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Biopanning of polypeptides binding to bovine ephemeral fever virus G₁ protein from phage display peptide library

Peili Hou , Guimin Zhao, Chengqiang He, Hongmei Wang* and Hongbin He*

Abstract

Background: The bovine ephemeral fever virus (BEFV) glycoprotein neutralization site 1 (also referred as G₁ protein), is a critical protein responsible for virus infectivity and eliciting immune-protection, however, binding peptides of BEFV G₁ protein are still unclear. Thus, the aim of the present study was to screen specific polypeptides, which bind BEFV G₁ protein with high-affinity and inhibit BEFV replication.

Methods: The purified BEFV G₁ was coated and then reacted with the M13-based Ph.D.-7 phage random display library. The peptides for target binding were automated sequenced after four rounds of enrichment biopanning. The amino acid sequences of polypeptide displayed on positive clones were deduced and the affinity of positive polypeptides with BEFV G₁ was assayed by ELISA. Then the roles of specific G₁-binding peptides in the context of BEFV infection were analyzed.

Results: The results showed that 27 specific peptide ligands displaying 11 different amino acid sequences were obtained, and the T18 and T25 clone had a higher affinity to G₁ protein than the other clones. Then their antiviral roles of two phage clones (T25 and T18) showed that both phage polypeptide T25 and T18 exerted inhibition on BEFV replication compared to control group. Moreover, synthetic peptide based on T18 (HSIRYDF) and T25 (YSLRSDY) alone or combined use on BEFV replication showed that the synthetic peptides could effectively inhibit the formation of cytopathic plaque and significantly inhibit BEFV RNA replication in a dose-dependent manner.

Conclusion: Two antiviral peptide ligands binding to bovine ephemeral fever virus G₁ protein from phage display peptide library were identified, which may provide a potential research tool for diagnostic reagents and novel antiviral agents.

Keywords: Bovine ephemeral fever virus, Phage display random peptide library, G₁ binding peptide, Antiviral peptide

Background

Bovine ephemeral fever (BEF) caused by bovine ephemeral fever virus (BEFV), also known as 3 day fever, is an acute febrile infection of cattle and water buffaloes. The typical clinical symptoms of BEF are characterized by the rapid onset and rapid recovery of clinical signs, such as fever, depression, muscle stiffness, oral and nasal discharges, joint pain and lameness [1–3]. The disease is more frequently distributed in a vast expanse of the

world including tropical, subtropical and temperate regions of Africa, the Middle East, Australia and Asia, and leads to serious economic losses to the cattle industry through loss of milk production, significant impacts on trade [4–6]. To date, no specific treatment and drug is available for BEFV.

BEFV belongs to the genus *Ephemerovirus* in the family *Rhabdoviridae*, and consists of a single stranded, negative-sense RNA genome with a lipid envelope and five structural proteins [7, 8]. The G protein plays an important role in inducing neutralizing antibodies, and it is also closely associated with cell tropism, pathogenicity, fusion and interaction with host cellular receptors [5, 9–12]. The

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protein G consists of five major neutralisation sites ($G_1, G_2, G_{3a}, G_{3b}, G_4$) defined by BEFV G protein specific monoclonal antibodies (MAbs) in competition ELISAs, and among these sites, site G_1 composed of two minimal B cell epitopes is a linear neutralisation site involving in eliciting neutralizing antibodies. It is reported that site G_1 is predicted to face the viral membrane in both the pre-fusion and post-fusion forms of the trimer and may be approachable to antibodies [13–15]. Therefore, G_1 protein can be used as a potential target for antiviral drug screening.

Phage display, a well-established powerful and popular technology, has been extensively used in many fields, including antibody engineering [16, 17], ligand screening [18, 19], peptide drug discovery and manufacture [20, 21], disease molecular diagnostic analysis [22], biosensing [23] and vaccine research and development [24]. The high capacity and abundance of random phage display library makes it appropriate for high-throughput screening of peptide ligands that specifically bind with the given targets. In virology, several peptides have been identified as potential antivirals against classical swine fever virus [25], transmissible gastroenteritis virus [26], influenza virus [27], newcastle disease virus [28], human immunodeficiency virus (HIV) [29] and hepatitis B virus [30] using phage display technology. However, there is no report about screening of polypeptides binding to BEFV by phage display library.

In this study, we identified specific peptides that were capable of binding to the G_1 protein of BEFV from the 7-mer phage display library using the immobilized BEFV G_1 protein as a target, and we analyzed their roles in the context of BEFV infection in vitro, which is of great significance for potential diagnosis and treatment of BEF.

