



Original Article

Development of Multiplex PCR for Simultaneous Detection of Avian Influenza and Newcastle Disease Viruses

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A study was undertaken to develop a rapid, sensitive and reliable molecular method for complete sub-typing of avian influenza virus (H5N1) either alone or simultaneous detection of avian influenza (H5N1) and Newcastle disease viruses prevalent among the poultry population of Bangladesh. Complimentary DNA of reference Newcastle disease (ND) and avian influenza (H5N1) viruses were used to develop a uniplex polymerase chain reaction then duplex and multiplex polymerase chain reaction. The band of the polymerase chain reaction products for F gene of Newcastle disease virus, hemagglutinin and neuraminidase genes of avian influenza virus appeared at 356 bp, 219 bp, and 616 bp on 2% NA agarose gel respectively. The newly developed and standardized multiplex polymerase chain reaction was applied on the field samples. For this, clinical and post-mortem samples were collected from naturally and experimentally Newcastle disease virus infected chickens and subsequently inoculated into 10-day-old chicken embryos for collection of allantoic fluid. All the samples showed the band at the position of 356 bp that indicated Newcastle disease virus positive. None of the samples were showed the band at the position 219 bp and 616 bp for hemagglutinin and neuraminidase genes of avian influenza virus respectively. Results of the present study clearly indicated that the multiplex polymerase chain reaction is a highly sensitive, specific and rapid test for complete sub-typing of avian influenza virus along with simultaneous detection of Newcastle disease virus.

Key words: Avian influenza virus, Newcastle disease virus, Polymerase chain reaction, Sub-typing

Introduction

Highly pathogenic avian influenza (HPAI) and Newcastle disease (ND) are considered as top ranking list. A viral diseases of the Office International des Epizooties which have been responsible for serious losses to the poultry industry^{1,2}. Avian influenza also has caused severe human losses throughout the centuries³. Nevertheless, avian influenza has been transmitted to human directly, as seen in Hong Kong⁴.

Three types of influenza viruses, types A, B, and C are known and they belong to a family of single-stranded negative-sense enveloped RNA viruses called *Orthomyxoviridae*. The viral genome is comprised of eight RNA segments (seven in type C). Influenza A viruses can be classified into subtypes based on antigenic difference in the two surface glycoproteins, name, hemagglutinin (HA) and neuraminidase (NA) which is required for viral attachment and cellular release. Other major

viral proteins include the nucleoprotein (NP) which is the main structural protein, membrane proteins (M1 and M2), polymerase proteins (PA, PB1 and PB2), and non-structural proteins (NS1 and NS2). Currently, sixteen subtypes of HA (H1-H16) and nine NA (N1-N9) antigenic variants are known in influenza A virus mostly related with veterinary significance⁵.

Newcastle Disease (ND) is caused by avian paramyxovirus serotype 1 (APMV-1) viruses, which, with viruses of the other eight APMV serotypes (APMV-2 to APMV-9), have been placed in the genus *Rubulavirus*, sub-family *Paramyxovirinae*, family *Paramyxoviridae*, in the current taxonomy⁶. The ND virus has a 15 kb RNA genome that codes for six viral proteins: an RNA-directed RNA polymerase (L), hemagglutinin-neuraminidase protein (HN), fusion protein (F), matrix protein (M), phosphoprotein (P) and nucleoprotein (NP). The F glycoprotein is responsible for fusion between the

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cellular and viral membranes, and subsequent virus genome penetration².

A variety of techniques are commonly used for the isolation and identification of AIV and NDV such as isolation in embryonated eggs, enzyme immunoassays, hemagglutination inhibition (HI) test, enzyme linked immunosorbent assay or direct immunofluorescence test^{3, 8-9}. With the advancement of science, various molecular methods have been established for complete subtyping of AIV and simultaneous detection of highly pathogenic AIV and NDV¹⁰⁻¹². Molecular methods of diagnosis can be used for type A influenza viruses for screening of samples using primers specific for nucleoprotein (NP) gene¹³⁻¹⁴ or matrix (M) protein gene¹⁵. It can also be used for complete subtyping of AIV using HA and NA gene specific primers^{14, 16-17}. Methods such as Multiplex RT-PCR assays allow for the simultaneous amplification of several genes, thereby minimizing the use of reagents and decreasing personnel time¹⁸.

