

Hepatitis E Virus Genotype 4 in Yak, Northwestern China

Technical Appendix

Technical Appendix Table 1. Frequency of hepatitis E virus detected by RT-PCR assay in fecal samples from domestic yaks of different ages in 2 provinces of northwest China

Province	Animal age, mo	No. (%) samples tested	No. (%) positive
Qinghai	≤12	56 (60.87)	3 (5.36)
	12–36	36 (39.13)	0
Gansu	≤12	48 (64.00)	0
	12–36	27 (36.00)	0

Technical Appendix Table 2. Sequences of primers for cloned hepatitis E virus genome sequence contained all open reading frames

Primer	Sequence, 5' → 3'	Site (nt)*
P1	F-CACGTATGTGGTCGACGCC	8–26
	R-GAAGAGCATAAGCCTGTCCCA	984–1004
P2	F-CTGCCTGCTCTACTAAATCCAYAT	937–960
	R-CGATTGAACCTRTACAAGGCTGA	1996–1974
P3	F-TGGCTGCGYGGYCCACATAGTC	1828–1848
	R-CGTGCCGTGTCCTCAGTAATA	2867–2887
P4	F-ATCTTACTGAGCCAGCCATAGC	2806–2827
	R-ACGAGACACATCACGGCTRCAC	4178–4199
P5	F-ACCTAGYCAGCGTAAAGCTGTC	3962–3983
	R-CCACATTCGTTAACTTTGCA	4962–4982
P6	F-GACCCTCCCTGATGTTGTTAGG	4859–4880
	R-CAATAGTGGACGTAAGCGGAGA	5609–5630
P7	F-CCGTTACGTCCACTATTGCTA	5612–5633
	R-AGTGCACCAAGTATAAGGCGTATTG	6055–6078
P8	F-CCTAGTGAGCGCCTGCACTAT	5027–5947
	R-CGAGAATAGAACAATTGTCCACCA	6361–6384
P9	F-AGYTACCCGCTTTATGAAAGYTCT	6223–6246
	R-TGAAATRCAGACRCGGTGRCC	6914–6934
P10	F-TGCTAATGACGTGCTCTGGCT	6586–6606
	R-TGCGTTCCGCGCTCCCTGA	7149–7241

*Site on the genome of China swine strain (GenBank accession no. GU119961). R = A/G; Y = C/T.