

# Detection of infectious dengue virus by selective real-time quantitative polymerase chain reaction 

## Dear Editor,

The dengue virus (DENV) is a single-stranded positivesense RNA virus that belongs to the family Flaviviridae (Gubler, 2002), and has four serotypes, $\mathrm{DENV}_{1}-\mathrm{DENV}_{4}$, which are transmitted via Aedes aegypti and Aedes albopictus (Rodriguez-Roche and Gould, 2013). It has been reported that more than 50 million dengue infections occur each year (Guzman et al., 2010), and a serious outbreak occurred in the Southern Provinces of China in the summer of 2014. The clinical presentations of dengue infection range from mild febrile illness to severe dengue characterized by dengue hemorrhagic fever and shock syndrome, which make the accurate laboratory confirmation of the diagnosis challenging but crucial. Currently, serological assays and real-time quantitative polymerase chain reaction ( qPCR ) techniques are most commonly applied in the diagnosis of dengue infection (Guzman et al., 2010; Bäck and Lundkvist, 2013; Guzman and Harris, 2015). However, the current methods have some major drawbacks, such as falsepositive results owing to cross-reactivity with other ar-thropod-borne flaviviruses, and inability to determine the infectiousness in individual patients (Schwartz et al., 2000). Therefore, a simple and accurate method is needed to detect the virus, especially its associated infectious particles.

Propidium monoazide (PMA) is a fluorescent, photoreactive dye with a high affinity for nucleic acids. Previous studies have indicated that PCR combined with PMA can discriminate between viable and inactivated cells, because of the reduction in PCR signal from DNA of dead cells (Nocker et al., 2006). The azide group of the compound generates highly reactive nitrene intermediates that readily form covalent nitrogen-carbon bonds with nucleic acids. The nucleic acids modified by PMA cannot be used as templates to be transcribed or amplified. However, the compound does not penetrate intact cell walls or membranes, and only reacts with DNA or RNA exposed after such barriers are damaged (Nocker et al., 2006). Hence, the compound may be used to selectively amplify templates from structurally intact organisms. The PMA-qPCR method has been widely
applied to detect and quantify viable particles of the echovirus (Parshionikar et al., 2010), bacteriophage T4 (Fittipaldi et al., 2010), influenza virus (Graiver et al., 2010), and norovirus (Kim and Ko, 2012). In this study, we investigated the feasibility and reliability of selective qPCR to detect $\mathrm{DENV}_{2}$.

Cytopathogenic $\mathrm{DENV}_{2}$ was obtained from the BSL-3 Laboratory at the Southern Medical University, China, and was propagated and assayed in BHK-21 cells. Semipurified stocks were subsequently produced from these cultures. Briefly, the cells were lysed by repeated freezethaw cycles at $-80^{\circ} \mathrm{C}$ (Low-temperature Refrigerator, SANYO, Osaka, Japan); the lysates were cleared by centrifugation for 15 min at 4000 rpm at $4^{\circ} \mathrm{C}$, and then stored at $-80^{\circ} \mathrm{C}$. The infectious titers were measured as a $50 \%$ tissue culture infectious dose in eight replicates. Clustal W was used to align the specific conserved cDNA fragment from $20 \mathrm{DENV}_{2}$ strains isolated from different geographical areas at different times. The primers for this fragment were designed by using the Primer 5.5, and assessed by using the Oligo 7.0 program (Supplementary Table S1). The fragment was also synthesized, inserted into the plasmid pMD18-T (TAKARA Co., Dalian, China) to construct the standard plasmid pMD-DENV 2 (Figure 1A). The plasmids were propagated in Escherichia coli DH5 $\alpha$ and purified by using the TAKARA MiniBEST plasmid purification kit. A standard curve was generated by amplifying 10 -fold dilutions of the standard plasmid (Supplementary Figure S1A), starting with a stock concentration of $279.1 \mathrm{ng} / \mu \mathrm{L}$, and then the cycle threshold ( $C t$ ) values were plotted against the concentrations of the template [Supplementary Figure S1B, $\mathrm{Y}=-3.258 \times \log (\mathrm{X}) \pm 9.79$, Eff. $=102.7 \%$ ].
For pretreatment with PMA, a $20 \mathrm{mmol} / \mathrm{L}$ stock solution was prepared by dissolving 1 mg of PMA (Biotium, Inc., Hayward, USA) in $98 \mu \mathrm{~L}$ of distilled water $\left(\mathrm{dH}_{2} \mathrm{O}\right)$, and the stock was stored at $-20^{\circ} \mathrm{C}$ until it was needed. The viral preparations were incubated in $50 \mu \mathrm{~mol} / \mathrm{L}$ PMA for 5 min in the dark at $20^{\circ} \mathrm{C}$, with occasional mixing. Then, the samples were crosslinked by exposing them to blue light-emitting diode (LED) light (LedActive Blue, Philips, Holland) for 15 min on ice. The RNA

