

Table1 : Primers used to sequence the HGyV genome by the Sanger method

Forward	Reverse	Size (bp)
5'-TCCGTTGCAGTGTGCTCGTTG-3'	5'-GCACTTAGAGGGCTTCCCAG-3'	642
5'-CTCATCTGCCGGTGCATTGG-3'	5'-CCGGGCTCCTATGTGGTAAG-3'	654
5'-AAAGCTTGAGCCTCCGGAATG-3'	5'-TAGGCAAGAGGGGCAACTTGG-3'	698
5'-TAGTTGTTGCTCGTCGGCGAG-3'	5'-CTTTCACCACGCACCAAGGG-3'	711

Table 2: Description of the Open Reading frames of HGyV and comparison with those of CAV (Emboss, Align Needle).

Protein	putative open reading frame (s)	frame	No of amino acids	theoretical mass kDa	CAV aa % identity	CAV nuc % identity
VP1	884-2281	+2	465	53.58	43.6	53.1
VP2	381-1076	+3	231	25.5	44.8	60.1
apoptin	508-882	+1	124	13.63	31.1	60.9

Table 3: Primers for the nested PCR used for prevalence studies

	Forward	Reverse	Size (bp)
External primers	5'-CAAAATCGGAGGCCCTAACCC-3'	5'-ATGCCTGAATAGCTGCCAGCC-3'	256
Internal primers	5'-GTCAGCACAAACGACGCAGG-3'	5'-AGGGTGCATCACCAGGAGAG-3'	115