JAST (Journal of Animal Science and Technology) TITLE PAGE

Upload this completed form to website with submission

ARTICLE INFORMATION	Fill in information in each box below
Article Type	Short communications
Article Title (within 20 words without abbreviations)	Nationwide patterns of PRRSV detection, seasonality, and PRRSV-PCV2 co-detection in pigs with respiratory symptoms in the Republic of Korea, 2022-2024
Running Title (within 10 words)	PRRSV epidemiology and PCV2 co-detection in the Republic of Korea
Author	Bog-hwa Kim[1,2], Doo-Sung Cheon[3], Eunjin Cho[1], Su-Jin Park[4], and Jun Heon Lee[1 *]
Affiliation	[1] Department of Animal Science and Biotechnology, Chungnam National University, 34134, Republic of Korea [2] Veterinary Diagnostic Center, Harim Bio Research Center (Jeil Feed Co., Ltd.), Republic of Korea [3] POSTBIO Inc., Namyangju 12106, Republic of Korea [4] Department of Animal Health and Welfare, College of Biohealth Sciences, Hoseo University, 20 Hoseo-ro, 79Bun-gil, Baebang-eup, Asan, Chungnam, 31499, Republic of Korea
ORCID (for more information, please visit https://orcid.org)	Bog-Hwa Kim (https://orcid.org/0009-0007-7774-6766) Doo-Sung Cheon (https://orcid.org/0000-0003-3306-9875) Eunjin Cho (https://orcid.org/0000-0003-4800-1603) Su-Jin Park (https://orcid.org/0000-0001-7299-8480) Jun Heon Lee (https://orcid.org/0000-0003-3996-9209)
Competing interests	The authors declare that they have no competing interests.
Funding sources State funding sources (grants, funding sources, equipment, and supplies). Include name and number of grant if available.	This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.
Acknowledgements	Not applicable.
Availability of data and material	The datasets generated and analyzed during the current study are not publicly available due to the confidentiality of farm-level diagnostic information but are available from the corresponding author on reasonable request.
Authors' contributions Please specify the authors' role using this form.	Authors' contributions Conceptualization: Lee JH, Kim BH, Cheon DS Data curation: Kim BH Formal analysis: Kim BH Methodology: Kim BH Software: Kim BH Validation: Lee JH, Kim BH, Cho E, Park SJ Investigation: Kim BH Writing - original draft: Kim BH Writing - review & editing: Lee JH, Kim BH, Cheon DS, Cho E, Park SJ.
Ethics approval and consent to participate	This study used post-mortem samples collected from pigs submitted for routine diagnostic testing. Therefore, approval from an Institutional Animal Care and Use Committee (IACUC) was not required. All procedures were conducted in accordance with relevant institutional and national guidelines for diagnostic services.

CORRESPONDING AUTHOR CONTACT INFORMATION

For the corresponding author (responsible for correspondence, proofreading, and reprints)	Fill in information in each box below
First name, middle initial, last name	Jun Heon Lee
Email address – this is where your proofs will be sent	junheon@cnu.ac.kr
Secondary Email address	
Address	Department of Animal Science and Biotechnology, Chungnam National University, Daejeon 34134, Republic of Korea
Cell phone number	+82-10-5172-0816
Office phone number	+82-42-821-5779
Fax number	+82-42-825-9754

Abstract

Porcine reproductive and respiratory syndrome virus (PRRSV) remains a major viral pathogen associated with respiratory symptoms in swine production systems. This study investigated nationwide patterns of PRRSV detection, seasonal variation, and co-detection with porcine circovirus type 2 (PCV2) using lung samples obtained from pigs with respiratory symptoms in the Republic of Korea from 2022 to and 2024. A total of 2,476 samples were analyzed using real-time reverse transcription–polymerase chain reaction, and 62.4% were found to be positive for PRRSV. The annual positivity rate increased from 59.7% in 2022 and 59.8% in 2023 to 67.8% in 2024. Among all samples, 38.0% were positive for PCV2, with positivity rates increasing from 28.4% in 2022 to 48.7% in 2024. PRRSV-2 was consistently the predominant genotype, whereas PRRSV-1 and co-detection infections were detected at lower frequencies. Marked seasonal variation was observed, with higher detection rates in autumn and winter than in summer. In addition, PRRSV positivity was significantly higher in PCV2-positive samples than in PCV2-negative samples, indicating frequent co-detection under field conditions. Multivariate logistic regression analysis identified season, PCV2 detection, and year as significant factors associated with PRRSV detection. These findings demonstrate that PRRSV remains widely prevalent in Korean swine farms, with clear seasonal patterns and frequent co-detection with PCV2, highlighting the importance of integrated respiratory symptoms management strategies.