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Figure 1. (A) Target fragment and primers. (B) Selective qPCR of viral suspensions $(n=3)$ with or without pretreatment with propidium monoazide (PMA). Dengue virus serotype $2\left(\mathrm{DENV}_{2}\right)$ was inactivated by heating at $100^{\circ} \mathrm{C}$. Titers were calculated using a standard curve generated by the amplification of a plasmid containing the target fragment. (C) Determination of infectious titer using cell culture and qPCR in DENV ${ }_{2}$ suspensions heated for 30 min at different temperatures. Selective qPCR indicates complete inactivation at $70{ }^{\circ} \mathrm{C}$.
was extracted using Buffer AVL-carrier RNA (Qiagen, Dusseldorf, Germany) according to the manufacturer's instructions, and then reverse transcription was performed at $37^{\circ} \mathrm{C}$ for 15 min , using the PrimeScript ${ }^{\mathrm{TM}}$ RT reagent kit (TAKARA Co., Dalian, China). The reaction was terminated by incubation at $85^{\circ} \mathrm{C}$ for 5 s . The samples were amplified in a Mx3005P Real-time PCR system (Stratagene, California, USA) with the following schedule: over 40 cycles of denaturation at $95^{\circ} \mathrm{C}$, annealing at $60^{\circ} \mathrm{C}$, and then elongation at $72^{\circ} \mathrm{C}$. The total reaction mixture volumes were $25 \mu \mathrm{~L}$ and consisted of 1 $\mu \mathrm{L}$ of Premix Ex Taq (TAKARA, Co., Dalian, China), $0.5 \mu \mathrm{~L}$ of each of the forward and reverse primers, 0.5 $\mu \mathrm{L}$ of TapMan probe, $0.5 \mu \mathrm{~L}$ of ROX II, $12.5 \mu \mathrm{~L}$ of cDNA, and $9.5 \mu \mathrm{~L}$ of double $\mathrm{dH}_{2} \mathrm{O}\left(\mathrm{ddH}_{2} \mathrm{O}\right)$.

To generate the particles, $140-\mu \mathrm{L}$ aliquots of the $\mathrm{DENV}_{2}$ stock were heated at $100^{\circ} \mathrm{C}$ for 10 min , and then the target fragments from both thermal inactivation viral particles and infectious viral particles ( $7 \times 10^{3} \mathrm{PFU} / \mathrm{mL}$ ) with or without pretreatment with PMA (Figure 1B) were amplified equally and efficiently. However, the compound significantly inhibited $(P<0.05)$ the amplification of the non-infectious viruses. It has been reported that high temperatures can inactivate numerous viruses, resulting in the loss of viral infectivity. Indeed, PMA has been demonstrated to prevent PCR-based detection of in-
activated viruses or bacteria, but not of infectious organisms (Nocker et al., 2009; Fittipaldi et al., 2010).

In addition, the ability of the cell cultures and selective qPCR to measure the infectious titers was evaluated by using $\mathrm{DENV}_{2}$ suspensions heated for 30 min at $56^{\circ} \mathrm{C}$, $60^{\circ} \mathrm{C}, 65^{\circ} \mathrm{C}, 70^{\circ} \mathrm{C}, 75^{\circ} \mathrm{C}, 80^{\circ} \mathrm{C}, 85^{\circ} \mathrm{C}$, and $100^{\circ} \mathrm{C}$. The qPCR performed without pretreatment with PMA detected $10^{7.84}$ to $10^{8.04}$ copies $/ \mu \mathrm{L}$ of $\mathrm{DENV}_{2}$, although the infectious particles were not detected by cell culture (Figure 1C). However, the infectious titer decreased linearly at the inactivation temperature when the samples were pretreated with PMA. Indeed, the infectious particles were undetectable in the samples heated above $70^{\circ} \mathrm{C}$, indicating their complete inactivation.

Serum samples of patients diagnosed with dengue fever were collected during the acute phase of the disease. qPCR with probes designed against all four dengue serotypes was performed for these samples within 1 h of the blood draws, to measure the viral titer. $\mathrm{DENV}_{2}$ was detected in two samples at $10^{7.48}$ and $10^{7.90}$ copies $/ \mu \mathrm{L}$. However, the titers were lower at $10^{7.01}$ and $10^{6.89}$ copies $/ \mu \mathrm{L}$, when the samples were pretreated with PMA, indicating that inactivated viral particles were present (Table 1).