Recently, Bangladesh is facing with a series of outbreak of avian influenza following emergence of HPAI virus (H5N1) at different location throughout the country such as at Rangpur, Narsingdi, Jampurhat, Jaldhaka Nilphamari, Sharishabari Jamalpur, Shankorpur Jessor, Savar Dhaka, Kashimpur Gazipur, Sonakanda Narayanonj, Hakimpur Dinajpur.

In the context of Bangladesh, ND of poultry is also a common disease and caused mostly by velogenic strains of NDV than mesogenic or lentogenic¹⁹⁻²⁰. The mortality rate incase of very virulent (vv) NDV up to 100% in young chickens and in varies from 80-90% in adults²¹. Thereby, 40-60% of the total mortality of poultry population in Bangladesh caused by this disease²² when appeared as in the epidemic form.

Hemagglutination (HA) and hemagglutination inhibition (HI) tests are used for the detection of NDV, which are time consuming, laborious and limited specificity and sensitivity. On the other hand, commercially available membrane immunoassay kits which is commonly known as rapid antigen test kit, has been used for primary screening of AIV, most of which can only detect type A group-specific antigen with the limitation of complete subtype determination and the sensitivity to the specific antigen varies from 60-70%. This assay is only applicable for initial screening of samples in the field level. Furthermore, membrane immunoassays are not so reliable test for routine surveillance upon which one can assure about the presence or absence of the antigen of AIV, as it is not able to detect a low level of infection. Presently, RT-PCR has been carried out for partial subtyping (only for HA) in different laboratories of Bangladesh.

Therefore, the present research work was carried out to develop a highly sensitive, specific and confirmatory molecular test for complete sub-typing of H5N1 and simultaneous detection of avian influenza and Newcastle disease viruses.

Materials and methods

Reference viruses

Reference NDV of Komarov strain collected from the repository of the Department of Microbiology and Hygiene, BAU, Mymensingh and cDNA from highly pathogenic avian influenza virus H5N1 subtype kindly provided by Dr. Hiroshi

Kida, Department of Disease Control, Graduate School of Veterinary Medicine, Hokkaido University, Japan were used in this study.

Clinical and post-mortem samples

Clinical (oro-nasal swab, faeces) and post-mortem samples (lungs, colon) were collected from a field outbreak of suspected ND and also from chickens of experimental infection with NDV.

Extraction of RNA

Extraction of total viral RNA of different samples was performed using QIAamp viral RNA Mini Kit (Qiagen, Germany) following manufacturer's protocol with all necessary safety precautions.

Primers

One set of primers²³ specified for amplification of 356 bp of F gene of NDV and two sets of AIV subtype specific primers²⁴ specified for amplification of 219 bp and 616 bp of HA (H5) and NA (N1) genes respectively were used in this study (Table 1).

Table 1. List of primers used for AIV (H5N1) and NDV genome detection

Primers	Sequence (5'-3')	Nucleotide Position	Amplification Size (bp)
WHO/HS-1(F)(HA) (Forward primer)	GCCATTCCCAACATMCACCC	943-963	219
WHO/HS-3(R)(HA) (Reverse primer)	CTCCCTGCRITGCTATG	1142-1161	
WHO/NI-1(F)(NA) (Forward primer)	TTGCTTGGTCGGCAAGTGC	490-508	616
WHO/NI-2(R)(NA) (Reverse primer)	CCAGTCCACCCATTGGATCC	1184-1105	
NDV (Forward primer)	GCAGCTGCAGGGATTGTGGT	158-177	356
NDV (Reverse primer)	TCTTTGAGCAAGGAGATGTTG	513-493	

Reverse transcription (RT)

Initially a volume of 4 µl of eluted RNA of NDV and 8.3 µl DEPC water were taken in a PCR tube, spinned and then placed in a forty eight wells thermocycler (MJ Mini thermocycler, BIORAD®, USA) following a thermal profile of 94° C for 5 minutes for linearization of coiled RNA followed by snap cooling. Then, the volume was made up to 25 µl by adding 12.7 µl of reaction mixture containing 4.0 µl 5x RT buffer, 2.0 µl 10 mM dNTP, 1.0 µl prime RNase inhibitor, 0.2 µl AMV-RT, 0.5 µl primer (RH 100 pmol) and 5.0 µl DEPC water. The RT was carried out at 42° C for 40 minutes followed by 85° C for 5 minutes. RT products were cooled on ice and stored at -20° C until use.

