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Characterization and antimicrobial resistance of *Staphylococcus hyicus* from swine exudative epidermitis in South Korea

Chi Sun Yun[1], Su-Min Kang[1], Dong Hyeon Kwon[1], Sanghyub Lee[1], Gyu-Tae Jeon[1], Hye Jeong Kang[2], Jongho Kim[1], Jae-Won Byun[1], Bok-Kyung Ku[1], Mi-Hye Hwang[1] and Ha-Young Kim[1*]

Abstract

Background *Staphylococcus hyicus* causes porcine exudative epidermitis, predominantly affecting suckling and weaned piglets. This bacterium produces various exfoliative toxins (ExhA, ExhB, ExhC, ExhD, SHETA, and SHETB), which are responsible for the clinical manifestations of exudative epidermitis. However, treatment failure is common due to frequent antimicrobial resistance in porcine strains. Therefore, this study aimed to identify the genes encoding exfoliative toxins and assess the antimicrobial resistance profiles of *S. hyicus*. A total of 17 *S. hyicus* isolates were collected from piglets with skin lesions from 2014 to 2021. All strains were subjected to species-specific polymerase chain reaction targeting *sodA* to confirm the presence of *S. hyicus*, and polymerase chain reaction amplification of exfoliative toxin genes (*exhA*, *exhB*, *exhC*, *exhD*, *sheta*, and *shetb*) was performed to differentiate toxigenic strains. Pulsed-field gel electrophoresis analysis and minimum inhibitory concentration tests using broth microdilution were conducted to further analyze the strains.

Results Exfoliative toxin genes were detected in 52.9% ($n=9$) of the *S. hyicus* isolates, with notable detection of *exhB* (17.6%), *exhC* (17.6%), *exhD* (11.8%), *exhA* (5.9%), *sheta* (0%), and *shetb* (0%). Pulsed-field gel electrophoresis analysis categorized the isolates into 11 pulsotypes with 70% similarity. Among 18 tested antimicrobials, all isolates exhibited 100% susceptibility to ceftiofur and sulfonamides and high susceptibility rates to neomycin, tilmicosin, and tetracyclines. Whereas the susceptibility rate of spectinomycin was 0% in all isolates, multidrug resistance was observed in 82.4% of the isolates, and in all toxigenic strains.

Conclusions These findings provide crucial insights for monitoring and devising effective treatment strategies for managing exudative epidermitis in pigs caused by *S. hyicus*.

Keywords Antimicrobial resistance, Exfoliative toxin, Exudative epidermitis, *Staphylococcus hyicus*, Piglets

*Correspondence:
Ha-Young Kim
kimhy@korea.kr; jnm4jesus@naver.com
[1]Animal Disease Diagnostic Division, Animal and Plant Quarantine Agency, 177 Hyeoksin 8-ro, Gimcheon 39660, Republic of Korea
[2]Bacterial Disease Division, Animal and Plant Quarantine Agency, Gimcheon 39660, South Korea

Background

Staphylococcus hyicus is an important pathogen on swine farms worldwide because it causes exudative epidermitis (EE), also known as greasy pig disease, in young pigs [1]. EE is characterized by skin exfoliation with crusts, vesicles, and pustules, leading to considerable economic losses due to high morbidity and moderate mortality rates in pig-producing countries. It also causes significant discomfort and distress to the affected animals [2, 3]. Furthermore, *S. hyicus* is known to infect various animal species, including horses, goats, and cattle, and poses a zoonotic risk to humans [4–6].

S. hyicus can be classified into toxigenic and non-toxigenic strains based on their ability to cause EE in pigs, with specific virulence genes identified [7]. Exfoliative toxins (ExhA, ExhB, ExhC, ExhD, SHETA, and SHETB) are critical virulence factors of *S. hyicus*, inducing the characteristic symptoms of EE by cleaving the cell-to-cell adhesion of keratinocytes in the stratum granulosum of the superficial epidermis [3, 8]. While toxigenic strains of *S. hyicus* have been extensively examined due to their direct association with EE, non-toxigenic strains also play a significant role in the epidermitis that EE causes in piglets and should be considered in EE research [7, 9].

