Research Articles - JCM

Performance assessment of Respiratory Viral ELITe MGB® assay for the quantitative detection of influenza A/B and respiratory syncytial viruses.

Antonio Piralla,[a*] Federica Giardina,[a*] Alice Fratini,[a] Davide Sapia,[a] Francesca Rovida,[a] Fausto Baldanti[a,b]

Molecular Virology Unit, Microbiology and Virology Department, Fondazione I.R.C.C.S. Policlinico San Matteo, Pavia, Italy[a]; Department of Clinical-Surgical, Diagnostic and Pediatric Sciences, Università Degli Studi di Pavia, Pavia, Italy[b]

Running title: Multiplex assays for the quantification of FluA/B and RSV.

*Antonio Piralla and Federica Giardina contributed equally to this article.

Address correspondence to Antonio Piralla, a.piralla@smatteo.pv.it

Text word: 1735

Abstract: 253 (max 250)

Abstract

Influenza (Flu) and respiratory syncytial virus (RSV) are responsible for lower respiratory tract infections (LRTIs) associated with significant hospitalization among young children. In the present study, the performances of a triplex PCR assay detecting Flu A/B and RSV were compared with our in-house single-plex assays using 160 stored respiratory specimens previously tested using a panel of laboratory-developed real-time RT-PCR. Of them, 61 were positive for FluA, 41 for FluB, and 58 for RSV. All samples were retrospectively quantified with Respiratory Viral (RV) ELITe MGB® Panel (ELITechGroup Molecular Diagnostics, Puteaux, France) processed using ELITe InGenius® system. Overall, the total percentage agreement observed was 93.4% (57/61) for FluA, 92.7% (38/41) for FluB, and 86.2% (50/58) for RSV. A significant correlation of VL values was observed between the two methods for FluA and RSV ($\rho = 0.91$ and 0.84). This finding was supported by the strength of agreement between the two methods, as showed by the linear regression analysis (R2 =0.84 and 0.80). FluB viral load values measured by RV Panel were less significantly correlated ($\rho = 0.77$ and R2 =0.56). The bland-Altman analysis showed how 84.2% (48/57) of FluA and 86.0% of RSV (43/50) samples fell within ±1.0 Log10 variation from our laboratory results, while only 21.1% (8/38) of FluB results fell within this range. The great majority of FluB samples (29/30) outside range had values higher than +1.0 Log10 (median +2.1 Log10 range +1.0 to +3.5 Log10). In conclusion, RV ELITe MGB® Panel constitutes a valid and robust system for simultaneous detection and quantification of Flu A/B and RSV.

Keywords: Multiplex PCR, Real-time, respiratory viruses, InGenius, Quantitative results.

Influenza viruses type A and B (Flu A/B) and respiratory syncytial virus (RSV) are responsible for lower respiratory tract infections (LRTIs) associated with significant hospitalization among young children, elderly and immunocompromised patients (1-5). The incidence, morbidity, and mortality of Flu as compared to RSV varies from season to season (6). A rapid diagnosis allowing an appropriate decision regarding treatment and/or improved cohorting and isolation strategies to prevent transmission is a major concern on respiratory virus infections (7-9). In fact, in the last decade, the introduction of nucleic acid amplification tests (NAATs) have shortened turnaround time (TAT) and increased sensitivity for respiratory viruses (10). Furthermore, the multiplex RT-PCR approach is a validated strategy to detect a large number of respiratory viruses (8). Quantitative NAATs have been useful in terms of monitoring the reduction of viral load and thus the clinical efficacy of specific therapy (11,12). Different viral load levels have been associated with a higher risk of complications and severe disease in adults and children (13-15). In addition, the determination of viral load for different viruses in co-infections could be useful to distinguish which virus is the real pathogen and which the bystander (16). All these issues have to be interpreted in the context of available clinical and diagnostic information in order to improve clinical management. However, the use of quantitative NAATs in the diagnosis of respiratory viruses has largely been debated.

In the present study, the performances of a triplex-PCR assay detecting and quantifying Flu A/B and RSV were compared with our laboratory developed single-plex assays using positive stored clinical specimens.

MATERIAL AND METHODS

Study samples. A total of 160 respiratory samples, stored at −80 °C in a universal transport medium (UTM™, Copan Italia SpA, Brescia, Italy) and collected from December 2014 through April 2016 at the Molecular Virology Unit of the Fondazione IRCCS Policlinico San Matteo were included in this study. All samples were previously tested using a panel of laboratory-developed

assays (LDA) real-time RT-PCR as previously described (9). Of them, 61 were positive for Flu A, 41 for Flu B and 58 RSV. Samples were categorized by viral load as high (>10^6 RNA copies/ml), medium (10^4-10^5 RNA copies/ml) and low (10^2-10^3 RNA copies/ml). All samples were retrospectively quantified with Respiratory Viral ELITe MGB® Panel (ELITechGroup Molecular Diagnostics, Puteaux, France) processed using ELITe InGenius® system.