Keywords: porcine reproductive and respiratory syndrome virus, porcine circovirus type 2, swine, epidemiology, seasonality

Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) is a major viral pathogen in the global swine industry, causing reproductive failure in breeding herds and respiratory symptoms in growing pigs. In growing pigs, PRRSV is a key component of porcine respiratory disease complex (PRDC), a

multifactorial condition involving interactions among viral and bacterial pathogens that increase disease severity and economic losses [1–4].

PRRSV is characterized by high genetic variability driven by mutation and recombination, resulting in substantial viral diversity within swine populations [5]. Two major genotypes, PRRSV-1 (European type) and PRRSV-2 (North American type), co-circulate in many regions. PRRSV-1 and PRRSV-2 differ genetically and antigenically and may vary in their epidemiological characteristics and pathogenicity [4,5]. Consequently, distinguishing between the two genotypes is important for surveillance and disease control programs. In the Republic of Korea, both genotypes have been detected for decades, with PRRSV-2 generally predominating in commercial production systems [11,13]. The continued detection of multiple genotypes indicates long-term endemic circulation and ongoing viral evolution under field conditions.

Environmental and management-related factors are also important in PRRSV transmission dynamics. Previous studies have reported increased PRRSV detection during colder seasons, suggesting that seasonal conditions may influence viral stability and transmission in intensive production systems [9,10]. In addition, farm density, pig movement networks, and farm-level biosecurity practices have been identified as important determinants of PRRSV transmission and regional disease dissemination [10,20].

Porcine circovirus type 2 (PCV2) is another major pathogen associated with PRDC and is frequently detected together with PRRSV in pigs with respiratory symptoms [3,4,6,7]. Concurrent detection of PRRSV and PCV2 has been associated with increased disease severity, altered immune responses, and aggravated respiratory lesions in both experimental and field studies [6–8]. Despite widespread vaccination, the continued co-detection of PRRSV and PCV2 highlights the complexity of porcine respiratory disease complex (PRDC), in which multiple pathogens may interact and contribute to disease occurrence under field conditions.

Previous studies on PRRSV in Korea have primarily focused on genotype distribution or region-specific epidemiology. However, nationwide epidemiological studies evaluating seasonal variation in PRRSV detection and its co-detection with PCV2 using routine diagnostic data remain limited. In particular, updated field-based evidence reflecting recent epidemiological changes is still lacking.

Therefore, the present study aimed to investigate nationwide patterns of PRRSV detection, seasonal variation, and PRRSV–PCV2 co-detection using lung samples obtained from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024. The analysis of a large-scale retrospective diagnostic dataset in this study provides updated epidemiological insights into PRRSV-associated respiratory symptoms under field conditions.

Materials and Methods

Sample collection and study design

This retrospective study analyzed lung samples collected from pigs with respiratory symptoms that were submitted for routine diagnostic testing in the Republic of Korea from January 2022 to December 2024. Samples were obtained from commercial swine farms across multiple regions through veterinary diagnostic services. Because samples were submitted for diagnostic testing from pigs with clinical respiratory signs, the dataset should not be considered representative of the general swine population. Instead, it reflects field cases of respiratory symptoms identified under commercial production conditions.

This study used post-mortem lung samples collected from pigs submitted for routine diagnostic testing. Therefore, approval from an Institutional Animal Care and Use Committee (IACUC) was not required. All procedures were conducted in accordance with relevant institutional and national guidelines for diagnostic services.

Only lung tissue samples were included to specifically evaluate respiratory-associated PRRSV detection under field conditions. A total of 2,476 lung samples collected from 2022 to 2024 were analyzed. Samples were submitted from commercial swine farms across multiple regions of the Republic of Korea, providing broad geographic coverage of routine diagnostic cases. Detailed characteristics of the study samples are summarized in Table 1.