Research on the characteristics and antimicrobial resistance of *S. hyicus* isolated from EE is limited in Korea, as most studies are conducted locally [10–12]. *S. hyicus* infections are a major concern for pig breeders, and antimicrobial therapy is commonly employed during acute disease outbreaks due to the absence of a vaccine [13]. However, effective treatment is frequently hindered by the emergence of antimicrobial resistance among *S. hyicus* strains. Moreover, comprehensive data on resistance patterns in *S. hyicus* are lacking. Therefore, this study aimed to evaluate the pathological and molecular characteristics and antimicrobial resistance profiles of toxigenic and non-toxigenic strains of *S. hyicus* isolated from piglets exhibiting clinical signs of EE in South Korea.

Methods

Samples and bacterial isolation

Piglets with skin lesions were presented to the Animal and Plant Quarantine Agency of Korea for differential diagnosis between 2014 and 2021. The piglets' bodies were covered with a moist, greasy exudate, and some exhibited thick, crusty lesions either covering the entire body or appearing as discrete, circumscribed lesions that did not coalesce. After necropsy, bacterial cultures were performed on selected skin samples corresponding to the gross lesions in each case. The samples were inoculated on 5% sheep blood agar plates (Asan Pharm Co., Seoul, Republic of Korea), and incubated aerobically at 37 °C. The suspected *Staphylococcus* colonies were isolated and identified as *S. hyicus* by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS; VITEK® MS; bioMérieux, Marcy I'Etoile, France).

Polymerase chain reaction (PCR) assay for exfoliative toxin genes

Genomic DNA was extracted using the Maxwell® RSC PureFood GMO Kit (REF AS1600; Promega, Madison, WI, USA) following the manufacturer's instructions. Extracted DNA from *S. hyicus* isolates was subjected to species-specific PCR targeting the *sodA* (superoxide dismutase A encoding gene) to confirm *S. hyicus* identity [14]. The presence of exfoliative toxin genes (*exhA*, *exhB*, *exhC*, *exhD*, *sheta*, and *shetb*) in the genomes of the isolates was confirmed using previously published primers and protocols [15, 16].

Pulsed-field gel electrophoresis (PFGE)

Following the CDC PulseNet protocol [17], DNA from *S. hyicus* isolates was digested using the *Sma*I enzyme (Takara Bio Inc., Shiga, Japan). Electrophoresis was conducted using the CHEF-DR® III PFGE system (Bio-Rad Laboratories, Hercules, CA, USA), and PFGE banding profiles were analyzed using BioNumerics software version 8.0 (Applied Maths, Sint-Martens-Latem, Belgium). The Dice coefficient and unweighted pair group method with arithmetic mean were employed for analysis. Isolates exhibiting a coefficient of similarity of ≥70% were considered genetically closely related [18].

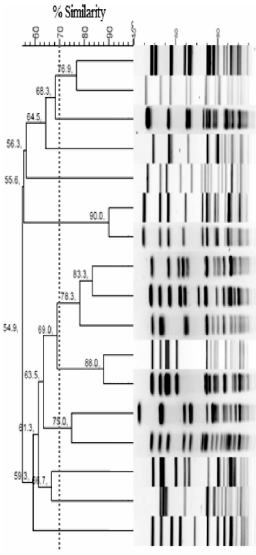
Antimicrobial susceptibility test

Minimum inhibitory concentrations (MICs) were determined using the standard micro broth dilution method, as recommended by the Clinical and Laboratory Standards Institute [19]. The Sensititre Standard Susceptibility MIC Plates BOPO6F panel (Trek Diagnostic Systems, Cleveland, OH, USA), which contains 18 antimicrobials, was used according to the manufacturer's instructions. *Staphylococcus aureus* (ATCC 25923) served as the quality control strain. Multidrug resistance (MDR) was defined as resistance to three or more antimicrobial subclasses.