Respiratory Viral ELITe MGB® Panel. The archived respiratory samples were processed according to the manufacturer's protocol on InGenius, a completely automated cassette based sample-to-results solution combining a universal extraction and independently controlled Real-time PCR thermal cycler (ELITechGroup Molecular Diagnostics, Puteaux, France). Briefly, 200 ul of respiratory were carefully transferred into a dedicated tube and loaded on the InGenius instrument for testing. Finally, the InGenius instrument was supplied with extraction/amplification Internal Control (IC), the RV ELITe MGB amplification Master mix, and extraction and amplification cassette consumables provided by the manufacturer (ELITechGroup Molecular Diagnostics, Puteaux, France). Results interpretation was performed according to the instruction manual of the RV ELITe MGB® assay. Quantitative results expressed as $\log_{10}$ RNA copies/ml were measured comparing the cycle threshold (Ct) values obtained and interpolated with a standard curve (serial dilutions of DNA plasmid) for FluA, FluB and RSV.

Statistical analysis. All viral RNA load (copies/ml) statistics were performed using $\log_{10}$ transformed viral load values. Quantitative variables were described as the mean and standard deviation, and/or median. Correlations between two quantitative variables were measured by the Spearman correlation test. The agreement between the assays was assessed with a Bland-Altman plot (17) and for graphical representation a ± 0.5 Log_{10} was considered an acceptable range of variability as also according to other publications (18). Descriptive statistics and linear regression lines were performed using Graph Pad Prism software (version 5.00.288). The correlation between

the quantitative results was computed as the concordance correlation coefficient (CCC) of the measurements, according to Lin (19) using MedCalc® software (Version 9.4.2.0).

RESULTS

A total of 160 respiratory samples with viral load ranging from 120 to 54574920 RNA copies/ml for FluA, from 180 to 31370040 RNA copies/ml for FluB and from 100 to 94513860 RNA copies/ml were analysed. Overall, the total percentage agreement observed was 93.4% (57/61) for FluA, 92.7% (38/41) for FluB and 86.2% (50/58) for RSV (Table 1). In detail, all FluA- (4/61) and FluB-positive (3/41) samples not detected by RV ELITe MGB® Panel belonged to low viral load group (10^2-10^3 RNA copies/ml), with viral load ranging from 270 to 900 RNA/copies ml for FluA and from 225 to 900 RNA/copies ml for FluB. Among 8 (13.8%) RSV-positive samples resulted negative by RV ELITe MGB® Panel, 1 (1.7%) had medium viral load (25650 RNA/copies ml) and 7 (12.1%) had low viral load ranging from 180 to 810 RNA/copies ml.

Positive samples were stratified based on viral load into three groups named high, medium and low (Figure 1). Viral loads were comparable in samples included in the high ($p=0.11$) and medium ($p=0.84$) group for FluA as well as for RSV ($p=0.07$ and $p=0.74$) (Fig. 1A and 1C). Conversely, a significantly difference of viral load was observed for FluA and RSV in low viral load group (Fig. 1A and 1C; $p<0.001$). For FluB samples, no difference in median viral load was observed in high group, while median viral load measured by RV ELITe MGB® Panel was greater in the medium and low groups (Fig. 2A, $p<0.001$).

A significant correlation was observed between the LDA and RV ELITe MGB® Panel for FluA and RSV assays ($\rho = 0.91$ and 0.84) also supported by the strength of agreement observed by the linear regression analysis ($R^2 = 0.84$ and 0.80) (Fig. 2A and 2C). In addition, the two assays showed good concordance, with a CCC of 0.86 (95% CI, 0.79 to 0.91) and 0.81 (95% CI, 0.70 to 0.88) for FluA and RSV assays, respectively (Table 2). FluB viral load values measured by RV ELITe MGB® Panel were less significant correlated to those quantified by LDA ($\rho = 0.77$ and R^2

=0.56). This finding was also confirmed by the low concordance with a CCC of 0.36 (95% CI, 0.22 to 0.49).

