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# Detection of Recombinant African Swine Fever Virus Strains of p72 Genotypes I and II in Domestic Pigs, Vietnam, 2023

## Appendix

**Appendix Table 1.** Information of primers used in this study.

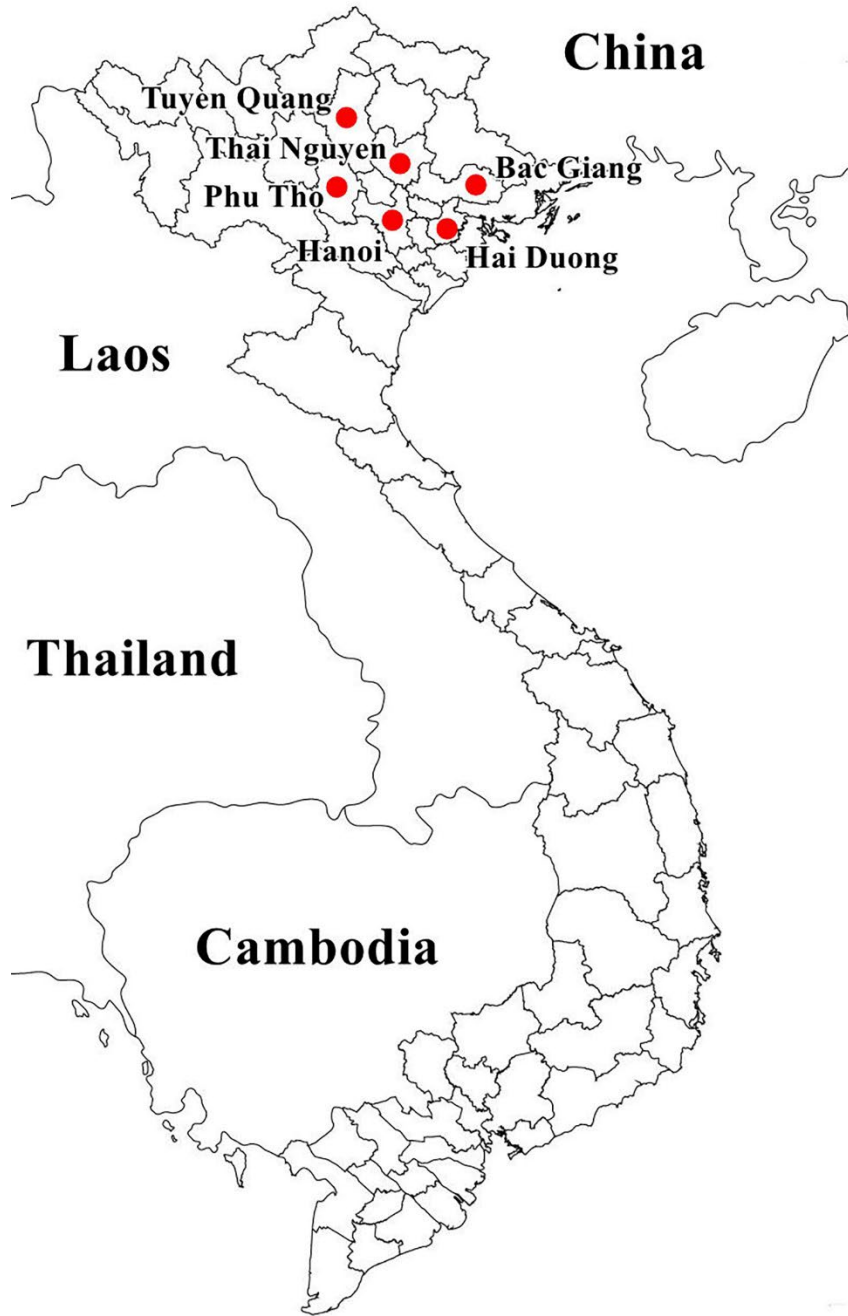
No.	Name	Sequence	Length (bp)	Gene	Reference
1	P72.U P72.D	GGCACAAAGTTCGGACATGT GTACTGTAACGCAGCACAG	478	B646L	(1)
2	PPA722 PPA89	CGAAGTGCATGTAATAAACGTC TGTAATTTTCATTGCGCCACAAC	676	E183L	(2)
3	CD2v-1F CD2v-1R CD2v-2F CD2v-2R	GTCGGGGCTACAATCCTTTTATC AAGTGTTGTTTCATTAGATGTAC GCTACTCCCCCAAATATCACAT GTTCTCGATGATCTGCTACTAG	690 847	EP402R	Designed in this study
4	B602L- 87070F B602L- 87872F	GTGGGGTTTGGGTAATTGCATCAA GCCTTCCTATTCAAAACCTACCC	803–900	B602L	Designed in this study
5	9GL/F 9GL/R	TAGAGATGACCAGGCTCCAA GTTGCATTGGGGACCTAAATACT	357	B119L	(3)
6	MGF MGR	GAGGATGATTTGCCCTTCACTCA CGCCACTAGTAAACATTGTCTATCT	422	MGF 505–1R	(4)
7	I177L-F I177L-R	TAGCTTGCCGGTAATGGCTAT TGCGACTCAAGGCAACAT	551	I177L	Designed in this study
8	UK-F UK-R	GTTGTCTGTGGATAATGCACC GGATGGAGCGCATTAGGGAT	210	DP96R	(4)
9	ECO1A ECO1B	CCATTTATCCCCGCTTTGG TCGTCATCCTGAGACAGCAG	356	Intergenic region between I73R and I329L genes	(5)
10	A238L-F A238L-R	GCGACAATCTTACGTCATGA CCAAGAATTACCGCACATATG	1082	A238L	Designed in this study
11	A137R-F A137R-R	CCACGTATAGCAACCTATATG CATGAGTTATTGGATGACCTCG	631	A137R	Designed in this study
12	MGF360– 12L-F MGF360– 12L-R	GCGGCCGAAACATTATTCTTAC CATACTTGGCAGAATGCCAGC	1238	MGF 360–12L	Designed in this study
13	I226R-F I226-R	GATAATGATACCACATGCAT TCGATGAGCCATCCACGATA	798	I226R	Designed in this study

