

Severe fever with thrombocytopenia syndrome virus in bats and ticks collected from bat habitats

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Background: The tick-borne zoonotic infectious disease, severe fever with thrombocytopenia syndrome (SFTS), caused by the SFTS virus (SFTSV), *Bandavirus dabieense*, was identified in bats and ticks collected from bat habitats in the Republic of Korea.

Methods: To investigate the relationship between bats and SFTSV, **1,200 ticks** were collected from 12 sites in 6 provinces within 1 km of bat habitats using flagging, and **147 bat sera** were collected via cardiac puncture after ether anesthesia between November 2021 and September 2022. Total RNA was extracted from the ticks and bat sera, and nested reverse transcription polymerase chain reaction (RT-PCR) was performed to amplify the S segment of SFTSV. Bat sera were analyzed for IgG antibodies against SFTSV by enzyme-linked immunosorbent assay (ELISA).

Results: Within 1 km of bat habitats, 881 *H. longicornis*, 209 *H. flava*, 96 *Haemaphysalis* spp., and 14 *Ixodes* (*I.*) *nipponensis* were identified. SFTSV was detected in 12.3% (147/1,200) of the ticks. Although no SFTSV RNA was detected in bat sera by nested PCR, 3.4% (5/147) were seropositive by ELISA.

Table 1. Detection of SFTSV in ticks collected within 1 km radius of bat habitat areas in the Republic of Korea

Provinces	Districts	Tick species	No. of positive	Detection rates (%)
Gyeonggi-do	Pocheon	<i>H. longicornis</i> (n=48)	14	29.2
		<i>H. flava</i> (n=26)	1	3.8
		<i>H. spp.*</i> (n=23)	1	3.8
		<i>I. nipponensis</i> (n=3)	0	0
Gangwon-do	Hwacheon	<i>H. longicornis</i> (n=82)	9	11.0
		<i>H. flava</i> (n=18)	2	11.1
	Inje	<i>H. longicornis</i> (n=24)	0	0
		<i>H. flava</i> (n=39)	2	5.1
		<i>H. spp.</i> (n=32)	0	0
Chungcheongnam-do	Gongju	<i>I. nipponensis</i> (n=5)	1	20
		<i>H. longicornis</i> (n=89)	17	19.1
		<i>H. flava</i> (n=10)	3	30
		<i>H. spp.</i> (n=1)	1	100
Gyeongsangbuk-do	Yeongyang	<i>H. longicornis</i> (n=75)	5	6.7
		<i>H. flava</i> (n=15)	0	0
		<i>H. spp.</i> (n=10)	0	0
	Goryeong	<i>H. longicornis</i> (n=83)	6	7.2
		<i>H. flava</i> (n=9)	3	33.3
Gyeongsangnam-do	Hapcheon	<i>H. longicornis</i> (n=81)	7	8.6
		<i>H. flava</i> (n=8)	1	12.5
		<i>H. spp.</i> (n=10)	1	1
		<i>I. nipponensis</i> (n=1)	0	0
	Sancheong	<i>H. longicornis</i> (n=41)	5	12.2
		<i>H. flava</i> (n=49)	1	2.0
		<i>H. spp.</i> (n=10)	1	1
	Hadong	<i>H. longicornis</i> (n=89)	10	11.2
		<i>H. flava</i> (n=6)	2	33.3
		<i>H. spp.</i> (n=1)	0	0
Jeollabuk-do	Muju	<i>I. nipponensis</i> (n=4)	0	0
		<i>H. longicornis</i> (n=100)	18	18
		<i>H. flava</i> (n=14)	9	10.5
	Jangsu	<i>H. longicornis</i> (n=86)	0	0
		<i>H. longicornis</i> (n=83)	24	29.0
	Imsil	<i>H. flava</i> (n=15)	2	13.3
		<i>H. spp.</i> (n=1)	1	100
6 provinces	12 districts	1,200 tested	147	12.3

Note: Adult and nymph ticks were used individually and larvae were used as pool samples (30 larvae per pool sample). *H.*, *Haemaphysalis*; *I.*, *Ixodes*.