A plot of the differences between Log_{10} values obtained with LDA and results obtained by RV ELITe MGB® Panel assay was reported using a Bland-Altman analysis. Overall, the mean difference between two assays were -0.09 (± 1.96 SD, range -1.52 to +1.34) for FluA, -1.58 (± 1.96 SD, range -3.7 to +0.54) for FluB, and -0.32 (± 1.96 SD, range -1.77 to +1.13) for RSV. Assuming that differences within ± 0.5 log_{10} from LDA results for RV ELITe MGB® Panel assay is the acceptable range, Bland-Altman analysis showed how 64.9% (37/57) of FluA and 64.0% of RSV (32/50) samples fell within ±0.5 Log_{10} variation from LDA results, while only 15.8% (6/38) of FluB results fell within this range. Regarding values outside the range of acceptability (values >+0.5 log_{10} or <−0.5 log_{10} difference), among results of FluA samples, 10/57 (17.5%) had had values >+0.5 log_{10} difference (mean +0.88 Log_{10} range +0.51 to +1.46 Log_{10}), while 10/57 (17.5%) had values <−0.5 log_{10} difference (mean -1.30 Log_{10} range -2.10 to -0.61 Log_{10}). Among RSV samples, 3/50 (6.0%) had values >+0.5 log_{10} difference (mean +0.79 Log_{10} range +0.61 to +1.13 Log_{10}) and 15/50 (30.0%) had values <−0.5 log_{10} difference (mean -1.14 Log_{10} range +3.25 to -0.51 Log_{10}) (grey circle, Fig. 3A and 3C). Almost all (31/32) FluB samples outside the acceptability range had a viral load difference greater than -0.5 Log_{10} (median -1.99 Log_{10} range -0.80 to -3.5 Log_{10}; Fig. 3B) as compared with our LDA. This means that overall RV ELITe MGB® Panel quantify 2 Log_{10} more than LDA.

DISCUSSION

In the field of respiratory infections, a rapid and accurate diagnosis is needed for reducing unnecessary antibiotic usage, preventing transmission, and initiation of specific antiviral therapy (20, 21). In the past decades, the conventional diagnostics methods have been replaced by molecular assays also in the diagnosis of respiratory virus infections. Although, these assays have significantly reduced the turnaround time (TAT) to less than six hours, sometimes most of them

resulted as complex to perform. In this perspective, it was of great introduction the newly designed diagnostic platform easy to handle with a further reduction of TAT. In the present study, the ELITe InGenius® system has been evaluated using the Respiratory Viral ELITe MGB® Panel in terms of performances including the semi-quantification of respiratory samples.

The overall agreement of the RV ELITe MGB® Panel compared to LDT was 93.4%, 92.7%, and 86.2% for influenza A, influenza B, and RSV, respectively. These findings are in keeping with the results of other rapid molecular assays when compared to LDT (22, 23). The main discordant results were observed in samples with low viral load (< 3 log10 RNA copies/ml). These results are commonly observed in comparison performed between multiplex syndromic PCR panels and single target LDT (24, 25). Linear regression showed good correlations between RV ELITe MGB® Panel and LDT for Flu A and RSV. Among Flu B samples, a greater viral load level with a median of 2 Log10 was observed using RV ELITe MGB® Panel.

RV ELITe MGB® Panel also provides a fully automated sample-to-result solution with a TAT of 2.5 hours for 12 samples but at this stage, only the panel does not include other respiratory pathogens. However, results of the present study encourage the availability of quantitative assays for respiratory virus detection but raise the question that also other respiratory viruses, such as rhinoviruses and parainfluenza viruses, could be included in a quantitative panel due to their increasing frequency of detection also in severe respiratory illness (26, 27).

Our study has a number of limitations. First, the RV ELITe MGB® Panel has been evaluated only in a series of previously tested-positive samples and therefore it could not be assessed an overall performance in terms of positive and negative predictive values. Our pilot study was mainly focused on the validation of the quantitative results obtained. It will be necessary, a more extended study should be performed, including also negative samples, in order to clarify the clinical impact of this sample-to-result solution within the laboratory workflow.

In conclusion, based on the data presented here, the robustness of quantification obtained by the RV ELITe MGB® Panel was demonstrated. Only a few samples with very low viral load have

not been detected by the new direct RV ELITe MGB® Panel assay described herein is a powerful tool for rapid and simple molecular diagnosis of seasonal influenza as well as RSV.

ACKNOWLEDGMENTS

The authors would like to thank Daniela Sartori for manuscript editing. Financial support and reagents were provided by ELITechGroup Molecular Diagnostics (Torino, Italy). The funding organization played no role in the collection, management, analysis, and interpretation of the data; or preparation, review, and approval of the manuscript.