Results

Detection of exfoliative toxin genes from *Staphylococcus hyicus*

A total of 17 *S. hyicus* isolates were obtained from different farms, with their clinical descriptions summarized in Fig. 1. All piglets were suckling ($n=8$) or weaned ($n=9$) and exhibited systemic atrophy and skin lesions, including erythema, skin thickening, and crust formation. Most cases demonstrated the following histological lesions, except for two cases with no records: hyperkeratosis and/



TOXIN GENE	YEAR	SEASON	REGION	AGE	CO-INFECTION	CR/HK/HP	ERO/ULC	PN-epi	PN-dermis	Antimicrobial Resistance Pattern	MDR
Non	2014	Fall	Central	Wean	PRRSV	+++	+++	+++	++	PEN-DAN/ENO-GEN/NEO-CLI-FFL-TYLT/TUL	6
exhD	2017	Fall	Nothern	Wean	None	++	++	+++	++	PEN-DAN/ENO-GEN-CLI-TYLT/TUL	5
exhD	2021	Fall	Central	Wean	None	+++	-	+++	+	PEN-DAN/ENO-GEN/SPE-CLI-TYLT/TUL-TIA	6
exhA	2016	Winter	Central	Wean	PRRSV/PCV2	NT	NT	NT	NT	SPE-CTC/OTC-CLI-TIL/TYLT/TUL-TIA	5
exhC	2018	Spring	Central	Suck	None	+++	++	+++	++	PEN-DAN/ENO-GEN/NEO/SPE-CLI-FFL-TIL/TYLT/TUL	6
Non	2018	Spring	Southern	Suck	PRRSV	+++	+	++	-	PEN-DAN/ENO-CTC/OTC-CLI-TIL/TYLT/TUL	5
Non	2021	Fall	Central	Wean	None	+	+	+	+	PEN-SPE-CTC/OTC-CLI-FFL-TIL/TYLT/TUL-TIA	7
exhC	2019	Spring	Central	Suck	None	++	+	+++	+	AMP/PEN-SPE-CLI-TIA	4
Non	2020	Fall	Central	Suck	None	+++	++	+++	-	PEN	1
exhB	2019	Spring	Central	Suck	None	++	-	++	-	DAN/ENO-GEN/SPE-CLI-FFL-TYLT/TUL-TIA	6
Non	2019	Winter	Central	Wean	None	+++	++	+++	+	PEN-FFL	2
Non	2019	Spring	Southern	Suck	None	++	+	++	+	PEN-FFL	2
exhB	2019	Spring	Central	Suck	None	NT	NT	NT	NT	DAN/ENO-GEN/NEO/SPE-CTC/OTC-CLI-FFL-TYLT/TUL-TIA	7
exhB	2020	Spring	Central	Wean	PRRSV	+++	+	++	+	PEN-DAN/ENO-SPE-CLI-FFL-TYLT/TUL-TIA	7
exhC	2015	Spring	Central	Suck	None	+++	++	++	+	AMP/PEN-DAN/ENO-GEN/NEO-CLI-FFL-TYLT/TUL	6
Non	2016	Fall	Central	Wean	PRRSV/PCV2/HPS/SS/PM	+	++	++	+	PEN-DAN/ENO-GEN/SPE-CTC/OTC-CLI-FFL-TYLT/TUL-TIA	8
Non	2017	Winter	Nothern	Wean	SS	++	+	+++	++	PEN-DAN/ENO-GEN/NEO/SPE-CTC/OTC-CLI-TIL/TYLT/TUL-TIA	7

Fig. 1 Dendrogram showing the relationship among 17 *Staphylococcus hyicus* pulsotypes, exfoliative toxin gene detection, pathologic features, and antimicrobial resistance profiles

or epithelial hyperplasia (n=15), erosion and/or ulceration in the epidermis (n=13), pyonecrotic epidermitis (n=15), and/or dermatitis (n=12). Additionally, one suckling piglet (12.5%) and five weaned piglets (55.6%) were co-infected with other viral or bacterial pathogens, including porcine reproductive and respiratory syndrome virus, porcine circovirus 2, *Streptococcus suis*, *Glaesserella parasuis*, and *Pasteurella multocida*. Overall, 9 of the 17 isolates (52.9%) were identified as toxigenic strains. The highest frequencies were for *exhB* (n=3) and *exhC* (n=3) at 17.6% each, followed by for *exhD* (11.8%, n=2) and *exhA* (5.9%, n=1), with neither *sheta* nor *shetb* detected. Toxigenic strains were predominantly found in the central region (n=8/9) and during spring (n=6/9), with no difference between suckling (n=5) and weaned (n=4) piglets (Fig. 1).