## References

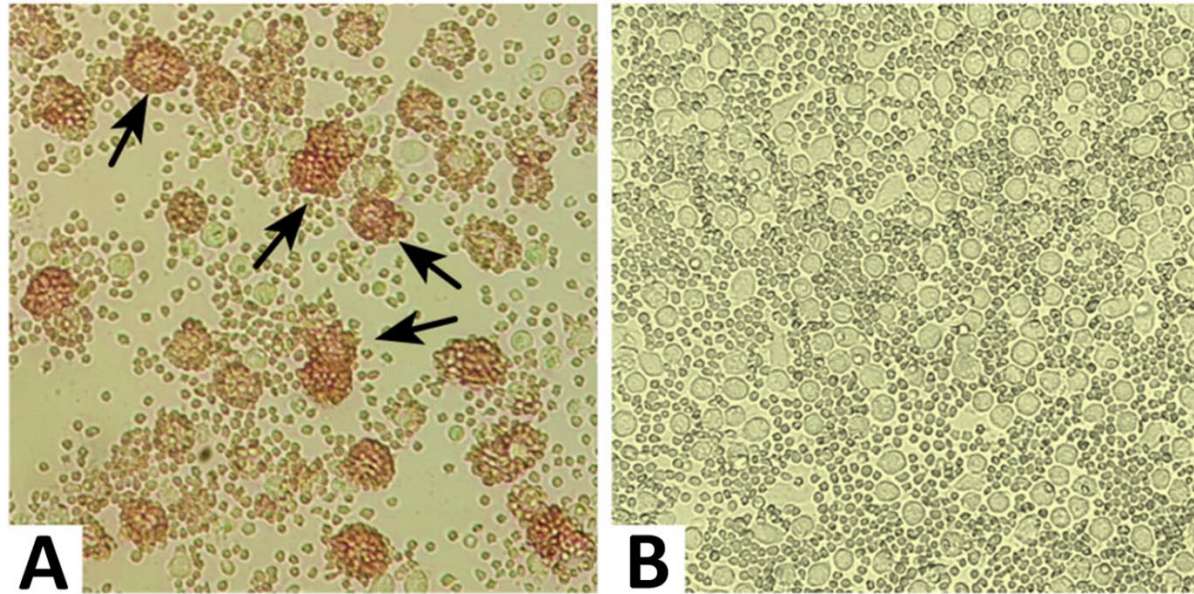
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**Appendix Table 2.** Genotype (based on the genes from the current pandemic p72 genotype II virus and low-virulent genotype I viruses reported in China) and percentage identity of the amplified genes of the Vietnamese rASFV I/II strains compared to those of the rASFV I/II strain JS/LG/21 from China. rASFV I/II and ASFV genotype II strains from Vietnam are highlighted in gray.