References

1. Malosh RE, Martin ET, Ortiz JR, Monto AS. 2018. The risk of lower respiratory tract infection following influenza virus infection: a systematic and narrative review. Vaccine **36**:141-147. https://doi.org/10.1016/j.vaccine.2017.11.018
2. Branche AR, Falsey AR. 2015. Respiratory syncytial virus infection in older adults: an under-recognized problem. Drugs Aging, 32:261-269. https://doi.org/10.1007/s40266-015-0258-9.
3. Hakim H, Dallas R, Zhou Y, Pei D, Cheng C, Flynn PM, Pui CH, Jeha S. 2016. Acute respiratory infections in children and adolescents with acute lymphoblastic leukemia. Cancer, **122**:798-805. https://doi.org/10.1002/cncr.29833.
4. Waghmare A, Campbell AP, Xie X, Seo D, Kuypers J, Leisenring W, Jerome KR, Englund JA, Boeckh M. 2013. Respiratory syncytial virus lower respiratory disease in hematopoietic cell transplant recipients: viral RNA detection in blood, antiviral treatment, and clinical outcomes. Clin Infect Dis **57**:1731-1741. https://doi.org/10.1093/cid/cit639.
5. Hijano DR, Maron G, Hayden RT. 2018. Respiratory Viral Infections in Patients With Cancer or Undergoing Hematopoietic Cell Transplant. Front Microbiol 9:3097. https://doi.org/10.3389/fmicb.2018.03097.
6. Kwon YS, Park SH, Kim MA, Kim HJ, Park JS, Lee MY, Lee CW, Dauti S, Choi WI. 2017 Risk of mortality associated with respiratory syncytial virus and influenza infection in adults. BMC Infect Dis **17**:785. https://doi.org/10.1186/s12879-017-2897-4.
7. Beckmann C, Hirsch HH. 2015. Diagnostic performance of near-patient testing for influenza. J Clin Virol **67**:43-46. https://doi.org/10.1002/jmv.24492.
8. Hirsch HH, Martino R, Ward KN, Boeckh M, Einsele H, Ljungman P. 2013. Fourth european conference on infections in leukaemia (ECIL-4): guidelines for diagnosis and treatment of human respiratory syncytial virus, parainfluenza virus, metapneumovirus, rhinovirus, and corona-virus. Clin Infect Dis **56**:258-266. https://doi.org/10.1093/cid/cis844.

9. Piralla A, Lunghi G, Percivalle E, Viganò C, Nasta T, Pugni L, Mosca F, Stronati M, Torresani E, Baldanti F. 2014. FilmArray® respiratory panel performance in respiratory samples from neonatal care units. Diagn Microbiol Infect Dis. 79(2):183-6. https://doi.org/10.1016/j.diagmicrobio.2014.02.010.

10. Ginocchio CC, Zhang F, Malhotra A, Manji R, Sillekens P, Foolen H, Overdyk M, Peeters M. 2009. Evaluation of multiple test methods for the detection of the novel 2009 influenza A (H1N1) during the New York City outbreak. **45**:191-195. https://doi.org/10.1128/JCM.43.6.2616-2623.2005.

11. Lee N, Chan MC, Lui GC, Li R, Wong RY, Yung IM, Cheung CS, Chan EC, Hui DS, Chan PK. 2015. High Viral Load and Respiratory Failure in Adults Hospitalized for Respiratory Syncytial Virus Infections. J Infect Dis. 212:1237-1240. https://doi.org/10.1093/infdis/jiv248.

12. Khanna N, Widmer AF, Decker M, Steffen I, Halter J, Heim D, Weisser M, Gratwohl A, Fluckiger U, Hirsch HH. 2008. Respiratory syncytial virus infection in patients with hematological diseases: single-center study and review of the literature. Clin Infect Dis. 46(3):402-12. https://doi.org/10.1086/525263.

13. Hasegawa K, Jartti T, Mansbach JM, Laham FR, Jewell AM, Espinola JA, Piedra PA, Camargo CA Jr. 2015. Respiratory syncytial virus genomic load and disease severity among children hospitalized with bronchiolitis: multicenter cohort studies in the United States and Finland. J Infect Dis. 211:1550-9. https://doi.org/10.1093/infdis/jiu658.

14. Kim YJ, Guthrie KA, Waghmare A, Walsh EE, Falsey AR, Kuypers J, Cent A, Englund JA, Boeckh M. 2014. Respiratory syncytial virus in hematopoietic cell transplant recipients: factors determining progression to lower respiratory tract disease. J. Infect. Dis. 209, 1195–1204. https://doi.org/10.1093/infdis/jit832.

15. DeVincenzo JP1, Wilkinson T, Vaishnaw A, Cehelsky J, Meyers R, Nochur S, Harrison L, Meeking P, Mann A, Moane E, Oxford J, Pareek R, Moore R, Walsh E, Studholme R, Dorsett P, Alvarez R, Lambkin-Williams R. 2010. Viral load drives disease in humans experimentally

infected with respiratory syncytial virus. Am J Respir Crit Care Med. 182(10):1305-14. https://doi.org/10.1164/rccm.201002-0221OC.