Available metadata for each sample, including year of submission, month, province, farm size, production stage, and PCV2 detection, were retrospectively extracted from diagnostic submission records

maintained by the Veterinary Diagnostic Center, Harim Bio Research Center (Jeil Feed Co., Ltd., Republic of Korea). Farm size was classified according to total herd size as small (≤1,000 pigs), medium (1,001–2,999 pigs), and large (≥3,000 pigs). Multiple samples from the same farm may have been included; however, farm-level clustering was not accounted for in the analysis.

Viral nucleic acid extraction and real-time reverse transcription–polymerase chain reaction detection

Total nucleic acids were extracted from lung tissues using an automated extraction system (NPA-32P; BIOMAX, Guri, Republic of Korea) according to the manufacturer's instructions. All samples were processed within 24 h of arrival at the laboratory.

The detection of PRRSV and PCV2 was performed using commercial real-time reverse transcription–polymerase chain reaction(PCR) assays (PostBio, Guri, Republic of Korea). Specifically, two separate assays were utilized for individual samples: a multiplex assay targeting both PRRSV-1 and PRRSV-2, and a singleplex assay targeting PCV2.

Amplification was carried out using a CFX Opus 96 Real-Time PCR System (Bio-Rad, Hercules, CA, USA). For PRRSV detection, the reaction conditions consisted of reverse transcription at 50°C for 15 min and initial denaturation at 95°C for 5 min, followed by 40 cycles of amplification at 95°C for 10 s and 60°C for 30 s. For PCV2 detection, PCR amplification was performed under identical cycling conditions, but with the omission of the 15-min reverse transcription step at 50°C.

Samples with cycle threshold (Ct) values < 35 were considered positive according to the manufacturer's recommended criteria. PRRSV-positive samples were further classified as PRRSV-1, PRRSV-2, or co-detection based on the amplification profiles. co-detection was defined as the simultaneous detection of both PRRSV-1 and PRRSV-2 targets within a single sample.

Statistical analysis

Descriptive analyses were performed to summarize PRRSV detection according to year, season, region, genotype, and PCV2 detection. Differences in PRRSV positivity across categorical variables were evaluated using chi-square tests.

Multivariate logistic regression analysis was conducted to identify factors associated with PRRSV positivity. PRRSV detection (positive/negative) was used as the dependent variable, and year, season, and PCV2 detection were included as independent variables. The reference categories were defined as 2022 for year, summer for season, and PCV2-negative samples for PCV2 detection.

Multicollinearity among candidate explanatory variables was assessed using the variance inflation factor (VIF). Variables with VIF values greater than 5 were considered to exhibit substantial multicollinearity and were excluded from the final multivariable logistic regression model. Other variables were also excluded because of incomplete data.

Odds ratios (ORs) and 95% confidence intervals (CIs) were calculated to estimate the strength of associations. Statistical significance was defined as $p < 0.05$. All analyses were performed using Python (Python Software Foundation, Wilmington, DE, USA).

Results

Overall PRRSV detection and genotype distribution

A total of 2,476 lung samples collected from pigs with respiratory symptoms from 2022 to 2024 were analyzed. Among these, 1,546 samples (62.4%) were positive for PRRSV.

Annual PRRSV positivity rates were 59.7% (463/776) in 2022, 59.8% (520/870) in 2023, and 67.8% (563/830) in 2024, showing a significant difference between years ($p = 0.0004$; Table 2, Fig. 1A).

PRRSV-2 was the predominant genotype throughout the study period, whereas PRRSV-1 and co-detection were observed at lower frequencies (Fig. 1B).

PCV2 detection

Among the 2,476 lung samples analyzed, 940 (38.0%) were positive for PCV2. Annual PCV2 positivity rates increased over the study period, from 28.4% (220/776) in 2022 and 36.3% (316/870) in 2023 to 48.7% (404/830) in 2024. PCV2 was consistently detected throughout the study period and represented a substantial proportion of respiratory disease cases submitted for routine diagnostic investigation. The annual distributions of PRRSV and PCV2 detection are summarized in Table 3.