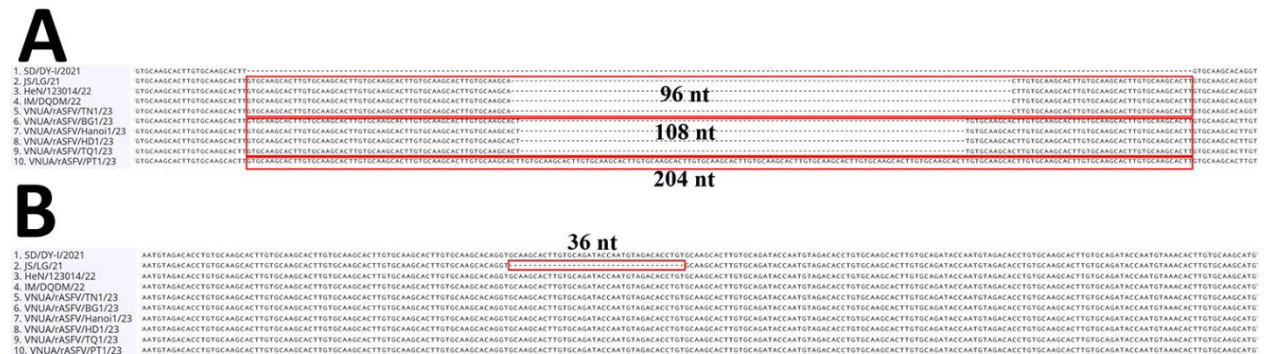
		Genotype/Percentage (%) Identity														
No.	Virus strain	B646L (P72)	B602L (CVR)	B119L (9GL)	A238L	A137R	E183L (P54)	EP402R (CD2v)	DP96R (UK)	I177L	MGF 505-1R	IGR	MGF 360- 12L	I226R		
1	VNUA/rASFV/HD 1/23	I 100	I 90.94	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
2	VNUA/rASFV/BG 1/23	I 100	I 90.94	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
3	VNUA/rASFV/Ha noi1/23	I 100	I 90.94	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
4	VNUA/rASFV/PT 1/23	I 100	I 77.47	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
5	VNUA/rASFV/TQ 1/23	I 100	I 90.94	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
6	VNUA/rASFV/TN 1/23	I 100	I 93.15	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
7	rASFV HeN/123014/22	I 100	I 93.33	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
8	rASFV IM/DQDM/22	I 100	I 93.33	I 100	I 100	I 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		
9	HeN/ZZ-P1/2021	I 100	I 73.33	I 100	I 100	I 100	I 96.42	I 78.05	I 99.05	I 96.88	I 0	I 86. 5	I 0	I 98.09		
10	SD/DY-II/2021	I 100	I 75.56	I 100	I 100	I 100	I 96.42	I 78.05	I 99.05	I 96.88	I 0	I 86. 5	I 0	I 98.09		
11	VN/HY- ASFV1(2019)	II 99.07	II 42.65	II 99.44	II 98.26	II 99.28	II 100	II 100	II 100	II 100	II 100	II 100	II 100	II 100		



**Appendix Figure 1.** Map of Vietnam showing the provinces from which rASFV I/II samples were collected.



**Appendix Figure 2.** Isolation of Vietnamese rASFV I/II strains on porcine alveolar macrophage (PAM) cells. Infected (A) and Un-infected (B) PAM cells with Vietnamese rASFV strains. Black arrows indicate hemadsorption (HAD), in which ASFV-infected PAM cells adsorb porcine red blood cells (RBCs).



**Appendix Figure 3.** Comparison of nucleotide (nt) sequences based on the CVR of the B602L gene between Vietnamese rASFV I/II strains and reference strains. A: insertion of 96, 108, and 204 nt; B: deletion of 36 nt.