Project DNA7 Comparing a DNA sequence to sequences in GenBank using BLAST

In the Project DNA7 Comparing a DNA sequence Zip File there are two trace files that will combine into a single DNA sequence, a fragment of a HVP2 DNApol gene. These files are sequencing traces using PCR product as template and each PCR primer as a sequencing primer. Once you have assembled and generated a consensus sequence, use this sequence to search GenBank using BLASTN and find homologous DNA sequences. Download 5 of the >200 homologous sequences that will appear. Align (and trim) them using the Mega. Remember to use your original DNA when deciding if the sequences need end trimming. Enter the files into the MEGA program to align and analyze the similarity between the sequences. Generate several DNA sequence-based trees using different methods. Save two of the trees.

For your information. The PCR product that was sequenced was amplified from the lungs of an infant baboon that died of pneumonia in December, 2003. The DNA preparation and diagnostic PCR were performed in Dr. Blewett’s lab in January, 2004. The infant had been diagnosed with CMV pneumonia and histology showed giant cells and other typical CMV lung pathology. Using a polyclonal anti-HCMV gB antisera and lung tissue sections, our collaborators showed the antibodies bound to the cells displaying cytopathic effect, confirming that the infant had baboon CVM (BaCMV).

**Based on your BLASTN searches and phylogenic trees, is this virus CMV? and is the diagnosis correct?**

Procedure:

1. Download the files from your BLAST searches as GenBank files, (\*.gb)
2. Import the sequences into a single Mega Project by starting Mega and selecting File > New alignment
3. Import all the files at once by clicking control I then browsing to the folder where you saved the files selecting all sequences and hitting open
4. The sequences will be open in the main Alignment Editor window.
5. Name and save the project as a Mega file (DNApol.mas).
6. Select the sequences to be aligned by clicking on the filenames in the lefthand window.
7. Align the sequences using Align > CLUSTALW multiple alignment.
8. Name and save the output file as DNApol aligned.mas.
9. You will likely need to trim each end of the files using the sequence editor to match the original DNpol sequence
10. Save the file with trimmed DNA sequences as DNApol trimmed
11. Import the DNApol.pir file into MEGA as in Project D6, align and produce two trees.

Data to be produced:

Computer files Acrobat documents

Dowloaded GenBank files None

DNApol.mas (MEGA)

DNApol aligned.mas

Answer the Experimental Question (in bold above)