Methods

Virus, cells and plasmid

Ph.D.-7 phage-displayed peptide library was purchased from New England Biolabs (Ipswich, MA, USA). The titer of this peptide library was up to 2×10^{13} plaque forming units (pfu/mL), containing about 2.8×10^9 independent random peptide sequences. BEFV(Shandong/China/2011) were isolated and stored by the Ruminant Disease Research Center, Shandong Normal University, Jinan, Shandong Province, China, and the 50% tissue culture infected dose (TCID₅₀) of BEFV determined by Reed-Muench method were $5.0 \times 10^{5.0}$ TCID₅₀/mL. Anti-BEFV antibody extracted from cattle was preserved in our laboratory. More concretely, clinical serum samples were collected from detected dairy cattle cases of BEFV infections in China. The antibodies against BEFV were identified by the microneutralization assay according to the instructions of the Agricultural Industry Criteria of the People's Republic of China (publication no. NY/T543–2002).

The anti-BEFV antibodies in this study were applied to analyze the bioactivity of purified recombinant G_1 protein in Western Blot. BHK-21 cells were incubated in Dulbecco's modified Eagle's medium (DMEM, Invitrogen, Carlsbad, CA, USA), supplemented with 10% fetal bovine serum (FBS, Gibco, USA) at 37 °C, 5%CO₂. Prokaryotic expression vector pET-32a(+) plasmid were maintained in our laboratory. The G genes of Shandong/China/2011 (GenBank: JX234571.1) was previously described [31], and the pMD18-T-G was used as template for PCR amplifying the G_1 gene using sense primer G_1 -F:5'-CGGGATCCAGAGCTTGGTGTGAATAC-3' and anti-sense primer G_1 -R:5'-CCGCTCGAGCCAACCTACAA CAGCAGATA-3'. Underlined parts of primers represent *Bam* HI and *Xho* I restriction sites, respectively. The amplified G_1 gene region and the points linked to the primers used were shown in Supplement Figure one with the size of 420 bp. The PCR product was cloned into the pET-32a(+) vector and the plasmids with G_1 gene was sequenced by BGI (BGI, China).

Expression and purification of BEFV recombinant G_1 protein in *E. coli*

The recombinant plasmid pET-32a(+)- G_1 was transformed into high efficiency chemical competent cells *E.coli* BL21(DE3) pLysS (TransGen Biotech Company, Beijing, China). BL21 cells were cultured in LB medium containing 100 mg/L Ampicillin. The LB medium was shaken at 37°C until the OD₆₀₀ reached 0.6–0.8, then isopropyl-d-thiogalactoside (IPTG) was added to a final concentration of 1 mmol/L to induce G_1 expression. The BL21 cells were further incubated for 6 h at 37 °C, and harvested by centrifugation at 8000×g for 5 min at 4 °C. The precipitation of BL21 cells were resuspended in lysis buffer including 10 mmol/L phosphate buffered saline (PBS, pH 7.4), imidazole (10 mmol/L), lysozyme (10 g/L), trypsin inhibitor (10 g/L), pepsin inhibitor (1.0 g/L) and PMSF (1.0 g/L) for sonication on ice. The cell lysate was centrifuged at 12,000×g for 20 min at 4 °C. The supernatant was collected and poured in a 10 mL Ni²⁺-Sepharose 6 Fast Flow column pre-equilibrated with lysis buffer. The column was then washed with imidazole (10, 50 and 100 mmol/L) in PBS (10 mmol/L, pH 7.4) to remove nonspecifically bound proteins, and eluted with 250 mmol/L imidazole. Meanwhile, the designated pET32a(+) vector control protein was also expressed and purified in *E. coli* in the same condition. The yield protein concentration was measured using the Pierce BCA-200 Protein Assay Kit. To verify the reactivity of purified G_1 protein, we conducted western blotting using purified G_1 protein and pET32a(+) vector control protein as antigen by incubating with anti-BEFV positive antibody (diluted at 1:1000) for 2 h, and then with goat anti-cattle IgG conjugated to peroxidase (diluted at 1:2000, Abcam, ab102150, USA). Full

immunoblots was visualized by enhanced chemiluminescence immunoassay (ECL kit, Thermo Fisher Scientific Inc., USA).

Biopanning and enrichment analysis of phage library using BEFV G₁ as target

The Ph.D.-7 peptide library (NEB, New England Biolabs, USA, E8100S) was used to screen for G₁ binding peptides according to the manufacturer's instructions with slight modifications. In short, 96-well plates were coated with 100 µL/well of the recombinant G₁ protein at a concentration of 100 µg/mL, biopanning was carried out by incubating the phage display library (10¹¹ phages/mL). After washing away the unbound phage with Tris-buffered saline (TBS + 0.1% Tween 20), a bound phage was eluted in TBS and titrated as described in the standard protocol, and then subjected to the next round of panning. The second, third and fourth rounds of panning were done under more stringent conditions using less amount of the target (100 µL/well of a solution at 75,50,25 µg/mL of the recombinant G₁ protein, and shorter incubation time (1.5 h, 1 h and 0.5 h in the 2, 3 and 4th round, respectively), and washed with higher concentrations of Tween 20-TBS (0.25%, 0.5% and 0.5%, respectively) for longer time (10 × 2 min, 10 × 3 min and 10 × 4 min). Inbetween each round of panning, the titer of the panning phages in binding buffer (here referred to as input) and that in the elution buffer (here referred to as output) was determined, and the ratio of output to input was analyzed to assess the enrichment efficiency. After four rounds of panning, individual clones were randomly picked and amplified in *E. coli* ER2738 strain to prepare their DNA.

