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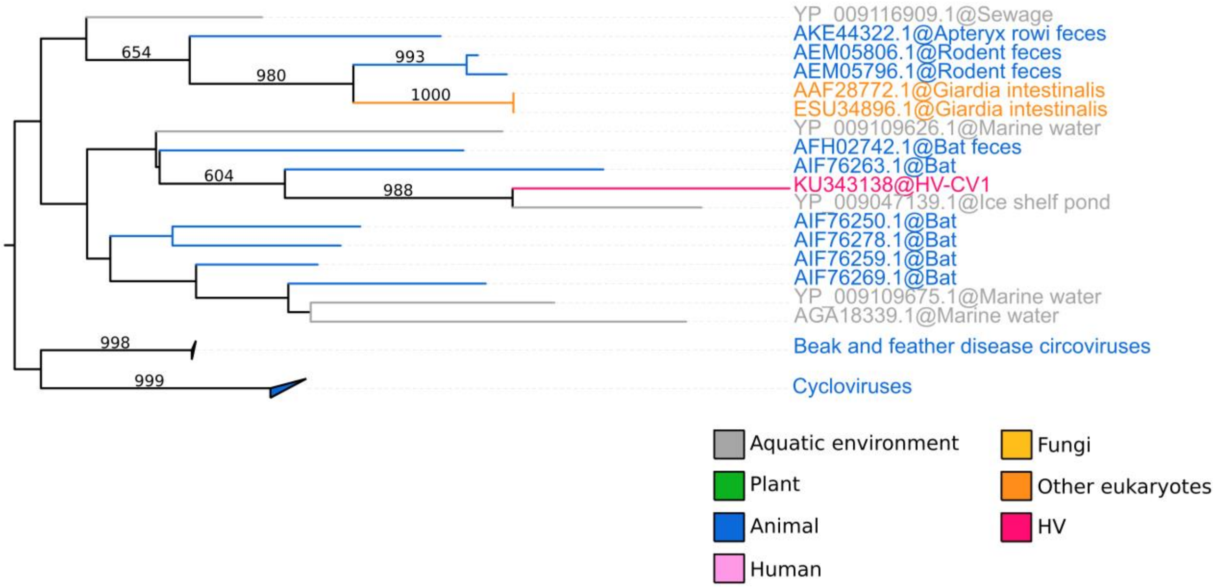
Novel Single-Stranded DNA Circular Viruses in Pericardial Fluid of Patient with Recurrent Pericarditis