Seasonal patterns of PRRSV detection

Monthly variation in PRRSV positivity was observed across the study period (Fig. 3A). Seasonal analysis showed significant differences between seasons ($p < 0.001$; Table 2, Fig. 3B).

PRRSV positivity rates were 53.1% in spring, 56.2% in summer, 68.0% in autumn, and 69.6% in winter. Detection was higher in autumn and winter than in summer.

Regional distribution of PRRSV detection

PRRSV positivity varied substantially across provinces (Table 2, Fig. 4). Relatively higher PRRSV positivity rates were observed in Chungnam, Gyeonggi, and Jeonbuk provinces. To ensure data reliability and avoid unstable estimates from extremely small sample sizes, provinces with fewer than five samples were excluded from the spatial visualization and regional comparison analyses.

PRRSV–PCV2 co-detection

Concurrent detection of PRRSV and PCV2 was frequently observed in lung samples from pigs with respiratory disease. Overall, 647 samples were positive for both PRRSV and PCV2, representing 41.8% of all PRRSV-positive samples. The proportion of PRRSV-positive samples with co-detected PCV2 increased from 30.2% in 2022 to 52.8% in 2024 (Fig. 2A).

PRRSV positivity was significantly higher in PCV2-positive samples than in PCV2-negative samples (68.8% vs. 58.5%, $p < 0.001$; Table 2, Fig. 2B).

To further characterize the epidemiological distribution of PRRSV–PCV2 co-detection, additional seasonal and regional analyses were performed. Co-detection rates were 21.5% in spring, 21.1% in summer, 30.9% in autumn, and 29.0% in winter, indicating that concurrent detection occurred more frequently during autumn and winter. Regionally, higher co-detection rates were observed in Chungnam, Gyeonggi, and Jeonbuk, whereas relatively lower rates were identified in the remaining provinces. Overall, the seasonal and regional distribution of PRRSV–PCV2 co-detection generally paralleled the overall distribution of PRRSV positivity.

Multivariate logistic regression analysis

Multivariate logistic regression analysis identified year, season, and PCV2 detection as significant factors associated with PRRSV positivity (Table 4, Fig. 5).

Compared with the reference categories, the odds of PRRSV positivity were significantly higher in 2024. Seasonal effects were also evident, with higher odds observed in winter (OR = 1.78, 95% CI = 1.39–2.28) and autumn (OR = 1.61, 95% CI = 1.26–2.05) than in summer. In addition, PCV2-positive samples had higher odds of PRRSV detection than PCV2-negative samples (OR = 1.45, 95% CI = 1.21–1.73).

Discussion

PRRSV was detected in 62.4% of lung samples collected from pigs with respiratory symptoms in the Republic of Korea between 2022 and 2024, confirming that PRRSV remains widely distributed in commercial swine production systems. Detection rates increased significantly in 2024, and PRRSV-2 remained the predominant genotype throughout the study period. In addition, clear seasonal variation was observed, with higher positivity during autumn and winter, while frequent PRRSV–PCV2 co-detection was identified among diagnostic submissions. Together, these findings indicate that PRRSV continues to represent a major component of porcine respiratory disease complex (PRDC) under contemporary field

conditions in Korea and emphasize the need for continuous epidemiological surveillance and integrated respiratory disease control strategies [1–4].

The overall PRRSV detection rate observed in the present study is consistent with previous reports describing the long-term endemic circulation of PRRSV in Korean swine populations. Both PRRSV-1 and PRRSV-2 have co-circulated in Korea for several decades, although PRRSV-2 has consistently predominated in commercial pig production systems [13]. Recent nationwide molecular surveillance has also demonstrated the continued circulation of both genotypes together with the emergence of highly pathogenic PRRSV-2 variants, indicating that the epidemiological landscape of PRRSV in Korea remains dynamic rather than static [14]. The predominance of PRRSV-2 observed in the present dataset therefore appears to represent a continuation of the established epidemiological pattern rather than a recent genotype replacement.