Polymerase Chain Reaction (PCR)

Standardization of uniplex PCR

Uniplex PCR was carried out for F gene of NDV, H5 and N1 of AIV separately in 50 µl reaction volume. In all cases, reaction mixture contained 10X LA buffer 5.0 µl, 25 mM MgCl₂ 2.0 µl, 10 mM dNTP 2.0 µl, LA-Taq 0.2 µl, cDNA 1.5 µl while concentration of primers varied from 0.3 µl to 0.8 µl. In case of NDV, 0.8 µl each of primers (NDVF-100 pmol and

NDVR-100 pmol) were used while 0.3 µl each of primers specific for H5 (WHO5-1/F - 100pmol and WHO5-3/R - 100pmol) and N1 (WHON1-1/F - 100pmol and WHON1-2/R - 100pmol) of AIV were used. In each case, DEPC water was added to make the volume up to 50 µl. In all cases, the reaction mixture was subjected to following thermal cyclic conditions: one cycle at 94° C for 2 min, 30 cycles each at 94° C for 30 sec, 45° C for 45 sec, and 60° C for 1 min followed by one cycle at 60° C for 5 min.

Duplex PCR for simultaneous detection of HA (H5) and NA (N1) of AIV

Duplex PCR for simultaneous detection of HA (H5) and NA (N1) of AIV was also carried out with same reaction mixture and following the same thermal profile as of uniplex PCR.

Multiplex PCR (mPCR)

Optimization of mPCR was done by varying reaction components and cyclic conditions. The volume of WHON1-1/F (100 pmol) and WHON1-2/R (100 pmol) was 0.3 µl each while the volume of primers for NDV, H5 and rest of the reaction mixture and cyclic conditions were as same as uniplex PCR.

Agarose gel electrophoresis

PCR products were analyzed on 2% agarose gel and visualized by ethidium bromide staining (0.5 µg/mL) under UV-transilluminator.

Results

This paper describes the development of a multiplex PCR for simultaneous detection of avian influenza and Newcastle disease viruses using the cDNA of H5N1 and field samples of NDV.

Standardization of uniplex PCR

A clear and distinct band of PCR product of the reference NDV appeared at the position at 356 bp on 2% agarose gel after electrophoresis (Fig. 1).

HA (H5) and NA (N1) genes of AIV were determined using uniplex PCR. The PCR products of HA and NA genes amplified by specific primers were appeared at 219 bp and 616 bp position, respectively after 2% agarose gel electrophoresis (Fig. 2).

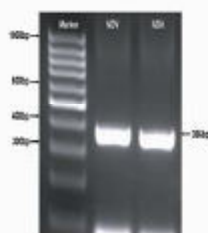


Figure 1. Uniplex PCR product of 356 bp of NDV after 2% agarose gel electrophoresis

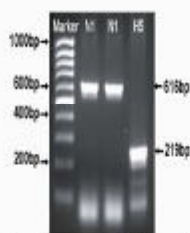


Figure 2. Uniplex PCR products of 219 bp and 616 bp of HA (H5) and NA (N1) genes respectively of AIV after 2% agarose gel electrophoresis

Standardization of duplex PCR for the detection of HA (H5) and NA (N1) genes of AIV

Specific primers were used for HA and NA genes in a single tube with other reagents for standardization of duplex PCR. The band of the PCR products appeared at 219 bp for HA gene and 616 bp for NA gene in a single column as appeared in uniplex PCR (Fig. 3).

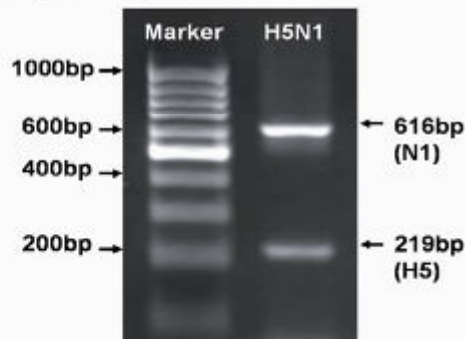


Figure 3. Duplex PCR products of 219 bp and 616 bp of HA (H5) and NA (N1) genes of AIV respectively in a same column after 2% agarose gel electrophoresis

Standardization of multiplex PCR

A multiplex PCR assay was standardized with three sets of primers specific for F gene of NDV, HA (H5) and NA (N1) genes of AIV in a single tube reaction with other reagents as mentioned in materials and methods section. The PCR products were found to be appeared at 356 bp, 219 bp, and 616 bp as band for reference NDV, HA (H5) gene and NA (N1) genes respectively in a single column (Fig. 4).