PFGE analysis of *Staphylococcus hyicus*

All isolates were categorized into 11 pulsotypes with 70% similarity. The dendrogram revealed no cluster formation based on toxin gene presence, years of isolation, season, region, age, or antimicrobial resistance patterns (Fig. 1).

Antimicrobial susceptibility of *Staphylococcus hyicus*

Table 1 describes the antimicrobial resistance and cumulative percentages of *S. hyicus* isolates, including nine toxigenic and eight non-toxigenic strains. All isolates were 100% susceptible to ceftiofur and sulfonamides, while neomycin (70.6%), tilmicosin (70.6%), and tetracyclines (64.7%) showed relatively high susceptibility rates. Conversely, susceptibility rates for spectinomycin (0%), clindamycin (17.6%), penicillin (17.6%), ampicillin (23.5%), florfenicol (23.5%), tylosin (23.5%), tulathromycin (23.5%), and fluoroquinolones (29.4%) were relatively low. Resistance to ampicillin, fluoroquinolones, aminoglycosides, clindamycin, tylosin tartrate, tulathromycin, and tiamulin was higher in toxigenic strains than in non-toxigenic strains, whereas resistance to penicillin, tetracyclines, and tilmicosin was higher in non-toxigenic strains. The prevalence of MDR was very high at 82.4%, excluding three non-toxigenic strains (Fig. 1). Additionally, toxigenic strains were all resistant to clindamycin and exhibited 100% MDR, whereas non-toxigenic strains were all resistant to penicillin.

Discussion

S. hyicus has been globally recognized as the causative pathogen of EE in pigs for over 180 years, establishing it as a significant staphylococcal skin disease. Clinical manifestations are most severe in piglets aged 3–32 days, often leading to dehydration and potential mortality [20, 21]. While extensive research has been conducted on staphylococcal-induced EE [22–26], studies specifically targeting *S. hyicus* remains sparse, both nationally and globally.

In this study, we investigated the exfoliative toxins produced by *S. hyicus* isolated from pigs with EE. Prior studies in South Korea have documented swine EE and associated mortality caused by *S. hyicus* on farms in the Gyeongsang [10], Chungcheong [27], and Jeolla provinces [12], with exacerbation of some cases due to concurrent viral infections. However, in-depth studies of the exfoliative toxins produced by *S. hyicus* are limited. These toxins are key virulence factors of *S. hyicus*, and ExhA, ExhB, ExhC, ExhD, SHETA, and SHETB toxins facilitate skin exfoliation in pigs [3, 15, 16]. All variants of these

Table 1 Antimicrobial resistance and cumulative percentage of *Staphylococcus hyicus* isolates in piglets with exudative epidermitis