Although PRRSV-2 accounted for most positive cases, the continued detection of PRRSV-1 and concurrent detection of both genotypes remains epidemiologically important. PRRSV possesses one of the highest evolutionary rates among RNA viruses because of its error-prone RNA-dependent RNA polymerase and frequent recombination events, resulting in substantial genetic diversity and continuous viral evolution [5,11]. The simultaneous circulation of multiple genotypes within intensive production systems increases opportunities for viral diversification and the emergence of novel variants with altered pathogenicity or antigenicity. Although lineage classification and recombination analyses were beyond the scope of the present study, the continued detection of both PRRSV genotypes highlights the importance of maintaining molecular surveillance to monitor future evolutionary changes in circulating field strains.

The findings of the present study are broadly consistent with recent epidemiological reports from other Asian countries, where PRRSV continues to evolve through the emergence of genetically diverse lineages[15,16]. In China, multiple studies have documented the widespread circulation of NADC30-like and NADC34-like PRRSV-2 strains, which have become increasingly prevalent despite routine vaccination and have substantially altered the molecular epidemiology of PRRSV in commercial pig populations [16–18]. Similar trends have recently been reported in Korea, where nationwide surveillance

identified the emergence and rapid dissemination of highly virulent PRRSV-2 variants [14]. Although molecular characterization was not performed in the present investigation, the increased PRRSV detection observed in 2024 may reflect the continued endemic circulation and ongoing genetic evolution of field viruses rather than a transient epidemiological event.

In contrast, the epidemiological situation in Europe differs substantially from that observed in East Asia because PRRSV-1 remains the dominant genotype in most European countries despite increasing genetic diversity within regional populations [21]. These regional differences highlight the distinct evolutionary trajectories of PRRSV across continents while emphasizing that continuous viral evolution represents a common challenge irrespective of genotype predominance. Consequently, sustained epidemiological surveillance integrating routine diagnostic data with molecular characterization remains essential for detecting emerging variants and supporting evidence-based disease control strategies.

A notable finding of the present study was the progressive increase in PCV2 detection during the study period, rising from 28.4% in 2022 to 48.7% in 2024. This observation indicates that PCV2 continues to circulate extensively in Korean swine herds and remains an important pathogen associated with respiratory disease cases submitted for diagnostic investigation. Although the present retrospective study was not designed to determine the underlying causes of this increasing trend, several factors may have contributed to the observed pattern. Continuous circulation of genetically diverse PCV2 strains, differences in vaccination practices among farms, changes in herd immunity, and increasing diagnostic submissions from clinically affected pigs may all influence annual detection rates under field conditions [7,23]. Because vaccination records, viral genotypes, and farm-level management information were unavailable in the present dataset, these potential contributing factors could not be evaluated directly. Therefore, the observed increase in PCV2 detection should be interpreted as an epidemiological observation rather than evidence of changes in viral pathogenicity or vaccine effectiveness. Furthermore, although PCV2 detection increased concurrently with PRRSV detection during the study period, the present findings do not support the interpretation that the increase in PRRSV positivity was solely attributable to the increasing prevalence of PCV2.

The present study also demonstrated that PRRSV was detected significantly more frequently in PCV2-positive samples than in PCV2-negative samples, and the proportion of PRRSV–PCV2 co-detection increased throughout the study period. This finding is biologically plausible because PRRSV preferentially infects porcine alveolar macrophages, which serve as one of the primary components of the innate immune defense system within the respiratory tract. Infection of these cells impairs macrophage function, alters cytokine responses, and reduces the host's ability to eliminate secondary pathogens, thereby creating conditions that may facilitate concurrent infections [25,26]. Experimental studies have consistently demonstrated that simultaneous infection with PRRSV and PCV2 can exacerbate respiratory disease by increasing viral replication, enhancing pulmonary lesions, prolonging viral persistence, and dysregulating both innate and adaptive immune responses [3,6–8,22]. Consequently, concurrent detection of these two pathogens in field cases is biologically reasonable and reflects the multifactorial nature of porcine respiratory disease complex. In addition to PCV2, PRRSV-induced immunosuppression has also been associated with increased susceptibility to other respiratory pathogens, including Mycoplasma hyopneumoniae, Streptococcus suis, and swine influenza A virus, further emphasizing the multifactorial etiology of PRDC [3,4,22].

