Construction of a recombinant bacmid DNA containing influenza A virus hemagglutinin gene using a site-specific transposition mechanism

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ABSTRACT

Introduction: In recent years, influenza viruses have caused moderate to severe infections all around the world while so far there is no influenza vaccine that can protect people with only one dose of injection. In this regard, producing a universal vaccine based on virus-like-particles (VLP) could be an ideal approach. Methods: In this study, the full-length ORF of influenza hemagglutinin (HA) gene from Influenza A virus of H9N2 subtype was amplified by RT-PCR using specific primers to produce HA cDNA. The amplicon was cloned firstly into a T/A cloning vector and then was subcloned into a pFastBacDual donor plasmid through SalI/HindIII restriction sites. The recombinant HA-pFastBacDual vector was transferred to Escherichia coli DH10Bac cells, to insert the HA gene into the bacmid DNA via a site-specific transposition process. The recombinant bacmid was then extracted and further analyzed by PCR. Results: Our data indicated that the HA-containing recombinant bacmid was constructed successfully using the transposition mechanism between pFastBacDual-HA and the bacmid. Conclusion: The recombinant baculovirus construct in this work had proper characteristics to be used in production of H9N2 VLP in Sf9 insect cell line in the future studies.

KEYWORDS: Influenza A virus, Hemagglutinin protein, Baculovirus.

INTRODUCTION

Influenza A viruses are members of Orthomyxoviridae family and are able to infect a large variety of animals as well as humans. These viruses have a segmented-negative strand genome and are classified based on the antigenic properties of their two distinct surface glycoproteins. These influenza glycoproteins, namely, hemagglutinin (HA) and neuraminidase (NA) are located on the outer host-cell-derived envelope. Influenza A viruses of H9N2 subtype have become highly prevalent in poultry facilities in many countries. Although these viruses can generally cause only mild to moderate diseases, they can infect a wide variety of species, including chickens, quails, turkeys, ducks, geese, pheasants, partridges and pigeons [1-4]. More importantly, the occasional transmissions of H9N2 viruses from land-based poultry to humans and pigs have been reported [5-7]. Some investigations suggest that a significant proportion of H9N2 field isolates have acquired human virus-like receptors specificity. For instance, a few isolates that could recognize α2, 6-linked sialic acid (SAα2-6) have been transmitted directly to humans [8-10, 6, 11]. In addition to possessing human virus-like receptor specificities, avian H9N2 viruses induce a typical flu-like illness in humans which can easily go unnoticed. Eventually, Such viruses have the opportunity to circulate, resort and improve their transmissibility [10, 6, 12-14]. Based on these global concerns, scientific efforts have focused on the prevention and treatment of H9N2 avian influenza virus infections. The prevention method against the avian influenza is mainly through vaccination. Currently, most avian influenza vaccines used in the clinics are the inactivated types that have been propagated in embryonated chicken eggs. However, the use of inactivated avian influenza vaccines can induce little or no cellular immune responses and hence cannot provide a wide and persistent protection against influenza while it would interfere with the serological monitoring of the virus. In addition, egg-based influenza vaccine production is dependent on the availability of embryonated eggs which might be in limited supply in the events of severe influenza outbreaks or pandemics. In view of these potential drawbacks of the old vaccines, the development
of a new type of H9N2 vaccine with emphasis on effectiveness and minimal side-effects and costs, is required. From three decades ago, it has been shown that antibodies against the influenza hemagglutinin and neuraminidase can establish protection, similar to immunization induced with inactivated influenza vaccines [1, 2]. One research avenue on this topic is the production of virus-like particles (VLPs). So far, VLPs have been expressed in different methods and hosts which one of the best expression systems among them is the production of VLPs by baculoviruses in insect cells [15]. The combination of recombinant baculovirus and insect cell expression systems provides high levels of recombinant proteins that undergo post-translational modifications such as glycosylation [16, 17]. Therefore, the application of such systems allows to produce large quantities of the target protein in its native conformation as a vaccine [18].

In this study, HA gene was isolated and amplified from H9N2 influenza virus and then the HA-containing recombinant bacmid was constructed via a site-specific transposition. It is envisaged that such constructs can be used to produce recombinant protein in Sf9 insect cells [19]. Such HA-containing recombinant bacmid could eventually be used to produce large scale preparation of hemagglutinin protein, suitable for influenza vaccine production.