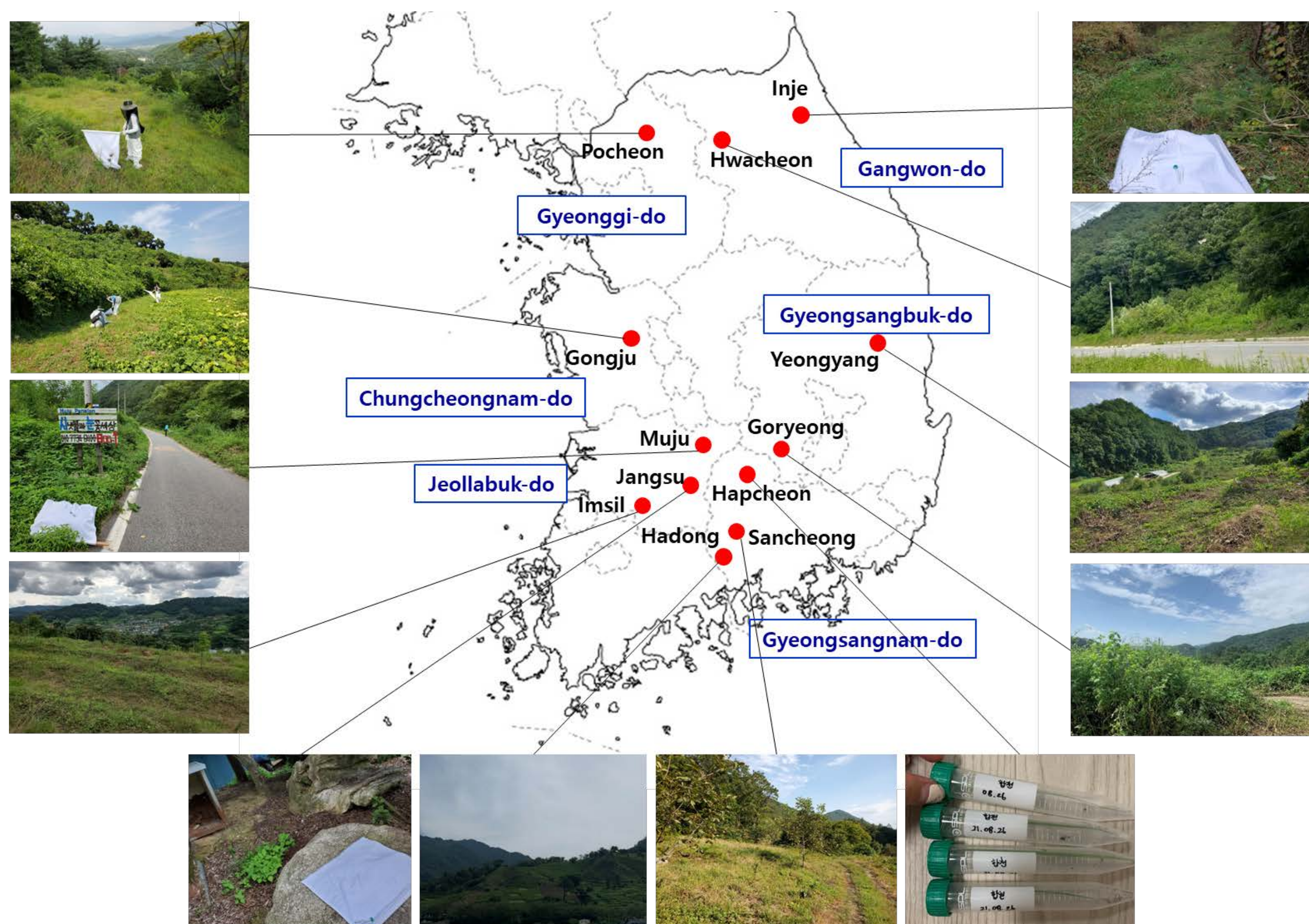


Fig. 1. Geographical map of tick collection sites within a 1 km radius of bat habitats. Blue words indicate provinces and black and red words indicate tick collection sites within a 1 km radius of bat habitats. Habitats include abundant forests and near the cave.

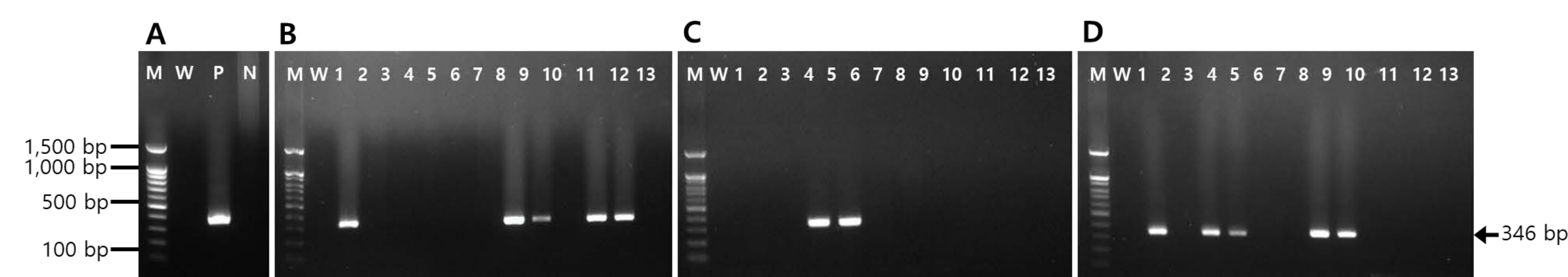


Fig. 2. Geographical map of SFTSV detection in ticks in the Republic of Korea. The number of SFTSV positive and negative at each site is shown. Blue words indicate provinces and black words and red indicate tick collection sites within a 1 km radius of bat habitats. One hundred ticks collected from each site were used in the experiment.

