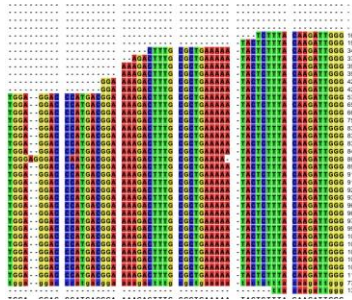


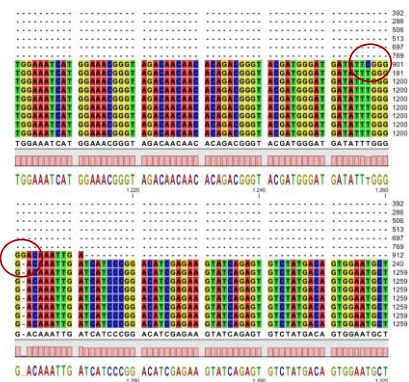
Common mistakes

- If primersites are not deleted
- If isolates are sequenced only in one direction. The EURL advises that isolates be sequenced in both the forward and reverse direction. If isolates are cloned it is recommended that at least 3 clones are sequenced.
- Improper reading/analysis of trace files



VHSV

- 13 laboratories sequenced the G-gene
 - 8 sequenced the full G-gene, 1 did not assemble sequences
 - 5 labs sequenced between 500 and 800 nt
 - 3 sequences contained mistakes, always at the end
- 12 laboratories sequenced the N-gene
 - Sequences varied between 264 and 723 nt
 - 5 sequences contained mistakes, always at the ends



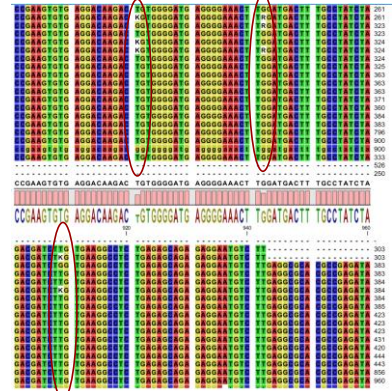
IHNV

- 21 laboratories sequenced the G-gene
 - They sequenced between 187 and 2035 nt
 - 6 sites where more than one lab found a difference to consensus or wobble bases
- 8 laboratories sequenced the N-gene
 - They sequenced between 236 nts and 748 nts
 - 8 sites where more than 1 lab found a difference to consensus or wobble bases
 - 1 lab found 22 wobble bases on a sequence of 748 nts on the N-gene.

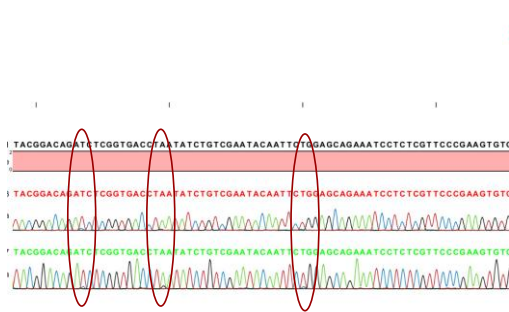
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G-gene

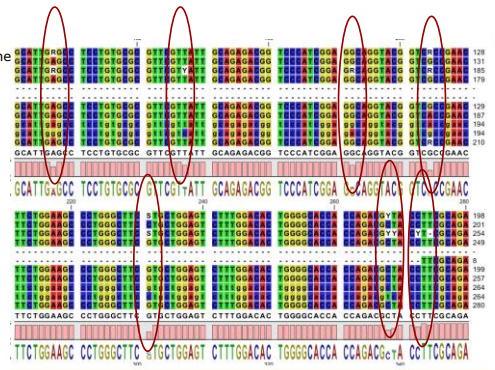


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N-gene



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Recommendations for next year

- Please assemble your sequences instead of sending several sequences for one isolate
- Request for chromatograms for further analysis
- Request for further information about sequencing methods