16. Martin ET, Kuypers J, Wald A, Englund JA. 2012. Multiple versus single virus respiratory infections: viral load and clinical disease severity in hospitalized children. Influenza Other Respir Viruses. 6(1):71-7. https://doi.org/0.1111/j.1750-2659.2011.00265.x.
17. Bland JM, Altman DG. 1986. Statistical methods for assessing agreement between two methods of clinical measurement. Lancet 1(8476):307-10.
18. Pang XL, Fox JD, Fenton JM, Miller GG, Caliendo AM, Preiksaitis JK; American Society of Transplantation Infectious Diseases Community of Practice; Canadian Society of Transplantation. 2009. Interlaboratory comparison of cytomegalovirus viral load assays. Am J Transplant. 9(2):258-68. https://doi.org/10.1111/j.1600-6143.2008.02513.x.
19. Lin LI. 1989. A concordance correlation coefficient to evaluate reproducibility. Biometrics 45:255–268.
20. Shah S, Bourgeois F, Mannix R, Nelson K, Bachur R, Neuman MI. 2016. Emergency department management of febrile respiratory illness in children. Pediatr Emerg Care 32:429–34. https://doi.org/10.1097/PEC.0000000000000721.
21. Klepser DG, Corn CE, Schmidt M, Dering-Anderson AM, Klepser ME. 2015. Health care resource utilizationand costs for influenza-like illness among midwestern health plan members. J Manag Care Spec Pharm. 21:568–73. https://doi.org/10.18553/jmcp.2015.21.7.568.
22. Popowitch EB, Miller MB. 2018. Comparison of the Xpert Flu/RSV XC and Xpress Flu/RSV Assays. J Clin Microbiol. 56(8): e00278-18. https://doi.org/10.1128/JCM.00278-18.
23. Voermans JJC, Mulders DGJC, Pas SD, Koopmans MPG, van der Eijk AA, Molenkamp R. 2020. Performance evaluation of the Panther Fusion® respiratory tract panel. J Clin Virol. 123:104232. https://doi.org/10.1016/j.jcv.2019.104232.
24. Bruning AHL, Leeflang MMG, Vos JMBW, Spijker R, de Jong MD, Wolthers KC, Pajkrt D. 2017. Rapid Tests for Influenza, Respiratory Syncytial Virus, and Other Respiratory Viruses: A

Systematic Review and Meta-analysis. Clin Infect Dis. 65(6):1026–1032. https://doi.org/10.1093/cid/cix461.

25. Ramanan P, Bryson AL, Binnicker MJ, Pritt BS, Patel R. 2017. Syndromic Panel-Based Testing in Clinical Microbiology. Clin Microbiol Rev. 31(1):e00024-17. https://doi.org/10.1128/CMR.00024-17.

26. Das D, Le Floch H, Houhou N, Epelboin L, Hausfater P, Khalil A, Ray P, Duval X, Claessens Y-E, Leport C, ESCAPED Study Group. 2015. Viruses detected by systematic multiplex polymerase chain reaction in adults with suspected com-munity-acquired pneumonia attending emergency departments in France. Clin Microbiol Infect 21:608.e1–8.23. https://doi.org/10.1016/j.cmi.2015.02.014.

27. Dunn JJ, Miller MB. 2014 Emerging respiratory viruses other than influenza. Clin Lab Med 34:409–30. https://doi.org/10.1016/j.cll.2014.02.011.

Figure legend

Figure 1. Comparison of the viral load measured with LDA (white circle) and RV ELITe MGB® Panel (black circle) for influenza A (A), influenza B (B) and RSV (C).

Figure 2. Linear regression analysis of log transformed viral load measured by LDA vs RV ELITe MGB® Panel assays for influenza A (A), influenza B (B) and RSV (C). Dashed red lines show the 95% confidence interval of the regression line (red line). Samples with undetectable results with RV ELITe MGB® Panel are reported with a grey circle.

Figure 3. Bland Altman analysis was performed to compare the viral load (Log_{10} difference) measured by the two methods, LDA and RV ELITe MGB® Panel assay, for influenza A (A), influenza B (B) and RSV (C). The acceptability range (+0.5 to -0.5 Log_{10} difference) is shaded in light grey and mean value is reported with a dotted line. Data outside the acceptability range are reported with a grey circle.