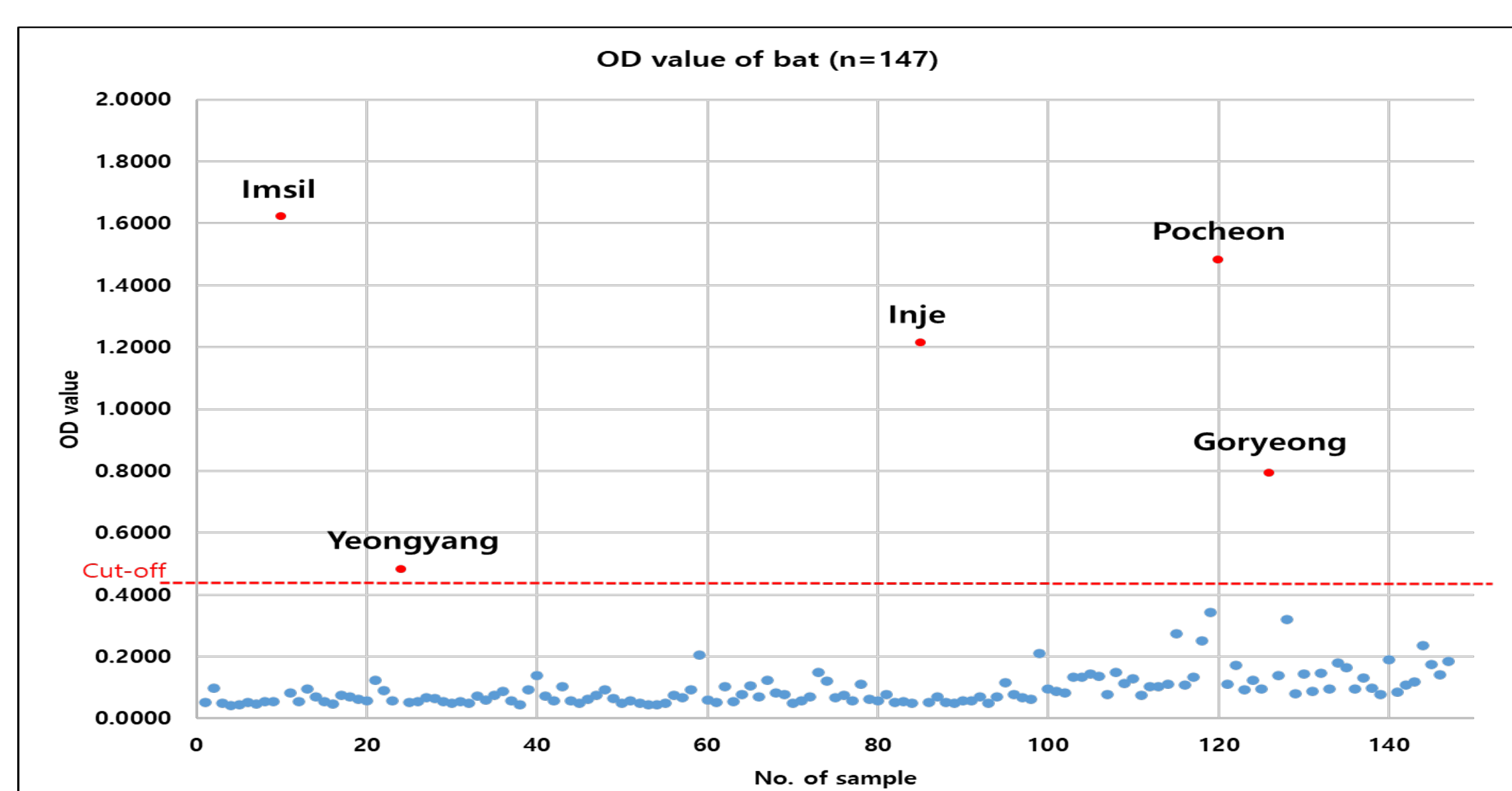


Fig. 3. The result of ELISA for SFTSV in bat sera. OD value and cut-off line (red dotted line) of the ELISA for SFTSV in bat sera. Red dots indicate five SFTSV positive samples.

