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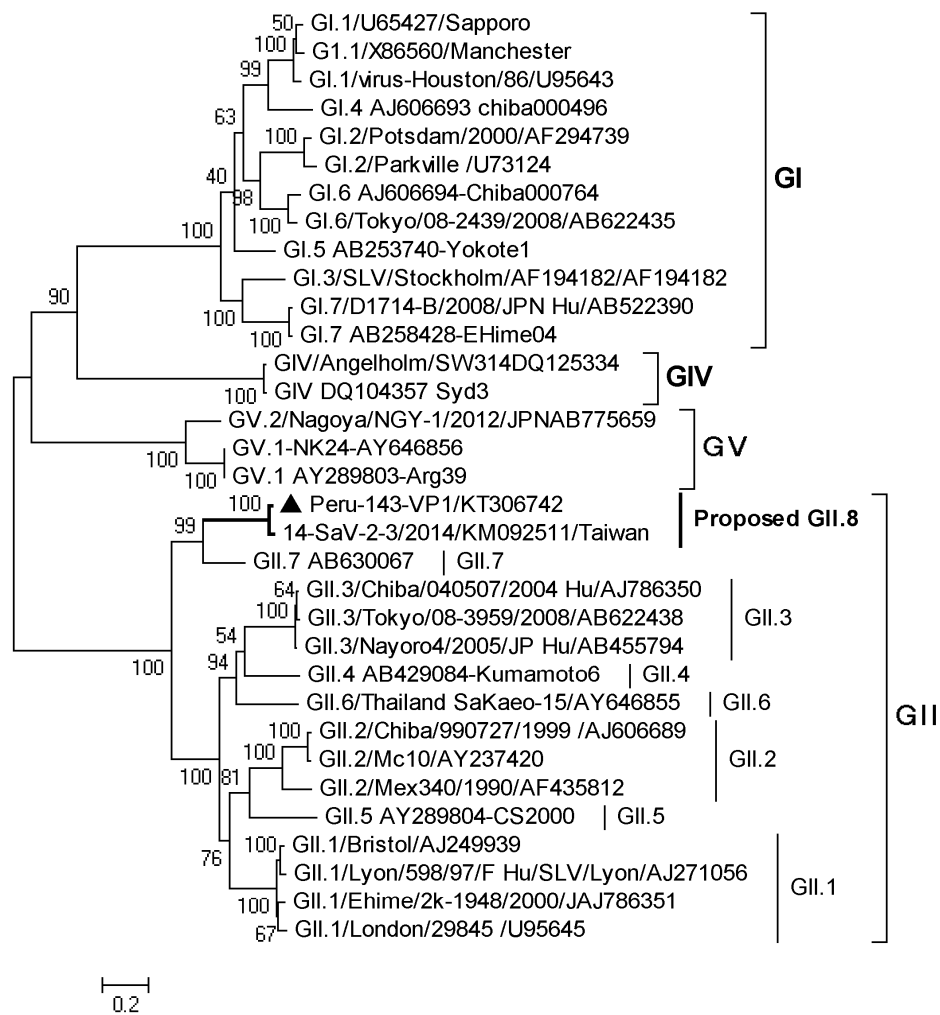


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Supplementary Table 1. Primer and probe sequences used in this case-control study

Usage	Primer/Probe	Nucleotide Sequence (5'-3')	Position	Reference
Real-time PCR	Sav 1F	TTGGCCCTCGCCACCTAC	5077-5094 ^a	1
	Sav 5F	TTTGAACAAGCTGTGGCATGCTAC	5112-5135 ^a	
	Sav124 F	GAYCASGCTCTCGCYACCTAC	5074-5094 ^a	
	Sav1245 R	CCCTCCATYTCAAACACTA	5159-5177 ^a	
	Sav124 probe	VIC-CCRCCTATRAACCA-MGB	5101-5117 ^a	
	Sav5 probe	VIC-TGCCACCAATGTACCA-MGB	5142-5157 ^b	
Genotyping	SV-F13	GAYYWGGCYCTCGCYACCTAC	5074-5094 ^a	2
	SV-F14	GAACAAGCTGTGGCATGCTAC	5074-5094 ^a	
	SaVF1245	TAGTGTTTGARATGGAGGG	5159-5177 ^a	
	SaV5857R-1	CWGGDGANAYHCCATTBTCCAT	5857-5878 ^a	
	SaV5857R-2	GGNGANMNNCCRTTNTSCAT	5857-5876 ^a	
Amplification of VP1	SV-F13	GAYYWGGCYCTCGCYACCTAC	5074-5094 ^a	Current
	SV-F14	GAACAAGCTGTGGCATGCTAC	5074-5094 ^a	study
	SaVGHIR	GCTCCWGTRAACCAAGACATTATTC	6851-6875 ^c	

- a. Position in complete sapovirus GI genogroup sequence (Manchester, X86560)
 - b. Position in complete genome of sapovirus GV genogroup (NongKhai-24/Thailand, AY646856)
 - c. Position in complete genome of GII genogroup (Bristol/98/UK, AJ249939)
1. **Oka T, Katayama K, Hansman GS, Kageyama T, Ogawa S, Wu FT, White PA, Takeda N.** 2006. Detection of human sapovirus by real-time reverse transcription-polymerase chain reaction. *J Med Virol* 78:1347-1353.
 2. **Okada M, Yamashita Y, Oseto M, Shinozaki K.** 2006. The detection of human sapoviruses with universal and genogroup-specific primers. *Arch Virol* 151:2503-2509.



Supplementary Figure 1. Phylogenetic analysis of full VP1 nucleotide sequences of sapovirus.

The phylogenetic tree was inferred using the maximum likelihood method (Kimura 2-parameter model) using MEGA5. The tree was drawn to scale, with branch lengths measured in the number of substitutions per site. The VP1 obtained in this study is marked with a filled triangle.