288 **TABLE 1 Cross table of clinical performance study.**

Assay	Virus target	Samples viral load category	RV ELITe MGB® results			% agreement
			pos	neg	total	
LDA	Flu A (n=61)	high viral load[a]	26	0	26	100.0%
		medium viral load[b]	17	0	17	100.0%
		low viral load[c]	14	4	18	77.7%
		Total	57	4	61	93.4%
	Flu B (n=41)	high viral load[a]	11	0	11	100.0%
		medium viral load[b]	14	0	14	100.0%
		low viral load[c]	13	3	16	81.3%
		Total	38	3	41	92.7%
	RSV (n=58)	high viral load[a]	13	0	13	100.0%
		medium viral load[b]	22	1	23	95.7%
		low viral load[c]	15	7	22	68.2%
		Total	50	8	58	86.2%

LDA, laboratory developed assay; influenza A, Flu A; influenza B, Flu B; positive, pos; negative, neg

[a] $>10^6$ copies/ml

[b] 10^4-10^5 copies/ml

[c] 10^2-10^3 copies/ml

289

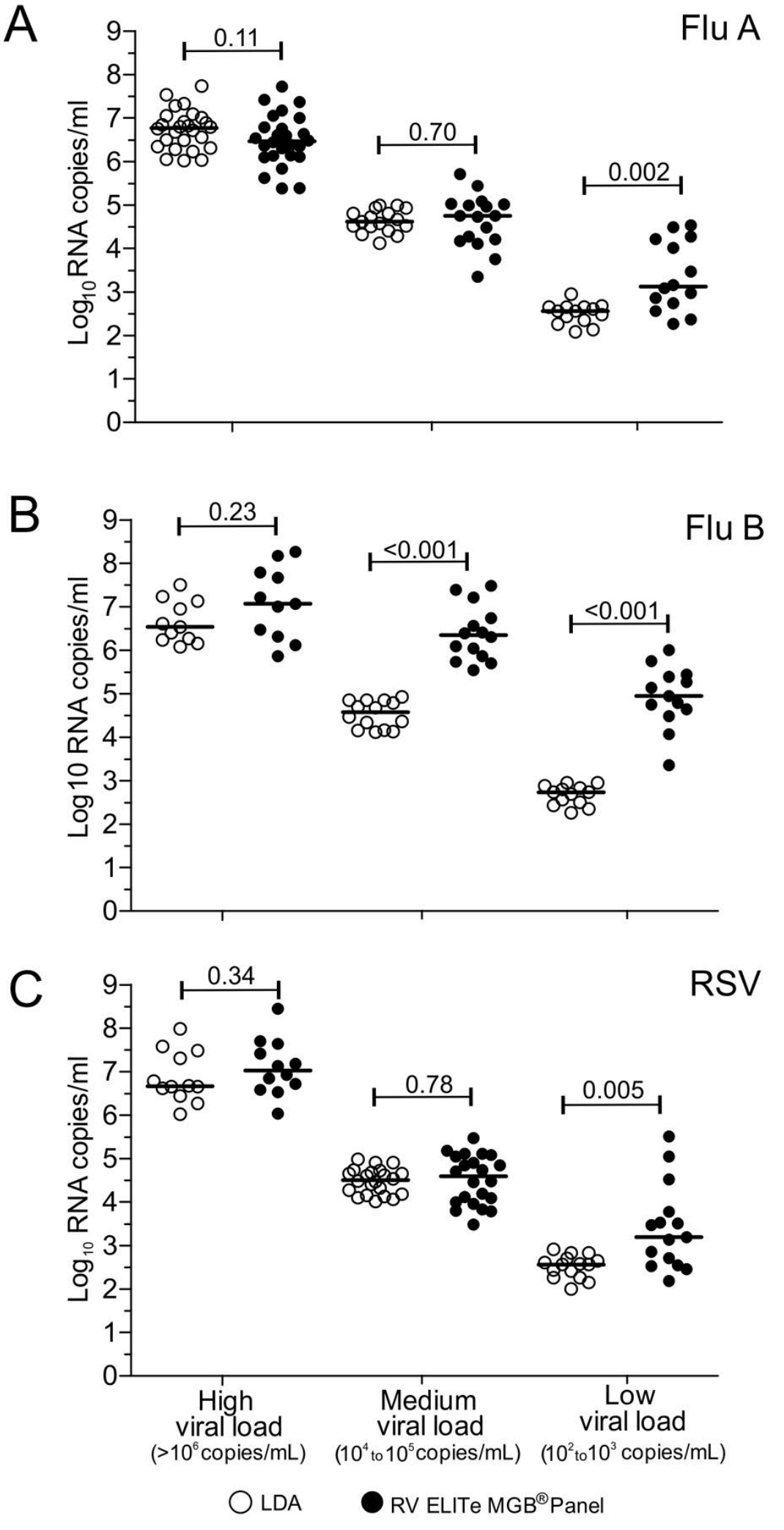
290 **TABLE 2. Results obtained from statistical analyses of two methods comparisons.**

