BIOINFORMATIC ANALYSIS OF HOST – PATHOGEN INTERACTION IN INFECTIOUS Bursal Disease of Chickens

Hari Mohan Saxena
Department of Veterinary Microbiology, College of Veterinary Science, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, India 141004.

ABSTRACT: The analysis of amino acid sequences of the Infectious Bursal Disease virus (IBDV) and chicken MHC II proteins was done to identify their features. Antigenicity plot of the 1011 residue long IBDV sequence revealed 38 potential antigenic sites of the virus. Eleven MHC II binding peptides of IBDV VP2 were also predicted. Protein interface recognition sites for IBDV VP2 and chicken MHC II were predicted using a software PIR. In case of IBDV VP2, 21 residues and in case of chicken MHC II, 26 residues were identified as very likely to be involved in protein interface formation. Protein docking of amino acid sequences of IBD Virus and chicken MHC II molecules indicated a possible receptor – ligand type relationship.

KEYWORDS: Infectious Bursal Disease, IBD virus, bioinformatic analysis, MHC II, chicken, host-pathogen interaction.

INTRODUCTION

Infectious Bursal Disease (IBD) is an acute contagious viral disease affecting young chickens upto six weeks of age causing high morbidity but low mortality. IBD Virus (IBDV) selectively affects the B Lymphocytes of chickens. It destroys B cells in the bursa of Fabricius causing significant depression of the humoral immune response. However, the specific moiety on chicken B cells, which is the putative site of predilection for IBDV is not known yet. Bioinformatic studies were therefore undertaken to explore the basis of host-pathogen interaction in Infectious Bursal Disease of chickens. Such an analysis could yield important clues to the identity of molecular target of IBDV.

MATERIALS AND METHODS

Amino acid sequences of Infectious Bursal Disease virus and chicken MHC II proteins were analyzed using various programs. Potential antigenic epitopes and MHC II binding peptides of IBDV protein were predicted on the basis of hydrophilicity profile using ANTIGEN program. Protein interface recognition sites of the IBD virus and chicken MHC II proteins were analyzed using a public domain software PIR. PIER value indicates how likely a particular residue is to be involved into a protein interface formation, with higher values meaning higher probability. PIER value above 30 means very likely interface residues, and below 0 very unlikely interface residues. Buried residues were not included into prediction. Protein docking of IBDV VP2 and chicken MHC II molecules was done using ZDOCK program and visualization was done using PYMOL software. ZDOCK is a Fast Fourier Transform based protein docking program. It takes two PDB files and outputs the predicted structure of their complex. The top 2000 ranked predictions are returned. ZDOCK searches
all possible binding modes in the translational and rotational space between the two proteins and evaluates each by an energy scoring function. Each protein's structure is converted to a digital signal and a Fast Fourier Transform technique reduces the computational time.

RESULTS AND DISCUSSION

The analysis of amino acid sequences of the Infectious Bursal Disease virus and chicken MHC II proteins was done to identify their features. Antigenicity plot of the 1011 residue long IBDV sequence revealed 38 potential antigenic sites of the virus (Table 1). The conserved heptapeptide of IBDV VP2 showed similarities to peptide amidase which interacts with chymotrypsin and to an uncharacterized antigen of *Leishmania major* and *Leishmania braziliensis* which infect macrophages. Eleven MHC II binding peptides of IBDV protein were identified (Table 2). Twenty one protein interface recognition sites of Infectious Bursal Disease viral proteins (Table 3) and 26 PIR sites of chicken MHC II (Table 4) were identified. Protein docking of amino acid sequences of IBD Virus and chicken MHC II molecules (Fig. 1 & 2) showed a good fit indicating a possible receptor – ligand type relationship.

The bioinformatic analyses yielded useful information on the identity, nature and functional aspects of putative molecular target of IBDV. Thirty eight potential antigenic sites and 11 MHC II binding peptides of IBDV protein were identified. Twenty six sites on chicken MHC II and 21 sites on IBDV proteins were identified as protein interface recognition sites. The protein docking studies suggest a possible receptor – ligand type of interaction between the IBDV VP2 and chicken MHC II protein. These studies offer valuable insight into the nature of the putative target and form the basis for useful and confirmatory experimental studies. Overall, the bioinformatic data lends credibility to the hypothesis that chicken MHC II molecule may be the possible target for IBDV binding on chicken lymphocytes and some other cells.

Table 1: Predicted epitopes of IBDV VP2 protein

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<th>S/no.</th>
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Table 2: Prediction of MHC II binding peptides of IBDV VP2

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<th>S. No.</th>
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### Table 3: Protein Interface Recognition for Infectious Bursal Disease Virus VP2

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### Table 4: Protein Interface Recognition for Chicken MHC II

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Table 5. Prediction of protein - protein binding of the heptapeptide of IBDV VP2

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<th>Amino acid</th>
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<td>-6</td>
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<tr>
<td>S</td>
<td>-20</td>
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Fig. Prediction of protein – protein binding of chicken MHC II protein

MAVLSGAAVPLLLLGVLGGVGAVLKPHVLLQAEFYQRSEG
P---------------------PP--PPPP-
PDKAWAQFGFHFDADELFHVELDAAQTVWRLPEFGRASF
-----P--------------------
EAQGALQNMAVGKQNLEVMIGNSRQQDFVTPELALFPA
-------P-------PP--------
EAVSLEEPNVLCYADKFWWPPVATMEWRRNGAVVSEGVYD
---PPP-------P-------------
SVYYGRPDLLFRKFSYLFPVPQRGDVYSCAVRHWGAEGPV
----P-P----PP---------------
QRMWEPEVPEPSESSATLWCAVGLAVGIAGIAAGTALIL
-------P---------------------
RAVRRNAANRPGLL
---------PP--PP
Fig. 1. A model of docking of IBD virus VP2 with chicken MHC II molecule.

Fig. 2. Another view of a model of docking of IBDV VP2 with chicken MHC II molecule.