|  |  |  |
| --- | --- | --- |
| **No of table** | **Name of Figure** | **Page No** |
| 2.1 | Herpes Virus Structure | 8 |
| 2.2 | Structure of ILTV | 12 |
| 2.3 | Map of the double-stranded DNA genome of ILTV, which is ca. 150 kbp in size and consists of long and short unique regions (UL, US), and of inverted repeats (IR, TR) flanking the US region. | 13 |
| 2.4 | Mettenleiter’s proposed summary diagram of herpesvirus (ILTV) | 14 |
| 2.5 | Nucleotide alignment of the Serva ILTV sequence and the concatenated ILTV reference sequence | 23 |
| 2.6 | Amino acid alignment of predicted translation products of homologous genes from the Serva ILTV strain, the concatenated ILTV reference sequence and other alphaherpesviruses. | 24 |
| 2.7 | Gaping of Bird  | 28 |
| 2.8 | Haemirrhages in comb,wattle and Swollen around eyes  | 28 |
| 2.9 | Severe epizootic form: expectoration of bloody mucous | 28 |
| 2.10 | Early ILT very similar to IB, ND | 29 |
| 2.11 | Hemorrhagic tracheitis due to infectious laryngotracheitis in a chicken. | 29 |
| 2.12 | Trachea: The submucosa is thickened by a dense cellular infiltrate | 32 |
| 2.13 | Mucosal epithelium is necrotic | 32 |
| 2.14 | Trachea: Mucosa contains syncytia and large eosinophilic intranuclear inclusions | 32 |
| 2.15 | Trachea: More epithelial intranuclear inclusions | 32 |
| 2.16. | The principles of LAMP DNA amplification and primer arrangement | 36 |
| 3.1 | Flowchart showing different steps to be followed during this study. | 47 |
| 4. 1. A | Normal CAM covering embryo (uninfected) | 63 |
| 4. 1.B | Infected CAM with desecrate pock like lesions  | 63 |
| 4. 1.C | Single pock like lesion on the CAM with centrally depressed area of necrosis. | 63 |
| 4.2 | 1% Agarose Gel Electrophoresis of mRT-PCR amplified products of individual CAM + field samples. | 64 |
| 4.3 | 1% Agarose Gel Electrophoresis of PCR amplified products of ICP4 gene of ILTV from individual CAM (+) filed samples | 65 |
| 4.4 | Partial chromatogram of the sequence of PCR product (R3). | 68 |
| **No of table** | **Name of Figure** | **Page No** |
| 4.5 | The snapshot from Jalview site showing variations in the ICP4 gene nucleotide sequences among the obtained field isolates. | 70 |
| 4.6 | The graphic summary of 119 blast hits on the query sequence, KC576526 | 73 |
| 4.7 | The sequence producing significant alignment with GenBank accession no. KC576526 | 74 |
| 4.8 | The similarity of sequence of Gen Bank: accession no KC576526 (Vaccine isolate) with that of GenBank: accession no.  | 75 |
| 4.9 | The graphic summary of 100 blast hits on the query sequence KC576525 | 76 |
| 4.10 | The sequence producing significant alignment with distinct GenBank accession number KC576525.1 | 77 |
| 4.11 | Pairwise alignment between Bangladesh field isolate KC576525 and Nobilis CEO vaccine isolate FJ477351 shows 99% similarity with nucleotide base Gaps in 3 positions and 1 SNPs | 79 |
| 4.12 | Snapshot from Jalview site showing similarity between targeted fragment of ICP4 gene sequences of USDA reference strain (EU104909), TCO vaccine strain (EU104908), Strain 1874C5 (JN542533), Live attenuated vaccine (Serva) strain (HQ630064), ILTV strain-Jiang (JN969100), CEO-high egg passage vaccine (JN580316) and CEO-low egg passage vaccine (JN580317) as well as vaccine isolate of Bangladesh (KC576526) and CVASU-1 ILTV field isolate of Bangladesh (KC576525.1). | 82 |
| 4.13 | Pairwise alignment shows variation in between the sequence of vaccine isolate (KC576526.1) and field isolate (KC576525.1) of ILTV from Bangladesh | 83 |
| 4.14 | The genetic inter relationship of Bangladeshi isolates and previously published reference sequences of ILT inferred from Phylogenetic tree constructed by average distance analysis method using BLOSUM62 with Jalview software. | 84 |
| 1 |  A glimpse of activities performed in Lab. | 117 |
| 2 | GenBank accession no. (KC576525) of ICP 4 gene specific field isolate (CVASU-01)of ILTV | 119 |
| 3 | GenBank accession no. (KC576526) of ICP 4 gene specific vaccine isolate of ILTV | 121 |