Antimicrobial class or subclass	Antimicrobials	Cumulative percentage of strains inhibited at antimicrobial concentration (μg/ml)												MIC_{50} (μg/mL)[a]	MIC_{90} (μg/mL)[a]	S (%)[b]	I (%) [b]	*R* (%) [b]	MIC breakpoint (μg/mL)[c]
		≤ 0.12	0.25	0.5	1	2	4	8	16	32	64	128	256						
Penicillinase-labile penicillins	Ampicillin		23.5	88.2	100									0.5	1	23.5	64.7	11.8	≥ 1
	Penicillin	17.6	23.5	35.3	64.7	94.1	100							1	2	17.6	ND [d]	82.4	≥ 0.25
Cephalosporin III	Ceftiofur				94.1	100								1	1	100	ND [d]	0	≥ 8
Fluoroquinolone	Danofloxacin	17.6	29.4	35.3	100									1	1	29.4	5.9	64.7	≥ 1
	Enrofloxacin	29.4			35.3		100							4	4	29.4	5.9	64.7	≥ 4
Aminoglycosides	Gentamicin				41.2		47.1	64.7	100					8	16	47.1	17.6	35.3	≥ 16
	Neomycin						35.3	70.6	88.2	100				8	32	70.6	ND [d]	29.4	≥ 16
	Spectinomycin										41.2	100		128	128	0	41.2	58.8	≥ 128
Tetracyclines	Oxytetracycline			64.7				100						0.5	8	64.7	ND [d]	35.3	≥ 2
	Chlortetracycline			64.7				100						0.5	8	64.7	ND [d]	35.3	≥ 2
Lincosamides	Clindamycin		17.6					23.5	100					16	16	17.6	ND [d]	82.4	≥ 4
Phenicols	Florfenicol					23.5	41.2	100						8	8	23.5	17.6	58.8	≥ 8
Macrolides	Tilmicosin						35.3	64.7	70.6		100			8	64	70.6	ND [d]	29.4	≥ 32
	Tylosin				23.5					100				32	32	23.5	ND [d]	76.5	≥ 4
	Tulathromycin					23.5					100			64	64	23.5	ND [d]	76.5	≥ 64
Sulfonamides	Sulfadimethoxine												100	256	256	100	ND [d]	0	≥ 512
	Trimethoprim/Sulfamethoxazole					100								2	2	100	ND [d]	0	≥ 4/76
Pleuromutilins	Tiamulin			41.2				47.1		100				32	32	47.1	ND [d]	52.9	≥ 32

n = 17 (piglets with exudative epidermitis)

The gray zone represents the tested concentration range for each antimicrobial on the BOPO6F plate

a. MIC_{50} and MIC_{90} concentrations at which isolate growth was inhibited by 50% and 90%, respectively

b. S, susceptible; I, intermediate; R, resistant

c. MIC breakpoints of 18 antimicrobials are indicated as vertical double lines according to CLSI guidelines (2018), except for neomycin, which follows the recommendations from a previous study (Moreno et al., 2023)

d. ND, not determined

Susceptibility and resistance are indicated by vertical double (sensitive) lines based on the reference guidelines for each antimicrobial

exfoliative toxins induce blister formation in porcine skin by cleaving desmoglein-1, though human desmoglein-1 is resistant to these toxins [3, 8]. Although toxigenic strains of *S. hyicus* have been isolated from both healthy and diseased pigs, the isolation rate is higher in pigs affected by EE than in healthy pigs [16, 22, 28]. In this study, 52.9% of the isolates were identified as toxigenic, consistent with the findings of Andresen et al. [22], who reported that 47.1–66.7% of *S. hyicus* strains isolated from pigs with EE appeared toxigenic. However, these findings contrast with those of Russian [29] and Brazilian [18] studies which reported that approximately 90% of isolates are toxigenic. The highest detection rates in this study were for *exhB* and *exhC* (17.6% each), followed by for *exhD* (11.8%) and *exhA* (5.9%). Although the number of isolates was insufficient for a robust comparison with other studies, previous research has shown variable detection rates of exfoliative toxins; for instance, 18–22% with the highest rate for *exhB* was observed in Denmark [30], 0.7–48.9% with the highest rate for *exhA* in Japan [28], 24.4–76.1% with the highest rate for *exhC* in Brazil [18], and 89.5% with the highest detection rate for *exhD* in Russia [29]. Additionally, studies within the same country have shown temporal changes in the distribution of toxin genes, such as a decrease in the prevalence of *exhB* [15, 18]. Therefore, distribution of exfoliative toxins and prevalence of toxigenic strains reported in the literature vary according to different countries and study periods.