Sequencing of positive phage clones

Individual positive phage clones were amplified, and phage single-stranded DNA was extracted and purified using M13 Phage DNA Rapid Extraction Kit (Spin-column, Signalway Biotechnology, USA), DNA was sequenced by Sangon sequencing (Sangon Biotech Co., Ltd., Shanghai, China) using the-96 gIII sequencing primer 5'-CCCTCATAGTTAGCG TAACG-3' provided by the Ph.D.-7 peptide library kit. Amino acid sequences were deduced from phage display peptide DNA sequences by ExPASy Translate tool (<http://web.expasy.org/translate/>). The polypeptides used in the study were synthesis and purified by the Beijing Science and Technology Co., Ltd. and an irrelevant control peptide (AEMLELS) acquired from another screening strategy was synthesized by China Peptides Co., Ltd. (Shanghai, China).

Binding analysis of individual phage using ELISA

The phage displayed peptide clones with different amino acid sequences were subjected to ELISA. Briefly, ELISA plates were coated with the G₁ protein at a concentration of 10 µg/well diluted in 0.1 mol/L NaHCO₃ (pH 8.6)

overnight at 4°C. Meanwhile, the purified pET32a(+) vector control protein coated with the same concentration was used as control group. All ELISA plates were blocked with 200 µL blocking buffer (5% BSA) for 2 h at room temperature. Ten-fold serial dilutions of the selected phages were added to both coated plates starting with 10¹² phages in the first well. Plates were incubated for 2 h at room temperature and then washed 6 times with TBST (TBS containing 0.5% Tween-20). Bound phage was then detected with 200 µL 1:1000 diluted horseradish peroxidase (HRP)-conjugated anti-M13 antibody (GE Healthcare, 27-9421-01, USA) in blocking buffer. Finally, the peroxidase activity was rapidly detected with substrate solution TMB upon addition of a sulfuric acid stop solution. The absorbance of the reaction was determined at 450 nm with an ELISA microplate reader (Shanghai Utrao Medical Instrument Co., Ltd., Shanghai, China).

Antiviral activity of positive phage clones and synthetic peptides

BHK-21 cells (1 × 10⁵/well) were plated in 12-well culture plates to 90% confluence. Amplified positive phage clones at concentrations of 10¹⁰(pfu/mL) and synthetic peptides at concentrations of 0, 10, 20, 40, 80, 160, and 320 µg/mL were incubated with 100TCID₅₀/0.1 mL BEFV at 37°C for 1 h, respectively, and then a mixture of virus and amplified positive phages or various concentrations of synthetic peptides transferred onto the cell monolayers for adsorption for 2 h. The medium was then replaced with maintenance medium containing 2%FBS in 1 mL DMEM and incubated for a further 36 h. The treated cells and their supernatants were collected followed by three cycles of alternate freezing and thawing and stored at -80 °C before use.

Plaque reduction assay

Vero cells (1 × 10⁵ cells/well) were seeded into 12-well plates for 12 h maintained in Dulbecco's modified Eagle's medium (DMEM, Invitrogen, USA), supplemented with 10% inactivated fetal bovine serum (FBS, Gibco, USA) and a mix of the antibiotics Penicillin (100 IU) and Streptomycin (100 µg/mL) at 37°C, 5%CO₂. Synthetic peptides at concentrations of 0, 10, 20, 40, 80, 160, and 320 µg/mL were incubated with 100TCID₅₀/0.1 mL BEFV at 37°C for 1 h, and then transferred onto the cell monolayers. After 2 h of incubation, discarding the supernatant, the cells were incubated under normal culture conditions at 37°C for 36 h. The monolayers were spread out with 2% low melting agarose, and formation of cytopathic plaque was visualized by staining the cell monolayers with 1%(W/V) neutral red solution (Sigma-Aldrich, USA). The effects of peptides on BEFV infection were evaluated by counting the plaques and calculating the titer (pfu/mL) and inhibitory rate.

Real-time reverse transcription polymerase chain reaction (RT-PCR)

Total RNA was extracted from 200 μ L treated samples using QIAamp[®] Viral RNA Mini Kit (QIAGEN, Valencia, CA, USA) and eluted into final volumes of 50 μ L. Reverse transcription was performed using PrimeScript RT reagent Kit (TaKaRa, Japan) according to manufacturer's protocols. The SYBR Green-based quantitative real-time RT-PCR was carried out using a Premix Ex Taq kit according to the manufacturer's protocols (TaKaRa, Japan) in a total volume of 25 μ L on a Roche LightCycler 480 Real Time PCR System (Roche Applied Science, Germany). The sequences of primer sets used in real-time RT-PCR with specific primers for BEFV N gene and endogenous glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene were listed in Table 1. Real-time RT-PCR was carried out as follows: 95 °C for 5 min, followed by 40 cycles of 94 °C for 20 s, 60 °C for 30 s and 30 s at 72°C. The threshold cycle (Ct) value related to RNA levels of each target gene was normalized to GAPDH expression and the relative expression of each sample was analysed by the $2^{(-\Delta\Delta C_t)}$ method.

