in parentheses.

^f One lab provided nine results.

^g Two labs provided nine results.

Of the 18 participating laboratories, 6 used COBAS Ampliprep/COBAS TaqMan HCV 2 (CAP/CTM) from Roche Diagnostics (range of quantification, 43 IU/ml to 6.9×10^7 IU/ml; limit of detection [LOD], 15 IU/ml) and 12 used Abbott M2000sp/Abbott Realtime HCV PCR (ART) from Abbott Diagnostics (range of quantification, 12 IU/ml to 10^8 IU/ml). According to the two manufacturers, the following three categories of results were possible: (i) RNA not detected when HCV RNA is under the detection limit of the test, (ii) HCV RNA detected when the value is below the lower quantification limit, and (iii) HCV RNA detected when the value falls within the linear quantification range of the assay. The samples were assayed in single testing according to the manufacturer's instructions.

The results were analyzed at two levels. The first one aimed to analyze the results obtained after the PCR process. In this case, the expected results were "negative" for samples in group 1, "negative or target detected but not quantifiable" for samples in group 2 (to take into account Poisson distribution, which can give alternatively positive or negative results when viral RNA approaches the detection limit of the technique), and "target detected with a quantifiable VL" for samples in group 3. For each laboratory and each group of samples, the score was calculated as the percentage of correct results among the number of expected results. The second level of analysis, which only focused on samples in groups 1 and 2, aimed to evaluate the interpretation of participants for results from a "clinical" point of view. These clinical interpretations were classified into two categories. The first included the conclusions recommended by the manufacturer ("absence of detectable HCV RNA" when the result of the PCR process was negative and "presence of RNA" when the result was positive); the second included all other ambiguous interpretations suggesting the presence of HCV RNA in negative samples (for example, "under the LoQ") or its absence in positive samples (for example, "negative, under the LoQ").

For samples in groups 1, 2, and 3, 59, 72, and 60 results were provided with CAP/CTM and 118, 144, and 120 were provided with ART, respectively. The global score of correct results was 97.4% (range, 93.7 to 100%) for CAP/CTM and 97.4% (range, 93.5 to 100%) for ART (Table 1). Two of the 6 laboratories using CAP/CTM and 8 of the 12 laboratories using ART gave 100% correct results. The highest score was obtained for CAP/CTM in groups 1 and 2, as 100% of the samples included in these groups were correctly classified, while ART had a better

score in group 3, with 100% of the results correct. CAP/CTM failed to correctly quantify five samples included in group 3, giving positive results but with a VL under the LoQ. ART provided one false-positive result in group 1 and overestimated nine samples in group 2. In group 2, the results obtained with CAP/CTM in a total of 72 cases were "not detected" in 23 cases (32%), "RNA detected but below the LoQ" in 49 cases (68%), and "quantifiable RNA" in none; those obtained with ART in a total of 144 cases were "RNA not detected" in 50 cases (35%), "RNA detected but below the LoQ" in 85 cases (59%), and "quantifiable RNA" in 9 cases (6%).

The two investigated HCV real-time PCR assays had good specificity, since only one false-positive result (with a sample with a VL under the LoQ) was observed among the 177 tests performed with HCV-negative samples.

Table 2 shows the mean VLs obtained with the two assays in samples in group 3. Coefficients of variation ranged from 23.2% to 37.6% for ART and from 19.4% to 44.6% for CAP/CTM. Despite the underestimation of the VL in five samples in group 3, CAP/CTM gave significantly higher VLs than ART in samples with VLs above 100 IU/ml ($P < 10^{-3}$). Furthermore, among the samples containing a VL below the LoQ, ART provided a slightly higher proportion of negative results than CAP/CTM (35% versus 32%).

Regarding the interpretation of the results analyzed for samples in groups 1 and 2, only 8 (44.4%) laboratories (4 using CAP/CTM and 4 using ART) followed the manufacturer's recommendations for the interpretation of the results obtained and 10 (63.6%) gave ambiguous interpretations for both groups ($n = 6$) or alternatively for negative ($n = 1$) or positive results ($n = 3$).