MATERIALS and METHODS

Viral and bacterial strains and the plasmids

The virus strain in this study was A/Chicken/Iran/11T99 (H9N2), Escherichia coli strain DH5α (Invitrogen, USA) was used for transformation and amplification of the recombinant vectors and E. coli strain DH10Bac (Invitrogen, USA) was used as an appropriate strain to perform the cloning processes. For cloning the HA gene, “T/A cloning vector” (RBC Bioscience, Taiwan) was used as the general vector. To generate the recombinant Bacmid, pFastBacDual was used as the transfer vector (Invitrogen, USA). E. coli strain DH10Bac contained the baculovirus modified DNA (Bacmid) with a mini-attTn7 target site and the helper plasmid. The helper plasmid harbored by DH10Bac strains, confers resistance to tetracycline and encodes enzymes needed for transposition of the gene of interest into the Bacmid.

Design and synthesis of the primers

All the sequences of HA protein in Iran were obtained from NCBI and were compared with each other. The amino acid sequences were converted into codons which were compatible for Sf9 cells using JAVA codon adaptation tool <http://www.genscript.com/cgi-bin/tools/rare_codon_analysis>. Cleavage sites for restriction enzymes Sall and HindIII were inserted at the beginning and the end of HA gene ORF and specific primers were designed by CLC Main Workbench 4.5 (QIAGEN Co.). The designed primers were synthesized by Metabion Company (Germany).

In silico folding prediction of the recombinant HA protein

The three-dimensional (3D) predictions of the recombinant HA protein folding were performed by Swissmodel, Raptorx and Antherprot 3D viewer web servers. Furthermore, the Ramachandran plots were depicted for each model by Rampage. The Ramachandran plot displays the main chain conformation angles (Phi and Psi) of the polypeptide chain of a protein molecule.

RNA extraction and cDNA synthesis

Viral RNA was extracted from 200 μl of harvested cell culture supernatant using a Roche commercial kit (Germany) according to the manufacturer’s instructions. The cDNA synthesis was performed using Thermo Script™ RT-PCR System (Invitrogen-USA) according to the manufacturer’s instructions using specific primers (at the concentration of 10 μM or 10 pmol/μl for each primer), dNTPs (10 mM for each base) and RNAase inhibitor in RNAase/DNase-free microtubes (Extra gene, USA). RT-PCR

Specific primers (forward and reverse) were designed by CLC Main Workbench 4.5 (QIAGEN Co.) in order to amplify the complete HA gene ORF of H9N2 influenza (1682 bp). Five μl of cDNA were added to a 20μl total volume of PCR mixture containing 10 pmol of each forward primer 5’ GTC-GAC-ATG-GAA-ACA-ATA-TCA-CT 3’ and reverse primer 5’ AAG-CTT-TTA-TAT-ACA-AAT-GTT-GCA-CC 3’ (underlined nucleotides correspond to Sall and HindIII restriction sites, respectively), 10 mM Tris-Cl pH 8.3, 50 mM KCl, 1.5 mM MgCl2, 10 mM dNTPs and high fidelity PCR Enzyme Mix (Genet Bio, Korea). The amplification reactions were performed in a thermocycler (ABI, USA) using the following program: 5 min at 95° C followed by 30 cycles at 95° C for 30 sec, 50° C for 30 sec and 72° C for 80 sec, with a final extension step at 72° C for 10 min. The PCR products were analyzed on 1% (w/v) electrophoresis agarose gel stained with safe view (Kiagen, IKR) [20, 21].

Cloning of HA gene

The RT-PCR product was extracted from low melting agarose gel using a DNA extraction kit (Vivantis, Korea) and the amplicon was subsequently cloned into the T/A cloning vector and then subcloned into the pFastBacDual donor plasmid through Sall/HindIII restriction sites. The HA-containing recombinant pFastBacDual donor vector was confirmed using PCR and enzymatic digestion analysis. Subsequently, it was subjected to perform automatic one-directed sequencing, using the forward and the reverse primers as described above for the HA gene amplification.

