Phylogenetic analysis

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MATERIALS TEXT

Twenty-eight published FAdVs hexon (Table 1) and fiber (Table 2) gene sequences were obtained from GenBank. Another two reference strains from different genus avian adenovirus was used which are Duck adenovirus (Atadenovirus) and Turkey adenovirus (Siadenovirus). Multiple sequence alignment of nucleotide and deduced amino acid were conducted using BioEdit Version 7.2.5 and Mega Version 5 software. A region of L1 loop in hexon gene with 198 amino acids and entire region of fiber gene was selected for construction of phylogenetic tree. Jones-Taylor-Thorton (JTT) model was used to compute distance matrix using MEGA software and followed by phylogenetic tree construction using Neighbour-joining method with 1000 boostrap replicates [Juliana et al., 2104].

Table 1.docx   Table 2.docx

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