Statistical analysis

Each treated sample was run in triplicate. Statistical analysis was performed by one-way analysis of variance and values were considered significant when $p < 0.05$. Figures were performed using the GraphPad[™] Prism 5.0 software (Graphpad Software Inc., San Diego, CA, USA).

Results

Purification of recombinant BEFV G₁ protein in *E. coli*

The G₁ gene region of 420 bp (Additional file 1: Figure S1) was amplified by PCR and cloned into pET32a(+) vector. G₁ protein was expressed in *E. coli* strain BL21 (DE3) and it mainly existed in the supernatant of the bacterial lysate, which indicated that G₁ gene had been efficiently expressed in prokaryotic expression system in a soluble form. Large amounts of highly expressed protein were purified using Ni²⁺-sepharose 6 Fast Flow affinity media. The results of SDS-PAGE indicated that we obtained the highly-pure recombinant G₁ protein with an expected size of ~ 37 kDa. Meanwhile, the expected thioredoxin protein encoded by empty pET-32a (+) vector alone was also clearly visible with the size of ~ 21 kDa (Fig. 1a). Western blot were performed to analyze the bioactivity of purified recombinant G₁ protein. The result indicated that purification of recombinant

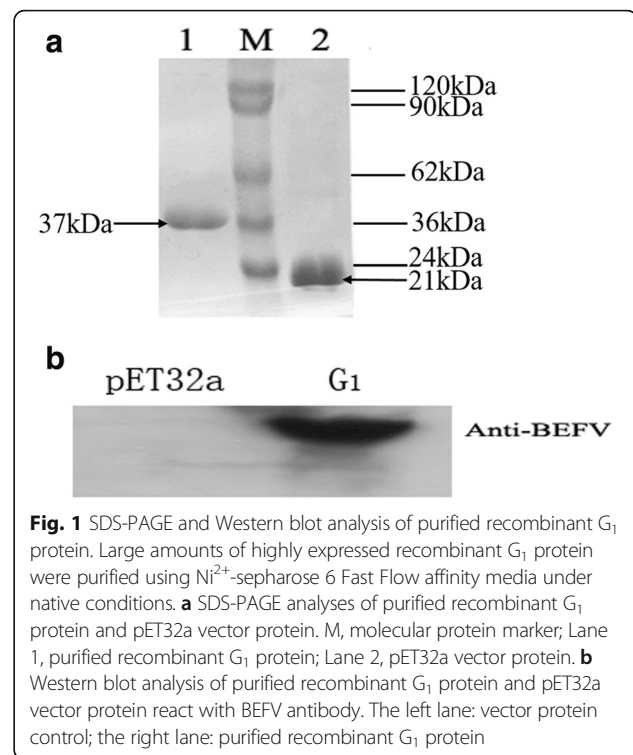


Fig. 1 SDS-PAGE and Western blot analysis of purified recombinant G₁ protein. Large amounts of highly expressed recombinant G₁ protein were purified using Ni²⁺-sepharose 6 Fast Flow affinity media under native conditions. **a** SDS-PAGE analyses of purified recombinant G₁ protein and pET32a vector protein. M, molecular protein marker; Lane 1, purified recombinant G₁ protein; Lane 2, pET32a vector protein. **b** Western blot analysis of purified recombinant G₁ protein and pET32a vector protein react with BEFV antibody. The left lane: vector protein control; the right lane: purified recombinant G₁ protein

G₁ protein could immunoreact with anti-BEFV antibody (Fig. 1b). Therefore, those data were indicated that the purified G₁ used in this study was biologically active. The concentration of purified G₁ and control pET-32a (+) vector protein determined by the absorbance at 280 nm were 1.65 mg/mL and 2.85 mg/mL.

Identification of phage-displayed peptides with BEFV G₁ protein

In this study, a Ph.D.-7[™] Phage Display Peptide Library was used to screen high-affinity ligands that could selectively bind to G₁ protein. Following four rounds of biopanning, the amounts of input phages and output phages were determined by titration, and the properties of phage recovery efficiency (output phages/input phages) in each round were calculated. As shown in Table 2, the recovery efficiency was 195-fold higher (from 7.2×10^{-3} to 3.7×10^{-5}) after four rounds of panning than after the first round, suggesting that the phages specifically bound to G₁ protein were successfully enriched.