The gold standard for measuring viral titers is titration in cell cultures, which is time-consuming. Furthermore, some viruses that pose significant public health concern

Table 1. Application of propidium monoazide (PMA)-qPCR to detect clinical samples ${ }^{a}$

|  | PMA+ |  | PMA- |  | $P^{\text {b }}$ |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | Ct Values | Quantification ( $\mathrm{Log}^{\text {copies }}$ ) | Ct Values | Quantification ( $\mathrm{Log}^{\text {copies }}$ ) |  |
| Patient 1 | $22.71 \pm 0.29$ | $7.01 \pm 0.09$ | $21.17 \pm 0.42$ | $7.48 \pm 0.13$ | $\leq 0.05$ |
| Patient 2 | $23.09 \pm 0.54$ | $6.89 \pm 0.17$ | $19.79 \pm 0.12$ | $7.90 \pm 0.04$ | $\leq 0.05$ |

Notes: ${ }^{\text {a }}$ Samples were collected from patients infected with dengue virus serotype $\left.2(\mathrm{DENV})_{2}\right)$ in acute phase. ${ }^{\text {b }}$ Data were analyzed using $t$-test, and $P$-values represent a comparison of selective (PMA+) and non-selective (PMA-) reactions. Each experiment was replicated thrice, and $\mathrm{DENV}_{2}$ titers were obtained by qPCR using a standard curve of pMD-DENV ${ }_{2}$ copies.
are either difficult to culture or are nonculturable (Pecson et al., 2009). For instance, cell culture systems for noroviruses have not been established (Wigginton and Kohn, 2012). On the other hand, viruses such as the hepatits A virus and rotaviruses are not cytopathic in buffalo green monkey kidney cells (Parshionikar et al., 2010). An alternative approach is to quantify the viral genomes by qPCR , which cannot assess infection risk because it measures both infectious and non-infectious particles (Fittipaldi et al., 2010). Therefore, it is necessary to pretreat samples with PMA to selectively amplify the viable organisms.

The result of this assay indicates that the envelopes and capsids are catastrophically lost only above $70^{\circ} \mathrm{C}$, while the infectivity is probably too low to induce obvious cytopathic effects when $\mathrm{DENV}_{2}$ suspensions are heated at $56^{\circ} \mathrm{C}-65^{\circ} \mathrm{C}$. Therefore, the PMA-qPCR produces weakly positive results, while the cell culture method produces negative results. It is also conceivable that a virus may lose its infectivity although the capsid remains intact, such as when it loses the ability to bind host cell receptors (Fittipaldi et al., 2010). This indicates that the selective qPCR may provide some information on the extent of damage to viral envelopes and capsids, therefore, may be appropriate for assessing disinfection practices. Furthermore, this study established a relationship between the temperature of the process condition and stability of intact $\mathrm{DENV}_{2}$ particles, which could contribute to the design of studies to investigate the features of $\mathrm{DENV}_{2}$.

In summary, to the best of our knowledge, this is the first report of a technique that involves pretreating samples with PMA to greatly enhance the specificity for infectious particles detection. For example, the nonselective PCR of the sera from convalescent patients may still produce positive results because of the presence of inactivated or non-encapsulated particles. Moreover, the positive results obtained by selective qPCR indicate that viruses continue to replicate and, therefore, the infection may progress further. While these results are clinically
significant, additional clinical samples of acute phase serum would be required to provide valuable information on the accuracy of the PMA-qPCR method. The technique, $q$ PCR combined with PMA pretreatment, is expected to be applied in the diagnosis of dengue infection. Factors that may affect this approach should be investigated in detail in future research.

## FOOTNOTES

This study was partly supported by the Joint Funds of NSFCGuangdong of China under Grant (No.U1132002), by the National Natural Science Foundation of China (No. 31270974, 31470271), and by the Technologies R \& D Program of Guangdong Province (No. 2013A020229004) and Guangzhou city (No. 201508020263). The authors declare that they have no conflict of interest. All participants provided written informed consent. The whole study was approved by ethics committee of Southern Medical University, China.

Supplementary figure/table are available on the websites of Virologica Sinica: www.virosin.org; link.springer.com/journal/ 12250.
 Shuai Yue ${ }^{2}$, Lixin $\mathrm{Wu}^{2}$, Yu Zhang ${ }^{2}$, Qian Xie ${ }^{1}$, Bao Zhang ${ }^{1 \boxtimes}$, Wei Zhao ${ }^{1 \boxtimes}$

1. Guangdong Provincial Key Laboratory of Tropical Disease Research, School of Public Health, Southern Medical University, Guangzhou 510515, China
2. Second clinical medical college, Southern Medical University, Guangzhou 510280, China
3. Nanfang Hospital, Southern Medical University, Guangzhou 510515, China
\# These authors contributed equally to this work.
$\measuredangle$ Correspondence:
Zhang Bao, Phone: +86-20-61648649, Fax: +86-20-61648649,
Email: zhangb@smu.edu.cn
ORCID: 0000-0003-0459-6406
Zhao Wei, Phone: +86-20-61648567, Fax: +86-20-61648567,

Email: zhaowei@smu.edu.cn
ORCID: 0000-0003-1414-4438

Published online: 30 May 2016

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