Nevertheless, the association observed in the present study should be interpreted with caution. Because the present investigation was based on retrospective diagnostic PCR results obtained from pigs with respiratory disease, detection of PRRSV and PCV2 in the same sample does not necessarily indicate simultaneous biological co-infection or a direct causal relationship between the two viruses. Likewise, the higher PRRSV detection observed in PCV2-positive samples should not be interpreted as evidence that the increasing annual PCV2 detection rate directly caused the increase in PRRSV positivity. Rather, both pathogens are endemic in Korean swine populations and frequently circulate within the same production systems, where shared epidemiological risk factors, including animal movement, farm density, biosecurity status, management practices, and host immunity, may contribute to their concurrent detection. Seasonal variation, the predominance of PRRSV-2, and regional production characteristics identified in the present study further support the conclusion that multiple epidemiological factors, rather than a single pathogen, contributed to the observed temporal increase in PRRSV detection. Future

longitudinal studies incorporating vaccination history, molecular characterization, production parameters, and sequential infection dynamics will be required to clarify the temporal and biological relationship between PRRSV and PCV2 under commercial field conditions.

The present study demonstrated a distinct seasonal pattern in PRRSV detection, with significantly higher positivity during autumn and winter than during spring and summer. Similar seasonal trends have been consistently reported in both Korea and North America, where PRRS outbreaks occur more frequently during colder months [9,10]. Lower ambient temperatures may prolong viral survival outside the host by enhancing the environmental stability of PRRSV and reducing viral degradation on contaminated fomites, thereby increasing opportunities for indirect transmission. Experimental studies have demonstrated that PRRSV remains infectious for longer periods under low-temperature conditions in both aerosols and contaminated manure, supporting the biological plausibility of increased transmission during colder seasons [27,28]. In addition, seasonal management practices commonly adopted during winter, including reduced barn ventilation, increased stocking density, and limited air exchange, may further facilitate viral transmission within intensive production systems [9,19]. Comparable seasonal patterns have also been reported in previous Korean surveillance studies conducted between 2018 and 2022, supporting the hypothesis that climatic conditions and management practices jointly influence the epidemiology of PRRSV under field conditions [13]. Nevertheless, environmental variables were not directly evaluated in the present study, and further investigations incorporating climatic, housing, and management data are warranted to better define their respective contributions to seasonal disease occurrence.

Regional variation in PRRSV detection was also observed, with the highest positivity rates identified in Chungnam, Gyeonggi, and Jeonbuk, which represent major swine-producing regions in the Republic of Korea. These provinces contain the largest swine populations in the Republic of Korea according to official livestock statistics [12] (Supplementary Fig. S1) and are characterized by high farm density, frequent animal movement, and extensive inter-farm transportation networks. Such production characteristics may increase opportunities for virus introduction and regional dissemination, thereby contributing to the spatial clustering of PRRSV observed in the present study [10,20]. Although regional

differences should be interpreted cautiously because diagnostic submissions were not evenly distributed among provinces, the observed spatial pattern is consistent with previous epidemiological studies demonstrating that farm connectivity and animal movement are major drivers of PRRSV transmission [9,10,20].

Several limitations should be considered when interpreting the findings of the present study. First, the study population consisted exclusively of pigs with respiratory disease that were submitted for routine diagnostic testing. Therefore, the results represent diagnostic detection among clinically affected animals rather than the true prevalence of PRRSV within the general swine population. Second, because individual farm identifiers were not consistently available, clustering of samples originating from the same farm could not be incorporated into the statistical analyses. Third, several potentially important epidemiological variables, including vaccination history, production management, biosecurity practices, and herd health status, were unavailable in this retrospective dataset and therefore could not be included in the multivariable model. In particular, vaccination records were unavailable, preventing evaluation of the relationship between vaccination status and PRRSV detection or PRRSV–PCV2 co-detection. Finally, molecular characterization, lineage classification, and whole-genome sequencing of circulating PRRSV strains were beyond the scope of this study. Future nationwide surveillance integrating molecular epidemiology with longitudinal production and vaccination data will provide a more comprehensive understanding of PRRSV evolution and transmission dynamics in Korean swine populations.

