Oct 06, 2019

Phylogenetic analysis

PLOS One

DOI

dx.doi.org/10.17504/protocols.io.7zihp4e

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DOI: https://dx.doi.org/10.17504/protocols.io.7zihp4e

External link: https://doi.org/10.1371/journal.pone.0225863

Protocol Citation: Norfitriah Mohamed Sohaimi, Mohd Hair Bejo, Abdul Rahman Omar, Aini Ideris, Nurulfiza Mat Isa 2019. Phylogenetic analysis. **protocols.io** https://dx.doi.org/10.17504/protocols.io.7zihp4e

Manuscript citation:
Sohaimi NM, Bejo MH, Omar AR, Ideris A, Isa NM (2019) Molecular characterization of fowl adenovirus isolate of Malaysia attenuated in chicken embryo liver cells and its pathogenicity and immunogenicity in chickens. PLoS ONE 14(12): e0225863. doi: 10.1371/journal.pone.0225863

Protocol status: Working
We use this protocol and it's working

Created: October 06, 2019

Last Modified: October 06, 2019

Protocol Integer ID: 28426

Keywords: analysis

Materials

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

Troubleshooting

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