Hepatitis C virus (HCV) RNA quantification is extensively used for therapeutic management of HCV chronic infection (1). The COBAS HCV Monitor v2.0 assay (HCM) was until recently one of the most used quantification methods worldwide. Two of its drawbacks are the labor-intensive manual extraction of HCV RNA and the frequent requirement of serum dilution for accurate quantification (>5.7 log_{10} IU/ml) (4). The COBAS Ampliprep TNAI/COBAS TaqMan 48 Roche assay (CAPP-CTM) combines automated HCV RNA extraction with real-time PCR on the COBAS TaqMan 48 instrument (CTM48). It is one of the first platforms for clinical laboratories tending towards fully automated nucleic acid isolation and quantification, and it ensures a broad dynamic quantification range (43 to 69,000,000 IU/ml).

Therefore, we aimed to evaluate this new assay by measuring HCV RNA levels (VL) in sera from 93 patients previously tested using HCM (results range, 723 to 21,400,000 IU/ml). The HCV genotype was previously determined for each sample (7). Thirty-seven patients were infected with HCV genotype 1, and 56 were infected with an HCV non-1 genotype, including genotypes 2, 3, and 4 in 6, 33, and 17 cases, respectively.

No HCV sample was found below the quantification threshold of 43 IU per ml with CAPP-CTM. For patients infected with HCV genotype 1, Spearman’s rank correlation coefficient was 0.941 (P < 0.01; R-square = 0.895), and the mean difference between RNA concentrations with CAPP-CTM and those with HCM was −0.11 ± 0.30 (range, −0.51 to 0.86); differences were between ±0.5 log_{10} IU/ml for 89% of samples (Fig. 1, left). For patients infected with HCV non-1 genotypes, Spearman’s rank correlation coefficient was 0.907 (P < 0.01; R-square = 0.836) and the mean difference was −0.77 ± 0.40 log_{10} IU/ml (Fig. 1, right). Differences varied broadly according to individual samples (from −1.61 to 0.03); they exceeded −0.5 and −1.0 log_{10} IU/ml in 71% and 30% of samples, respectively.

Comparisons between VL measured with CTM48 and HCM were previously reported, but they focused only on clinical samples containing HCV genotype 1. They showed poor agreement, which differs from our findings. For instance, VL obtained with CTM48 were, on average, either twofold lower than with HCM or higher by +0.45 log_{10}, while large differences for individual samples were also observed (2, 3, 5). HCV RNA isolation procedures differed between the different studies, having been performed with either Roche MagNA Pure LC or QIAGEN BioRobot 9604 instruments. HCM was also found to overestimate a genotype 1 international standard concentration by approximately 0.5 log_{10} (6).

Our findings revealed large underestimations of VL in clinical samples containing HCV genotypes 2, 3, and 4 with the CAPP-CTM assay in comparison with HCM, with large differ-

FIG. 1. Correlation between HCV RNA quantitative results using COBAS Ampliprep HCV Monitor and COBAS Ampliprep TNAI/COBAS TaqMan 48 HCV assays for HCV genotype 1 (left) and non-1 genotype (right) strains. Dashed lines, virtual equivalence between the two assays; ◆, genotype 2; □, genotype 3; ×, genotype 4.
ences for individual samples. These genotypes represent approximately half of HCV-infected patients in our laboratory (7). Mean differences in VL between the two assays differ for samples infected with HCV 1 and non-1 genotypes. Thus, our data highlight the need for caution towards sequential measurements of non-1 genotype HCV RNA using different generations of Roche assays.

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