Both toxigenic and nontoxigenic strains of *S. hyicus* have been reported to induce hyperkeratosis and inflammatory cell hyperplasia of the epidermis in pigs [7, 9, 31]. Consistent with this, our findings showed no correlation between the presence or type of exfoliative toxins and clinicopathological presentation of skin lesions. For instance, 47.1% of the *S. hyicus* isolates were identified as non-toxigenic strains, yet al.l were isolated from skin displaying mild-to-severe pathological lesions of EE. The absence of toxins in the isolates even in cases with severe skin lesions suggests the involvement of other virulence factors in EE, necessitating further research utilizing whole-genome sequencing to identify potential virulence determinants beyond exfoliative toxins involved in EE in pigs. Additional predisposing factors that may contribute to *S. hyicus* colonization and virulence in pigs include viral diseases, nutritional deficiencies, dermatophytosis, pityriasis rosea, parasitism, poor hygiene, inadequate ventilation, high humidity, trauma, and genetic predisposition [20].

The current study demonstrated a high diversity of both toxigenic and non-toxigenic *S. hyicus* strains in South Korea, irrespective of the year of isolation, season, region, age, or antimicrobial resistance pattern. Consistent with our finding, previous studies have reported significant diversity in the PFGE patterns of *S. hyicus* strains isolated from pigs [18, 31–33], with no clustering based on toxigenic strains or resistance profiles. Furthermore, various PFGE patterns have been identified on the same farm [32]. PFGE analysis of *S. hyicus* strains isolated from other animal species has shown diverse patterns and high variability in chickens and bovine milk [32, 34]. Given these studies, the high diversity observed in the PFGE results of this study appears to be inherent to the characteristics of *S. hyicus*. Therefore, PFGE results have limitations in cross-national comparative analyses for epidemiological research, necessitating the application of other molecular analysis techniques.

Antimicrobial susceptibility testing revealed that all *S. hyicus* isolates were 100% susceptible to ceftiofur and sulfonamides. However, the isolates demonstrated low susceptibility to penicillins (17.6–23.5%) and fluoroquinolones (29.4%). Among the macrolides, resistance to tilmicosin was 29.4%, while resistance to tylosin and tulathromycin was 76.5%. Consistent with our findings, other studies have shown low resistance rates to ceftiofur (0–0.97%) and sulfadimethoxine (1.9–5.2%) in Brazil and trimethoprim/sulfamethoxazole (9.7–25.8%) in Brazil and Japan among *S. hyicus* isolates from porcine EE [18, 28]. Despite the low resistance to ceftiofur, third-generation cephalosporins are classified as highest priority critically important antimicrobials (HPCIA) for humans and veterinary critically important antimicrobials (VCIA) for animals, according to the WHO (in 2024) [35] and WOAH (in 2021), respectively [36]. Fluoroquinolones are also classified into the HPCIA and VCIA categories. However, our results indicated a higher fluoroquinolone resistance rate at 64.7% compared to 0–13.2% in European countries, except for that reported by one Brazilian study [13, 18, 37]. Thus, there is an urgent need to address the high rate of fluoroquinolone resistance. Penicillin resistance rates vary widely across different countries and study periods, including 25.0% in Germany and 76.8% in Japan, and even fluctuate within the same country over time [13, 18, 28, 37]. However, a direct comparison of the MDR results obtained in this study with those reported by previous Korean studies poses challenges due to differing antimicrobials and testing methods used, even though a previous Korean report indicated a 12.6% MDR rate [10]. Furthermore, MDR has been observed to increase over time [18] and is predominant in toxigenic strains [28]. Consistent with this, 82.4% of isolates were MDR, with 76.5% ($n=13$) resistant to five or more antimicrobial subclasses, and all toxigenic strains were 100% MDR. These findings showed that *S. hyicus* isolates from EE exhibited increased resistance to most antimicrobials, which was unlike the findings of previous studies. Ensuring that bacteria do not develop resistance to antimicrobials is crucial for both animal and human health. Therefore, it is essential to confirm diagnoses using

susceptibility tests rather than base diagnoses on clinical symptoms alone to select appropriate antimicrobials [20]. Likewise, developing a vaccine against *S. hyicus* should also be considered, as autogenous vaccines using strains isolated from affected herds have reduced metaphylactic antimicrobial treatment and lowered morbidity and mortality rates in weaned pigs [20, 38].