DNA sequencing of the selected phage clones

After the 4th panning round, a total of 27 phage clones were randomly selected and amplified. The DNA of selected positive phage clones was extracted and sequenced. The DNA sequencing reports showed that 11 deduced peptides were finally obtained among the 27 phages and presented in Table 3. Alignment of the peptides revealed probably putative G₁ binding conservative

Table 1 The sequences of primers used in real-time RT-PCR

| Gene | | Sequences (5'-3') | Amplicon size(bp) |
|--------|---------|-----------------------|-------------------|
| BEFV N | N-F | TCCTTCACCATGTA CTGCAC | 138 |
| | N-R | ACCTTG TGGCACTCTCAAC | |
| GAPDH | GAPDH-F | TCATGACCACAGTCCATGCC | 144 |
| | GAPDH-R | GGATGACCTTGCCACAGCC | |

Table 2 Enrichment of phage peptides from library by BEFV G₁ protein biopanning

| Item | First round biopanning | Second round biopanning | Third round biopanning | Fourth round biopanning |
|--------------------------------|------------------------|-------------------------|------------------------|-------------------------|
| G1(μg) | 10 | 7.5 | 5 | 2.5 |
| Concentration of Tween20 (v/v) | 0.1% | 0.25% | 0.5% | 0.5% |
| Input/PFU (pfu/ml) | 1 × 10 ¹¹ | 1 × 10 ¹¹ | 1 × 10 ¹¹ | 1 × 10 ¹¹ |
| Output/PFU (pfu/ml) | 3.7 × 10 ⁶ | 5.2 × 10 ⁷ | 8.7 × 10 ⁷ | 7.2 × 10 ⁸ |
| Recovery (Output/input) | 3.7 × 10 ⁻⁵ | 5.2 × 10 ⁻⁴ | 8.7 × 10 ⁻⁴ | 7.2 × 10 ⁻³ |

consensus motifs. Phages 4, 11, 12, 23 and 25 had a consensus sequence YSLRSDY named T25, which bear YSLR similarity with other 11 phage clones. The overlapping motif sequence derived from Phages 3 and 18 was HSIRYDF named T18.

Binding analysis of individual phage with G₁ using ELISA

In order to test the binding ability of the selected phage clones, 11 independent phage clone groups encoding different amino acid sequences were selected and detected by ELISA using the purified recombinant G₁ protein as target. As shown in Fig. 2, the absorbance obtained from each phage combined with the target G₁ protein was significantly higher than that of the control pET-32a (+) vector protein. Among these G₁ binding peptides, T18 and T25 showed the higher binding ability to G₁ protein when compared to the other clones. Although there is no criterion for judging the positive clones, it is suggested that the T18 and T25 clone might have a higher affinity to G₁ protein than the other clones.

Inhibition of peptides on BEFV replication

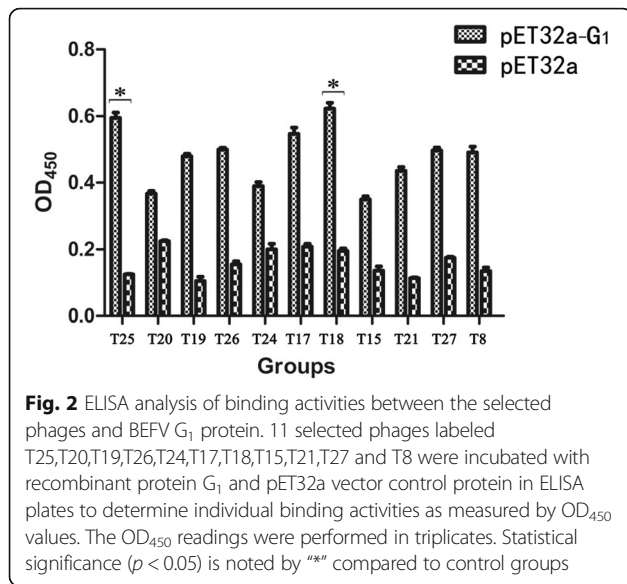
To further determine whether the phages that displayed G₁-binding peptides have the potential to inhibit BEFV infection, we performed virus-blocking assays in BHK-21 cells. Briefly, 100 TCID₅₀/0.1 mL BEFV was incubated with individual clone with a titer of 10⁹pfu/0.1 mL that

displayed G₁-binding peptide or irrelevant phage, respectively, and then inoculated into BHK-21 cells. Meanwhile, the non-phage treated BEFV was included as a control. After incubation for 36 h, the SYBR Green-based real-time RT-PCR was performed to determine the RNA copies of BEFV in different phage-treated cells. The results showed that T25 and T18 peptides significantly exerted antiviral activity, and the phage polypeptide T25 could reduce BEFV RNA copy number by 2 times, while T18 decrease by 1.5 times compared to control group. Obviously, T25 was the greatest antiviral peptide among all these selected peptides (Fig. 3).