Despite the indisputable performance of the two PCR assays, even though some slight differences have been observed between the two methods, a heterogeneity was noted in the interpretations given by the participating laboratories, irrespective of the method used, especially with critical samples (negative or containing a VL close to the LoQ). Indeed, 55.6% of the labs did not follow the manufacturers' recommendations for the clinical interpretation of their results. However, the study was performed out of any clinical context, and this certainly contributed to the ambiguity of the conclusions provided by some labs, especially for "negative" samples. In any case, these ambiguous conclusions underline the necessity of the knowledge of the clinical context to give a reliable interpretation of such results.

TABLE 2. Mean VLs of samples with more than 50 IU/ml (group 3)

Specimen and theoretical VL (IU/ml)	CAP/CTM			ART			<i>P</i> ^a
	No. of determinations	Measured VL (IU/ml)	CV (%)	No. of determinations	Measured VL (IU/ml)	CV (%)	
1							
50	11	40	30.6	24	40	37.6	NS ^b
100	12	99	19.4	24	74	24.1	<10 ⁻³
500	6	807	20.7	12	333	29.5	<10 ⁻⁴
2							
50	10	34	44.6	24	40	36.1	NS
100	10	71	41.1	24	84	23.2	NS
300	6	396	32.8	12	242	29.2	<10 ⁻³

^a *P* = probability obtained after analysis of variance (F test) comparing the mean VLs obtained with the two assays. The difference was considered significant when *P* was <0.05.

^b NS, not significant.

Distinguishing the absence of HCV RNA and its presence at an unquantifiable RNA level remains a delicate point largely depending on the clinical context. When an early infection is suspected, especially when anti-HCV antibodies are not yet detectable, detection of viremia, even at a low level, is crucial in order to initiate early antiviral therapy. Furthermore, “eradication” of HCV, which is the goal to be achieved to assess treatment efficacy (7), remains to be defined. It is thus important for clinicians to have reliable biological results reflecting the reality of the eradication status. In this matter, the true question is whether we need to reach a “zero” viremia level or an undetectable RNA level that would be arbitrarily determined as the detection limit of the assay to consider that HCV eradication has been attained. This issue should be resolved with the availability of more-sensitive PCR methods, but today it remains of importance.

This work was supported by a grant from the Agence Nationale de Recherches sur le SIDA et les Virus des Hépatites.

We thank Annie Razer and Christine Portal for their technical assistance.

REFERENCES

1. Barbeau, J. M., J. Goforth, A. M. Caliendo, and F. S. Nolte. 2004. Performance characteristics of a quantitative TaqMan hepatitis C virus RNA analyte-specific reagent. *J. Clin. Microbiol.* **42**:3739–3746.
2. Caliendo, A. M., et al. 2006. Multilaboratory comparison of hepatitis C virus viral load assays. *J. Clin. Microbiol.* **44**:1726–1732.
3. Forman, M. S., and A. Valsamakis. 2004. Verification of an assay for quantification of hepatitis C virus RNA by use of an analyte-specific reagent and two different extraction methods. *J. Clin. Microbiol.* **42**:3581–3588.
4. Konnick, E. Q., S. M. Williams, E. R. Ashwood, and D. R. Hillyard. 2005. Evaluation of the COBAS Hepatitis C Virus (HCV) TaqMan analyte-specific reagent assay and comparison to the COBAS Amplicor HCV Monitor V2.0 and Versant HCV bDNA 3.0 assays. *J. Clin. Microbiol.* **43**:2133–2140.
5. McGovern, B. H., et al. 2009. Improving the diagnosis of acute hepatitis C virus infection with expanded viral load criteria. *Clin. Infect. Dis.* **49**:1051–1060.
6. Nübling, C. M., et al. 2009. Experience of mandatory nucleic acid test (NAT) screening across all blood organizations in Germany: NAT yield versus breakthrough transmissions. *Transfusion* **49**:1850–1858.
7. Pawlotsky, J. M. 2006. Therapy of hepatitis C: from empiricism to eradication. *Hepatology* **43**:S207–S220.
8. Zeuzem, S., et al. 2009. Expert opinion on the treatment of patients with chronic hepatitis C. *J. Viral Hepat.* **16**:75–90.