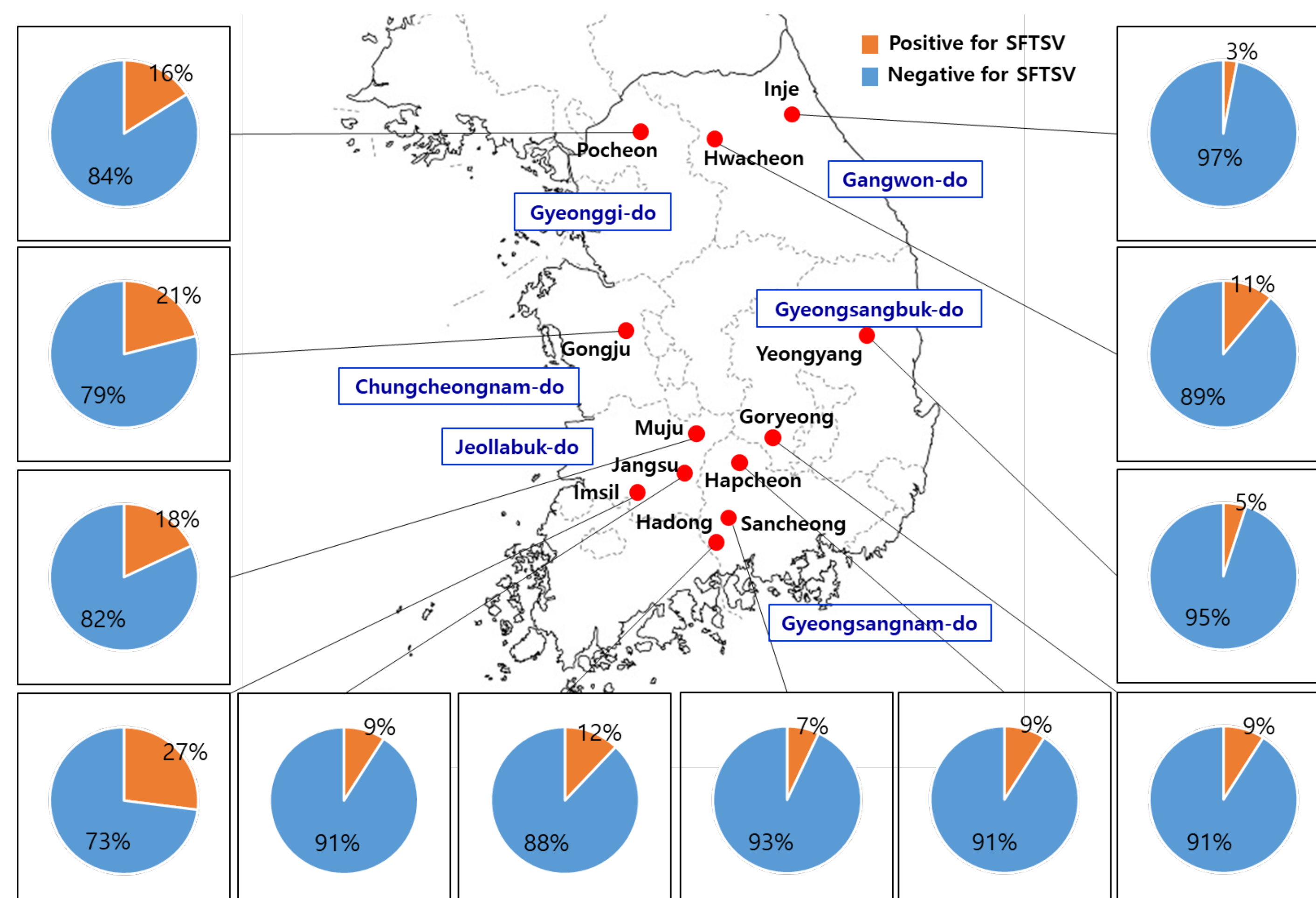


Fig. 4. Geographical map of SFTSV detection in ticks in the Republic of Korea. The number of SFTSV positive and negative at each site is shown. Blue words indicate provinces and black words and red indicate tick collection sites within a 1 km radius of bat habitats. One hundred ticks collected from each site were used in the experiment.

Conclusion: While molecular evidence of SFTSV infection was not observed in bats, a few serological positives suggest possible past exposure. The detection of SFTSV in ticks collected from bat habitats suggests potential ecological interactions involving bats, ticks, and other wildlife species. These findings highlight the importance of considering both wildlife reservoirs and the indirect role of bats in the geographical spread of SFTSV.