Despite pigs developing disease resistance with age, *S. hyicus* can still be recovered from older pigs' skin, and these asymptomatic carriers can contaminate naïve herds [39]. Research has shown that suckling piglets are primarily infected by dams, some of whom are vaginally infected at birth [20]. Moreover, *S. hyicus* has been isolated from healthy pigs. However, this study included limited samples for the differential diagnosis of piglets with skin lesions. Therefore, further studies are warranted to determine the overall distribution of *S. hyicus* based on clinical manifestations, age groups, and pig farm environments in South Korea.

Conclusion

This study analyzed the pathological findings, toxin types, and antimicrobial resistance of *S. hyicus* isolated from EE lesions from affected pigs in the Republic of Korea. All exfoliative toxins (ExhA, ExhB, ExhC, and ExhD) were detected, except for *sheta* and *shetb*. Ceftiofur and sulfonamides exhibited 100% antimicrobial susceptibility. Additionally, most *S. hyicus* isolates were found to be MDR. Thus, our study showed that selecting effective antimicrobials is crucial for enhancing treatment efficiency and preventing antimicrobial resistance. Owing to the limited number of samples available for disease diagnosis, further nationwide prevalence studies are necessary, regardless of clinical symptoms.

The results were calculated using the Dice coefficient and the unweighted pair group method with arithmetic averages (UPGMA), shown with a similarity greater than 70%. Seasonal divisions: Spring, March-May; Summer, June-August; Fall, September-November; Winter, December-February. Regional divisions: Northern, Gyeonggi and Gangwon; Central, Chungbuk, Chungnam, Gyeongbuk, and Jeonbuk; Southern, Jeonnam and Gyeongnam. Age categories: Wean: Weaned piglets (25–70 days old); Suck: Suckling piglets (1–24 days old). Co-infections: PRRSV: Porcine reproductive and respiratory syndrome virus; PCV2: Porcine circovirus type2; SS: *Streptococcus suis*; HPS: *Haemophilus parasuis*; PM: *Pasteurella multocida*. Pathological features: CR/HK/HP: Crust, Hyperkeratosis, or Hyperplasia in the epidermis; ERO/ULC: Erosion or Ulceration; PN-epi: Pyonecrotic epidermatitis; PN-dermis: Pyonecrotic dermatitis. Severity indicator: +++, severe; ++, moderate; +, weak; -, no histological lesion; NT, not tested. Anitmicrobial resistance profile: AMP, ampicillin; PEN, penicillin; XNL, ceftiofur; DAN, danofloxacin; ENO, enrofloxacin; GEN, gentamicin; NEO, neomycin; SPE, spectinomycin; CTC, chlortetracycline; OTC, oxytetracycline; CLI, clindamycin; FFL, florfenicol; TIL, tilmicosin; TYLT, tylosin tartrate; TUL, tulathromycin; SDM, sulfadimethoxine; SXT, trimethoprim/sulfamethoxazole; TIA, tiamulin; MDR, multidrug resistance.

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Author contributions
Conceptualization: Kim HY, Yun CS Data curation: Kim HY, Yun CS Formal analysis: Yun CS, Kang SM Methodology: Kim HY, Hwang MH Software: Yun CS Validation: Kim HY, Byun JW, Ku BK Investigation: Kwon DH, Lee S, Jeon GT, Kang HJ, Kim J Writing - original draft: Yun CS, Kang SM, Kwon DH, Lee S, Jeon GT, Kang HJ, Kim J Writing - review & editing: Kim HY, Hwang MH, Byun JW, Ku BK.

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Data availability
Upon reasonable request, the datasets of this study can be made available by the corresponding author.

Declarations

Ethics approval and consent to participate
This study did not require ethics approval because the piglets' bodies were submitted to the Animal and Plant Quarantine Agency for diagnosis by veterinarians and animal owners with their consent.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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