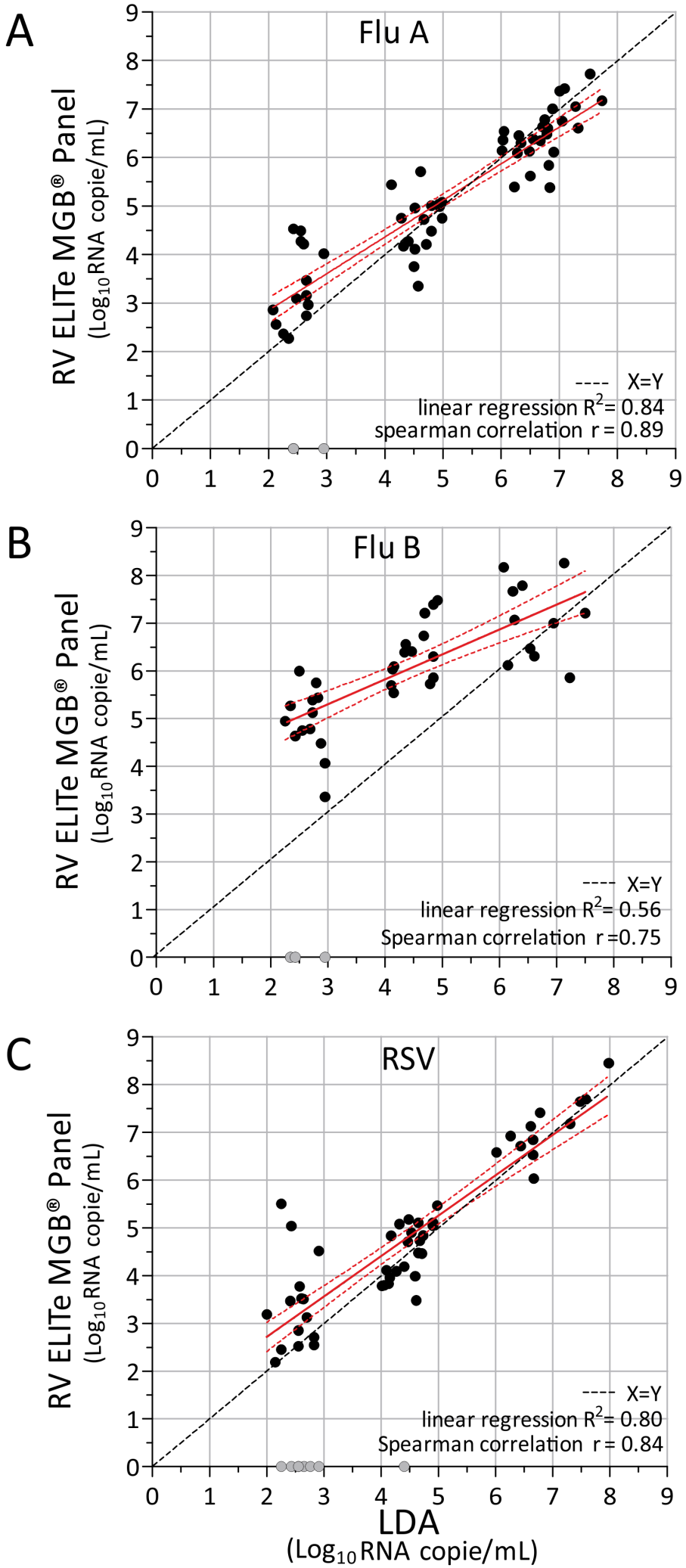
Methods comparison	LDT *vs* RV ELITe MGB® Panel		
	Influenza A	Influenza B	RSV
Arithmetic mean (95% CI[a])	-0.09	-1.58	-0.33
Lower limit	-2.10	-3.50	-3.25
Upper limit	+1.46	+1.38	+1.13
SD	0.73	1.08	0.74
Concordance correlation coefficient	0.86	0.36	0.81
Person ρ (precision)	0.89	0.75	0.84