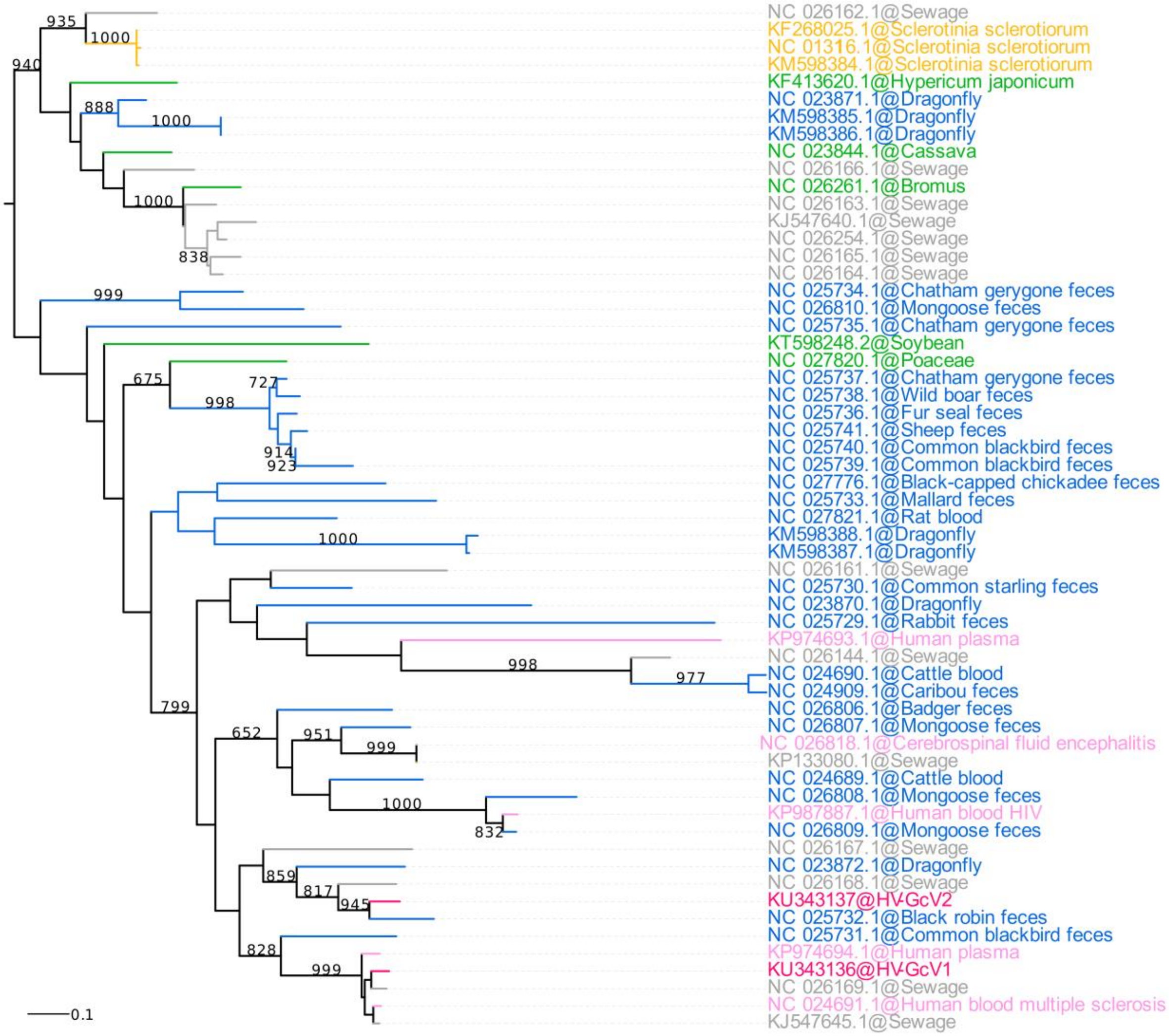
Technical Appendix

Technical Appendix Table. PCR primer pairs used to recover whole-genome sequences of gemycircularviruses

Primer pair	Forward primer sequence 5′→3′	Reverse primer sequence 5′→3′
HV-GcV1–1	TTATATGCCCAGACGGACCC	ATTGTGCGGCGGATAGGATA
HV-GcV1–2	CGAATTTAACCCCGGATGCA	AAGGATGCCACCCGAATGTA
HV-GcV1–3	TTGTTCGATCAGACCACCGA	GTTCCTTCCGAGCTACAAGT
HV-GcV1–4	TCGATGTTAACTCCCTCCGG	GAAACGTGTAGATCGGCGAC
HV-GcV2–1	TTGCTCTCAACCGAAAACGG	GCCTGTTACATCGCCGATTT
HV-GcV2–2	TCCGCGTCTTTTGTAGGTCT	AAAGCGTGTGATACCCAAGC
HV-GcV2–3	TCCTTCACCAGCCTCAAGTG	TCTCCGCATGATCAGATCCG
HV-CV1–1	GGAGTTGCATGGGATCGAAC	ACCTTGAGTGACATGAGCCA
HV-CV1–2	TGGGAGTTTGGGGAGATGTC	GAATGTAGTTGGTGCAGGGC
HV-CV1–3	ACGGGCTACACATTCAGCAT	TAGACGCAGAGGATGGATCG
HV-CV1–4	AAGCTTCTTCTCGAACGTCTT	GTTGAAGGACTGGCGGAATC



Technical Appendix Figure 1. Maximum likelihood phylogenetic inference of gemycircularvirus replication initiation proteins. Numbers on branches correspond to bootstrap values deduced from 1,000 replicates. Only scores >600 are displayed.



Technical Appendix Figure 2. Maximum likelihood phylogenetic inference of the closest homologues of the HV-CV1 replication initiation protein. Numbers on branches correspond to bootstrap values deduced from 1,000 replicates. Only scores >600 are displayed. Scale bar represents 0.1 residue substitution per site.