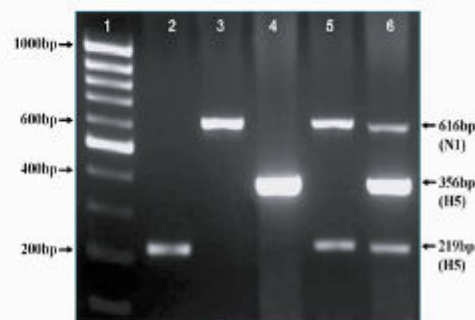


Figure 4. Multiplex PCR products of 219 bp, 616 bp and 356 bp of HA (H5) and NA (N1) genes of AIV and F gene of NDV respectively after 2% agarose gel electrophoresis

Lane 1: DNA marker (100 bp); Lane 2: PCR product of 219 bp HA gene of AIV; Lane 3: PCR product of 616 bp NA gene of AIV; Lane 4: PCR product of 356 bp F gene of NDV; Lane 5: PCR products of 219 bp and 616 bp HA and NA genes of AIV respectively; Lane 6: mPCR products HA and NA genes of AIV and F gene of NDV.

Detection of viruses in clinical and post-mortem samples using the newly developed multiplex PCR

The newly developed multiplex PCR was applied on the clinical and post-mortem samples collected from a field outbreak of suspected NDV and also from chickens of experimental infection with NDV. Clear and distinct band of PCR product was found at 356 bp position after 2% agarose gel electrophoresis in all cases which was indicative of NDV infection. No samples of that outbreak were positive for AIV (H5N1) (Fig. 5).

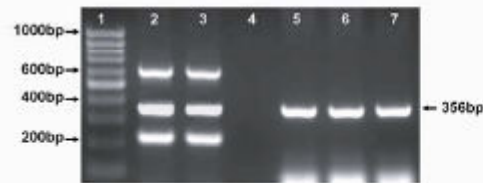


Figure 5. Multiplex PCR products visualized on 2% agarose gel after electrophoresis obtained from clinical and post-mortem samples using three sets of primers

Lane 1: DNA marker (100 bp); Lane 2-3: Multiplex PCR products of reference HA and NA genes of AIV and F gene of NDV; Lane 4: Negative control (PBS); Lane 5: mPCR product obtained from sample of experimentally NDV infected chickens; Lane 6-7: mPCR products obtained from samples of field outbreak of suspected NDV.

Discussion

The present research work was undertaken to develop and standardize molecular methods e.g. multiplex PCR for simultaneous detection of avian influenza and Newcastle disease viruses using cDNA of AIV (H5N1) and reference NDV.

The primer sets for the genome detection of NDV and AIV (H5N1) were highly specific, no cross reactivity was noticed between the nucleic acid amplification of the two viruses. Specific primers were used for the amplification of cDNA of reference NDV and the PCR product gave a band at 356 bp position in the uniplex PCR which corresponds to the findings of earlier researchers²⁵⁻²⁶.

Reference cDNA of AIV (H5N1) was used for the detection of HA (H5) and NA (N1) genes in uniplex, duplex and multiplex PCR in this study. In every case the band of PCR product for HA (H5) gene appeared at the position 219 bp and for NA (N1) gene at 616 bp. Many researchers^{13,19,20,21,27} also detected PCR product of different sub-types of AIV using cDNA as a template in the PCR assay.

As AIV (H5N1) and NDV are the viruses of two different families, usually separate sets of primers were required for the amplifications of their individual gene. It was found that the bands of the amplified products HA (H5), NA (N1) of AIV (H5N1) and NDV were always appeared at 219 bp, 616 bp, and 356 bp respectively in each occasion. The use of multiplex PCR for the detection of AIV and NDV in a single tube reaction was also previously described²⁸⁻³⁴.

The bands of NDV were found more dense and distinct than the bands of AIV though minimum amount of cDNA of NDV were used compared to that of cDNA of AIV (H5N1). This might be due to the variation of virus concentration of NDV and the RNA used for the synthesis of cDNA of NDV compared to the cDNA of AIV during PCR assay.

While the goal of development of molecular based test was to achieve a simpler, more reliable, rapid test, this was combined with maximum operator safety. Separation and visualization of the PCR products were carried out by agarose gel electrophoresis stained with ethidium bromide that was a mutagenic compound as reported earlier³⁵⁻³⁶.

In conclusion, results of the present study clearly indicated that the newly developed multiplex PCR is highly sensitive, specific and rapid for complete sub-typing of AIV and simultaneous detection of NDV and AIV in a single tube reaction. However, it would be worthwhile to evaluate this mPCR on AIV suspected samples from different parts of Bangladesh.

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