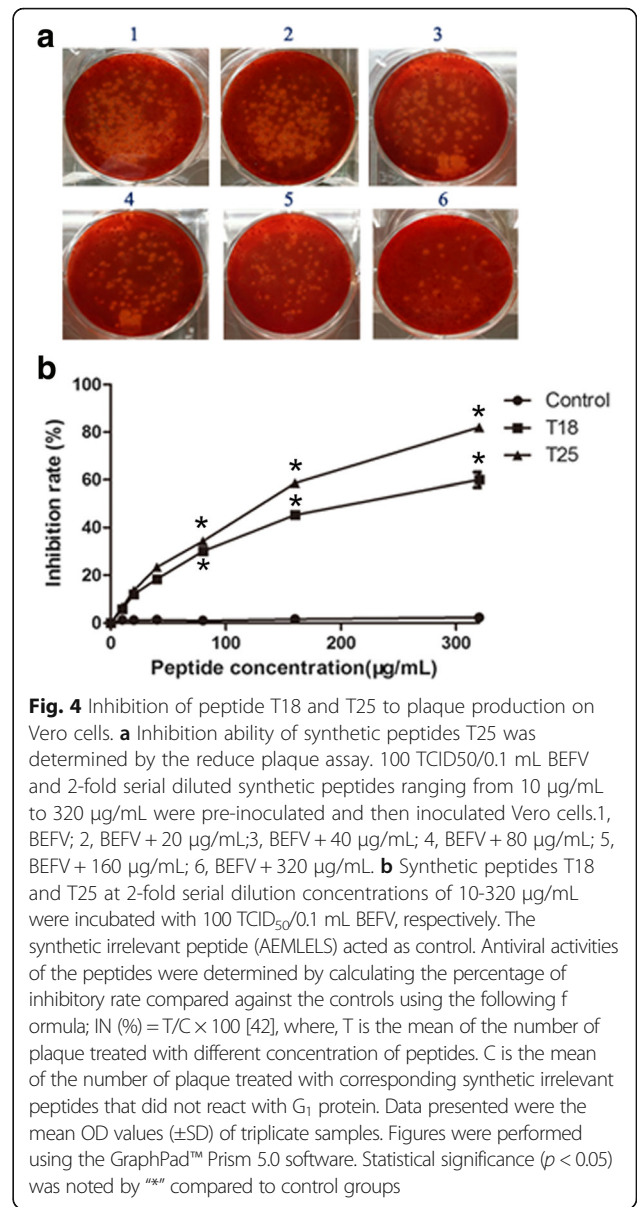
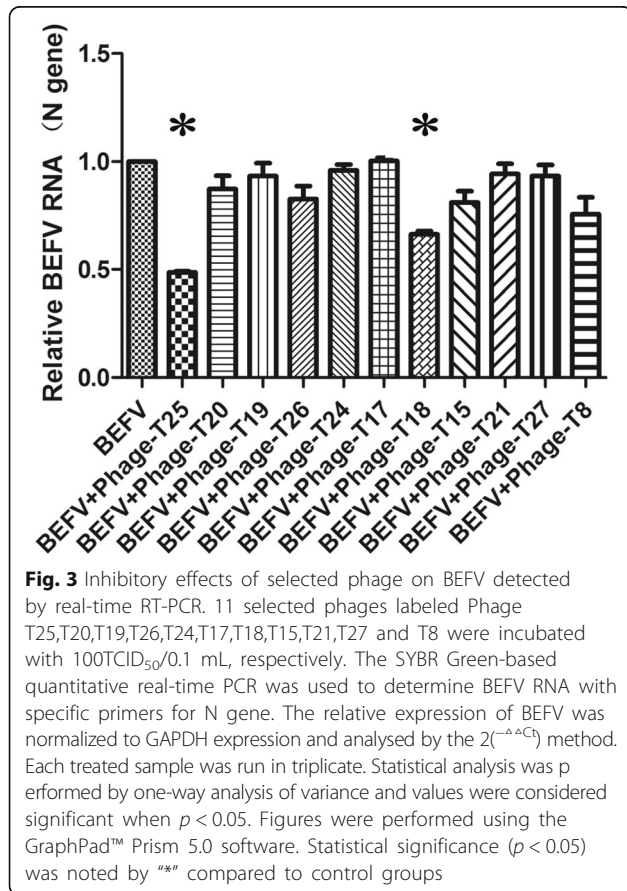
To further investigate the antiviral activity of selected polypeptide (T18 and T25), firstly, we synthesized the peptides borne by phages T18 and T25 and conducted the dose-dependent effect of synthetic peptides T18 and T25 on inhibition of BEFV replication by virus plaque assay. At indicated concentration points, the reduce plaque assay showed the synthetic peptides could significantly inhibit the formation of cytopathic plaque at a concentration of 80 μg/mL, while the group of 320 μg/mL nearly abolished plaque formation in Vero cells, and the reduce plaque result of serial diluted synthetic peptides T25 was shown in Fig. 4a. Then antiviral activities of synthetic peptides T18 and T25 were determined by calculating the percentage of inhibitory rate compared against the controls. The results suggested that the similar