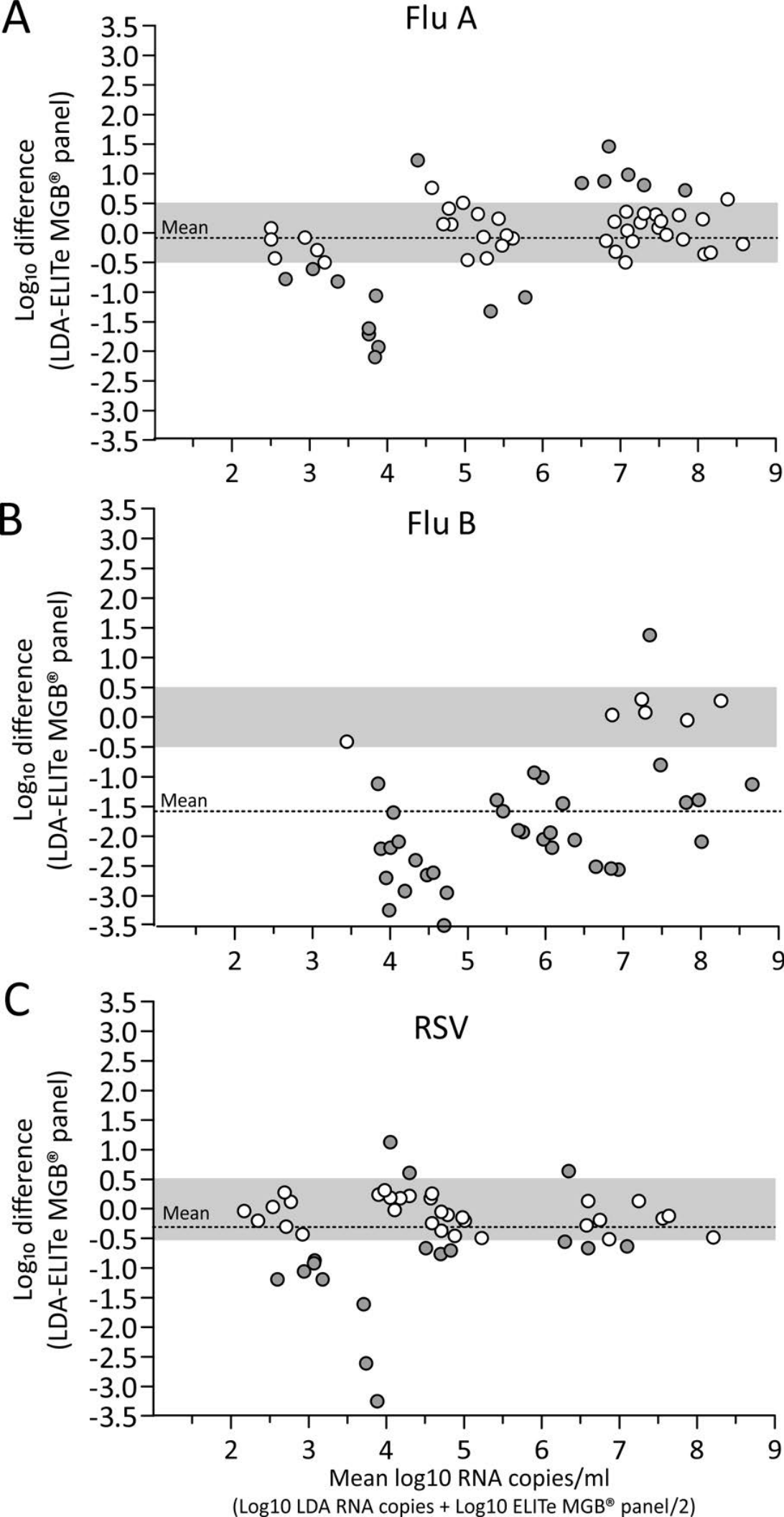
Confidence interval, CI; standard deviation, SD

291

292


A
Flu A
Log10 RNA copies/ml
0.11
0.70
0.002
B
Flu B
Log 10 RNA copies/ml
0.23
<0.001
<0.001
C
RSV
Log10 RNA copies/ml
0.34
0.78
0.005
High viral load (>10^6 copies/mL)
Medium viral load (10^4 to 10^5 copies/mL)
Low viral load (10^2 to 10^3 copies/mL)
LDA
RV ELITe MGB® Panel


A
Flu A
RV ELITe MGB® Panel
(Log10 RNA copie/mL)
---- X=Y
linear regression R2= 0.84
spearman correlation r = 0.89
B
Flu B
RV ELITe MGB® Panel
(Log10 RNA copie/mL)
---- X=Y
linear regression R2= 0.56
Spearman correlation r =0.75
C
RSV
RV ELITe MGB® Panel
(Log10 RNA copie/mL)
---- X=Y
linear regression R2= 0.80
Spearman correlation r = 0.84
LDA
(Log10 RNA copie/mL)


A
Flu A
B
Flu B
C
RSV
Mean
Log10 difference
(LDA-ELITe MGB® panel)
Mean log10 RNA copies/ml
(Log10 LDA RNA copies + Log10 ELITe MGB® panel/2)