Comparison of the new Hologic Aptima HIV-1 Quant Dx Assay with the established Abbott RealTime in HIV-1 viral load measurement

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Introduction and Purpose:

Hologic's Aptima HIV-1 Quant Dx assay is a HIV-1 RNA quantitative assay based on real-time Transcription Mediated Amplification (TMA) that runs on the fully automated Panther system with random access. A comparison with the Abbott m2000 RealTime assay was performed. Special focus was put on linearity, viremia near the limit of detection of the assays, non-B subtypes, and integrase inhibitor resistant samples.

Methods

Fresh (n=282), frozen (non-B, n=117; with integrase mutations, n=22) and diluted (n=559) patient samples spread over the clinical relevant range of viral load were tested. The Aptima assay is a dual target assay with targets in pol (integrase) and LTR-region, whereas RealTime uses a single target in the integrase region. Samples with integrase mutations were additionally tested with the Roche Cobas TaqMan v2.0, with targets outside the integrase region. For linearity comparison we set up and optimized two linear models minimizing the residual sum of squares (RSS) for each set of log-scaled viral loads measured by Aptima respectively Abbott.

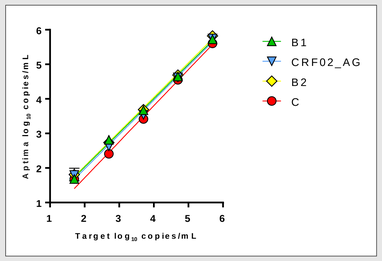

Figure 1: Linearity

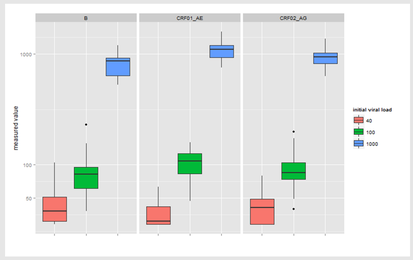

Figure 2: Inter-assay variance

Table 1: Intra-assay variance

Viral Load	Assay	CRF02_AG	B	CRF01_AE
1.7 log c./mL	Aptima	6,8%	6,9%	8,4%
	m2000	9,5%	8,2%	7,5%
2 log c./mL	Aptima	7,7%	6,9%	4,0%
	m2000	7,2%	4,7%	5,9%
2.3 log c./mL	Aptima	5,4%	5,0%	5,1%
	m2000	4,3%	4,0%	3,0%

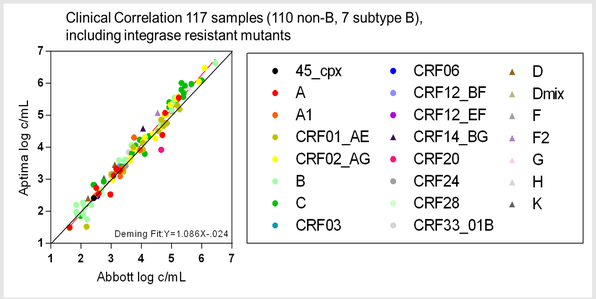

Figure 3: Subtypes

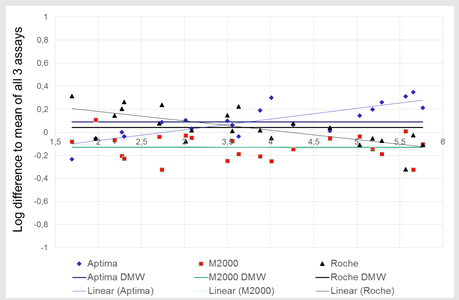

Figure 4: Integrase resistant samples

Tabele 2: Correlation in clinical samples

		Aptima			Total
		und	<30	quant	
Abbott	und	40	25	2	67
	<40	1	3	2	6
	quant	0	2	25	27
Total		41	30	29	100

Results

Aptima HIV-1 Quant Dx assay showed excellent performance in high throughput, routine use even in samples with low viremia and with mutations in the integrase region. With a lower limit of quantification (LLOQ) of 30 cps/mL and a lower limit of detection (LLOD) of 13 cps/mL, the Aptima assay classified more samples as "detected" (30 versus 6) than the RealTime assay in 100 unselected fresh samples (s. Tab. 2). Bland Altman plots demonstrated high concordance between the two assays. High concordance was also shown for non-B subtypes (s. Fig. 3). The mean difference was below 0.1 log cps/mL. Intra- and inter-assay variation was low and comparable to RealTime with intra-assay %CV ranging from 4.0% for samples with a viral load of 2.0 log cps/mL to 8.4% with 1.7 log cps/mL (s. Tab. 1 and Fig. 2). Linearity was shown by serial dilution (subtype B, C and CRF02_AG) from 5.7 log cps/mL to 1.7 log cps/mL (s. Fig. 1). Calculation yielded RSS values of 0.967 for Abbott and 0.944 for Aptima, testing for difference of both models resulted in a p-value <0.05 indicating values measured by Aptima are characterised slightly more linear than Abbott samples. Mutations associated with resistance in the integrase region were not found to impact results in the Abbott and the Aptima assay as compared to the Roche assay (s. Fig. 4).

Conclusions

The Aptima HIV-1 Quant Dx assay showed excellent correlation with RealTime with high sensitivity, linearity and accuracy in the therapeutic relevant range for all tested HIV-1 subtypes. With random access, the ability to continuously load samples and time to first result of about 150 minutes this assay is a major improvement in the viral load monitoring of HIV-1 infection.