Table 3 Sequencing results of positive phage colonies with specifically binding to BEFV G₁ protein

| Groups | Phage clones | Phage displayed peptide DNA sequence | Phage displayed peptide amino acid sequence | Poly-peptide names |
|--------|-------------------|--------------------------------------|---|--------------------|
| 1 | 4, 11, 12, 23, 25 | TATTCTCTTCGTTCTGATTAT | YSLRSDY | T25 |
| 2 | 5, 6, 20 | TATTCTCTTCGTCAGGATTGG | YSLRQDW | T20 |
| 3 | 1, 13, 19 | TATAGTTTGCGTACTGATTGG | YSLRTDW | T19 |
| 4 | 16, 22, 26 | TATTCTCTTCGTCAGGAGAGG | YSLRQER | T26 |
| 5 | 14, 24 | TATAGTTTGCGTGCGGATCGT | YSLRADR | T24 |
| 6 | 10, 17 | GCTCTGAGTAGTCTGCGTAAT | ALSSLRN | T17 |
| 7 | 3, 18 | CATTCTATTCGGTATGATTTT | HSIRYDF | T18 |
| 8 | 2, 15 | CATAGTATTCGTGTTGATTGG | HSIRVDW | T15 |
| 9 | 21 | GATTGGATTTTCTGCGTTT | DWIFPAF | T21 |
| 10 | 9, 27 | AAGGTTTGGATTGTTCTTCT | KVWIMPS | T27 |
| 11 | 7, 8 | AAGGTTTGGTTGCTTCATTCT | KVWLLHS | T8 |



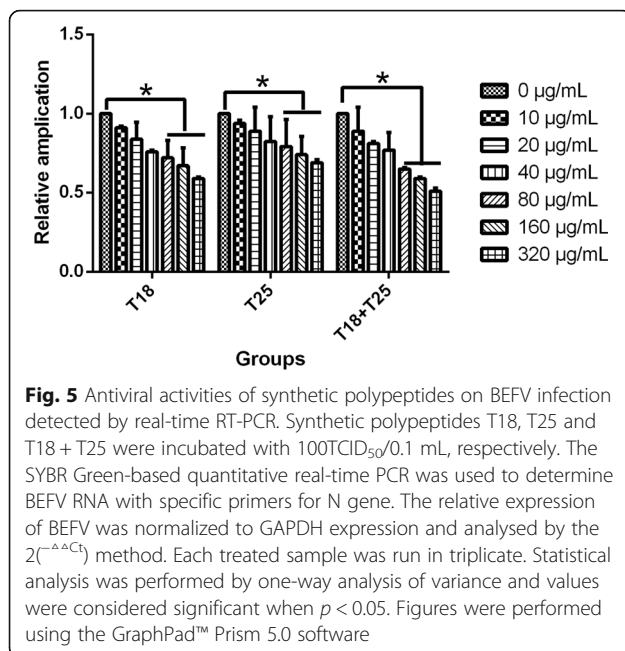
trend was at work on the inhibition of T18 and T25 on BEFV infection. It turned out that 80 $\mu\text{g/mL}$, 160 $\mu\text{g/mL}$ and 320 $\mu\text{g/mL}$ of synthetic peptides could significantly interfere with BEFV formation of cytopathic plaque ($p < 0.05$) (Fig. 4b).



We further analyzed dose dependence of antiviral activity of the synthetic peptide T18 and T25 alone, and compared the synergistic effects of combined use on BEFV replication. As shown in Fig. 5, the results of real time RT-PCR showed that 320 $\mu\text{g/mL}$, 160 $\mu\text{g/mL}$ and 80 $\mu\text{g/mL}$ of synthetic peptides alone and combined use could significantly inhibit BEFV RNA replication ($P < 0.05$), and both T18 and T25 exerted inhibition on BEFV replication of BHK-21 cells in a dose-dependent manner. However, the effects of peptides T18 and T25 combined were similar to that of peptide T18 or T25 alone ($P > 0.5$) (Fig. 5).

Discussion

The study of the molecular mechanism of virus infection is the basic and vital approach for prevention and control



of the disease. As for BEFV infection, it has been proposed that the attachment of virus to the host cell membrane via the interaction of the viral envelope G protein with cell surface receptors is considered to be the initial step of BEFV infection [32]. And G₁ protein is considered to be the main protective antigen of BEFV that only reacts with sera against BEFV, currently some molecular and serological diagnostic methods to detect BEFV were established based on G₁ protein [12, 33]. In this study, we aimed at utilizing G₁ protein as target protein for screening its ligands and preliminary investigating the role of binding peptides during BEFV infection. The highly effective prokaryotic system is exemplified an optimal choice for heterologous protein, and the BEFV G₁ protein was purified in a moderately form of soluble (Fig. 1a), ensuring the target protein's native configuration in vitro. Furthermore it can specifically react with anti-BEFV antibodies as an antigen protein (Fig. 1b). Taken together, the G₁ glycoprotein used in this study is biologically active.