Generation of the recombinant bacmid

The HA-containing recombinant pFastBacDual donor plasmid was transferred into E. coli DH10Bac competent cells for site-specific transposition of the HA DNA from the transposing vector to a Bacmid DNA through lacZ gene disruption. The transformed cells were cultured on a LB agar plate containing kanamycin (50 μg/ml), gentamicin (7 μg/ml), tetracycline (10 μg/ml), X-gal (100 μg/ml) and isopropyl-thio-galactoside (IPTG, 40 μg/ml) and incubated at 37° C for 24 h. The high-molecular-weight bacmid DNA was isolated from the overnight cultures by an alkaline lysis purification method, according to the instructions supplied by the manufacturer (Invitrogen-USA). Successful transposition was verified by PCR analysis using both M13/pUC and HA specific primers.

RESULTS

Codon optimization and structural prediction of HA protein

Codons of the selected sequence of HA protein from H9N2 influenza strains isolated in Iran were analysed for their expression in Sf9 insect cells by online software tools and expression of this gene in the insect cells was optimized by converting the codons into those suitable for expression by Sf9 cells which resulted in Codon Adaptation Index (COI) of 0.84. (Fig. 1). The optimized sequence was re-investigated in terms
of average GC content which was determined to be 42.38% as shown in Fig. 2. Therefore, the most appropriate GC-content and the highest value of adaptation with codons were used in order to express the gene in Sf9 cells. The study of the protein’s secondary structure using SOPMA program predicted that the protein product of the gene of interest was containing 116 alpha helices (Hh), 147 extended strands (ES) and 191 random coils (CC) as depicted in Fig. 3A. The 3D structure of the protein, predicted by Antheprot 3D viewer program is shown in Fig. 3B. The Ramachandran plot (Fig. 3C) of the refined model estimated that the number of residues in the favored region to be 141.5 (98.8%), the number of residues in the allowed region to be 2 (1.2%) and the number of residues in the outlier region to be 0 (0%).

Fig. 1. The distribution of codon usage frequency along the length of the target gene using GenScript rare codon analysis tool. The possibility of high protein expression level is correlated to the value of CAI. A CAI of 1.0 is considered to be ideal while a CAI of > 0.8 is rated as good for expression in the desired expression organism.

Fig. 2. The primary sequence of the designed gene using GenScript rare codon analysis tool which was adapted to usable codons in Sf9 cells. The ideal percentage range of GC content is between 30-70%. Any peaks outside of this range will adversely affect the transcriptional and the translational efficiency.
RT-PCR and T/A cloning

The full-length sequence of HA gene with an expected size of 1686 bp was amplified by RT-PCR using the designed specific primers (Fig. 4). The amplicon was cloned into a T/A cloning vector after extraction from the agarose gel and was confirmed by PCR (Fig. 5A) and enzymatic digestion analysis (Fig 5B). The ORF accuracy of the HA gene in T/A cloning vector was confirmed by nucleotide sequencing. The sequencing analysis was accomplished by Chromas software (version 1.45, Australia). Subsequently, the HA fragment was subcloned into the pFastBacDual donor plasmid, as described previously in the methods section. The integrity of the recombinant vector was confirmed by PCR and subsequently by enzymatic digestion (results not shown).
**Construction of the recombinant bacmid DNA**

The HA gene was subcloned into a pFastBacDual donor plasmid and the construct was verified by endonuclease digestion in comparison with a non-recombinant pFastBacDual vector, as a control. Following the transformation and plating of the cells on X-gal/IPTG LB agar, the transposed colonies were visible as large white colonies among the blue ones which harbored the unaltered bacmids. The selected white colonies were re-streaked on the agar plates to ensure whether they had a true white phenotype. Since verification of the high molecular weight recombinant bacmid DNA is not convenient by digestion, PCR was performed using both M13/pUC and HA-specific primers to ensure the proper transposition of the target gene in the recombinant bacmid. The bacmid DNA contains M13 forward and reverse priming sites, flanking the Tn7 mini-att site within the LacZ α-complementation region. A panel of PCR was done using M13/pUC universal primers, HA gene specific forward and reverse primers, HA gene specific reverse and M13 forward primers, and finally HA gene specific primers, respectively. The amplification of the non-recombinant bacmid using M13/pUC primers generated a band with estimated size of 303 bp (Fig. 6).

**REFERENCES**

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**CONFLICT OF INTEREST**

The authors declare that they have no conflict of interest.