In recent years, using purified protein or whole virus particle as the targets of phage peptide library screening provides an ideal approach to identify multifunctional peptides [22, 34–36]. In this study, we used a phage-displayed heptapeptide library to identify G₁ protein interactors, and the conditions of the selection were strictly limited to enrichment specific G₁-binding phages (Table 2). After four rounds of panning, 11 deduced peptide amino acid sequences from 27 selected candidate phage clones exhibited high affinity to G₁ protein according to ELISA (Fig. 2). And these peptide sequences showed partial consensus motifs (Table 3), indicating that the screening process was

successful. Meanwhile, partial consensus motifs which is possibly typical functional motifs of more complex proteins would be promising to discover the ligands of G₁ glycoprotein and analyze their roles in the context of BEFV infection. In addition, there has no report about BEFV receptor, and the consensus motif may mimic the discontinuous binding site as receptor agonists/antagonists or regulate the biological function of receptors [37–39].

Phage-display technology provides an effective way of identifying peptides with affinities to specific proteins for diagnostic analysis and the discovery of mimic antibodies [22, 40]. As the phages bearing the specific affinity peptides to BEFV G₁ protein, they have the potential to develop a phage-mediated diagnostic assay to BEFV. It is reported that the BEFV G₁ protein located at the C-terminal stalk of the G protein is one target of virus-neutralizing antibodies, and G₁ protein is a linear neutralization site (Y487-K503) that comprises two minimal B cell epitopes [5, 11]. The potential significant achievement of our work is the discovery of mimic antibodies, synthetic peptide in vitro could be used as a specific antibody mimic to detect BEFV in virus-infected cells.

Peptide ligands targeting a specific protein surface obtained by phage-display technology are widely used as therapeutic agents by interfering with protein-protein interactions [20, 21, 25–29, 41]. Interestingly, the phage clone T18 and T25 exhibited binding affinity to G₁ protein and antiviral activity against BEFV (Fig. 3), whereas other phages with high affinity to G₁ protein did not effectively inhibit the replication of BEFV. This means that the binding affinity of other phages do not necessarily connection with antiviral activity. In addition, a possible explanation of antiviral activity is that the G₁ protein binding phage ligand mediates an inhibitory effect of BEFV infection by competitive binding to receptor binding sites or neutralizing epitopes and thus inhibits the virus attachment/entry. In order to exclude the effect of phage itself on protein binding and antiviral activity against BEFV, we synthesized T18 and T25 peptides in vitro and conducted the reduce plaque assay in vero cells that significantly formed cytopathic plaque during BEFV infection. The results showed that the synthetic peptides could significantly inhibit the formation of cytopathic plaque (Fig. 4) and inhibit BEFV replication in a dose dependent way (Fig. 5). Altogether, T18 and T25 peptides are potentially potent antiviral molecules worthy of further development and test. This study provides an inexpensive way to discover functional motif for BEFV infection using the phage-display technology, which is possible to find the potential protein to mediate the interaction between BEFV and the host.

Conclusion

In summary, we successfully isolated G₁ protein binding peptides from phage display library. Antiviral effect assay showed that G₁-binding peptides were dose-dependently effective against BEFV infection at the cellular level, which might have potential applications in the diagnosis and treatment of BEFV.

Additional file

Additional file 1: Figure S1. Schematic drawing of BEFV G and the points linked to the primers of cloned G₁ used. (A) The number of amino acids region about full length G gene and Region G₁ (from 390 aa–529 aa) were indicated. (B) Presentation of G₁ nucleotides sized and gene sequence amplification locus and positions of the forward (G1-F) and reversed (G1-R) primers used in this study. (TIFF 11694 kb)

Abbreviations

BEF: Bovine ephemeral fever; BEFV: Bovine ephemeral fever virus; BHK-21: Baby Hamster Syrian Kidney; BSA: Bovine serum albumin; DMEM: Dulbecco's modified Eagle's medium; ELISA: Enzyme linked immunosorbent assay; FBS: Fetal bovine serum; GAPDH: Glyceraldehyde 3-phosphate dehydrogenase; IPTG: Isopropyl-d-thiogalactoside; NEB: New England Biolabs; PBS: phosphate buffered saline; PMSF: Phenylmethanesulfonyl fluoride; RT-PCR: Reverse transcription polymerase chain reaction; TBS: Tris-buffered saline; TCID₅₀: 50% tissue culture infected dose

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Not applicable.

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Availability of data and materials

The data supporting our findings of this article are included within the manuscript.

Authors' contributions

The study was conceived, designed and critically revised by HHB and WHM. Data collection, study execution and the drafted manuscript were done by HPL and ZGM. Laboratory data analysis was performed by HCQ. All authorship gave final approval and agreed to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

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