Despite these limitations, the present study provides updated nationwide epidemiological evidence regarding PRRSV detection in pigs with respiratory disease in the Republic of Korea. The continued predominance of PRRSV-2, significant seasonal variation, regional differences in detection, and the increasing frequency of PRRSV–PCV2 co-detection collectively highlight the complex epidemiology of PRDC under commercial production conditions. These findings provide valuable baseline information for improving diagnostic surveillance, optimizing disease control strategies, and guiding future epidemiological and molecular investigations aimed at reducing the burden of PRRSV in Korean swine production systems [23,24].

Conclusion

This nationwide retrospective study demonstrated that PRRSV is widely detected in lung samples from pigs with respiratory symptoms in the Republic of Korea, with PRRSV-2 as the predominant genotype. Detection rates varied by year and showed clear seasonal patterns, with higher positivity rates during autumn and winter. Frequent co-detection of PRRSV and PCV2 was also observed under field conditions. These findings provide updated epidemiological insights into PRRSV-associated respiratory symptoms and support the need for integrated disease management strategies in commercial swine production systems.

This study provides an updated synthesis of recent PRRSV epidemiological patterns in the Republic of Korea and discusses their implications for the swine industry. Although limited by the retrospective nature of diagnostic data, the findings offer a valuable foundation for future research, including molecular epidemiology studies, network-based transmission analysis, and quantitative assessments linked to production performance. In the long term, the development of data-driven surveillance systems integrating diagnostic, molecular, and production data is expected to enhance PRRSV control strategies and support the establishment of sustainable swine production systems in the Republic of Korea.

References

1. Zimmerman JJ, Karriker LA, Ramirez A, Schwartz KJ, Stevenson GW, Zhang J. Diseases of swine. 11th ed. Ames (IA): Wiley-Blackwell; 2019.
2. Holtkamp DJ, Kliebenstein JB, Neumann EJ, Zimmerman JJ, Rotto HF, Yoder TK, et al. Assessment of the economic impact of porcine reproductive and respiratory syndrome virus on United States pork producers. J Swine Health Prod. 2013;21:72–84. https://doi.org/10.54846/jshap/754
3. Opriessnig T, Giménez-Lirola LG, Halbur PG. Polymicrobial respiratory disease in pigs. Anim Health Res Rev. 2011;12:133–148. https://doi.org/10.1017/S1466252311000120
4. Chae C. Porcine respiratory disease complex: interaction of vaccination and porcine circovirus type 2, porcine reproductive and respiratory syndrome virus, and Mycoplasma hyopneumoniae. Vet J. 2016;212:1-6. https://doi.org/10.1016/j.tvjl.2015.10.030
5. Kappes MA, Faaberg KS. PRRSV structure, replication and recombination: origin of phenotype and genotype diversity. Virology. 2015;479–480:475–486. https://doi.org/10.1016/j.virol.2015.02.012
6. Harms PA, Sorden SD, Halbur PG, Bolin SR, Lager KM, Morozov I, et al. Experimental reproduction of severe disease in CD/CD pigs concurrently infected with type 2 porcine circovirus and porcine reproductive and respiratory syndrome virus. Vet Pathol. 2001;38:528–539. https://doi.org/10.1354/vp.38-5-528
7. Opriessnig T, Meng XJ, Halbur PG. Porcine circovirus type 2 associated disease: update on current terminology, clinical manifestations, pathogenesis, diagnosis, and intervention strategies. J Vet Diagn Invest. 2007;19:591–615. https://doi.org/10.1177/104063870701900601
8. Darwich L, Mateu E. Immunology of porcine circovirus type 2 (PCV2). Virus Res. 2012;164:61–67. https://doi.org/10.1016/j.virusres.2011.10.003
9. Arruda AG, Tousignant SJP, Sanhueza JM, Vilalta C, Corzo CA, Torremorell M, et al. Risk factors associated with recurrent porcine reproductive and respiratory syndrome virus outbreaks

in breeding herds in the United States and Canada. Prev Vet Med. 2018;151:135–142. https://doi.org/10.1016/j.prevetmed.2018.01.018

10. Vilalta C, Sanhueza JM, Alvarez J, Corzo CA, Arruda AG. Spatial analysis of porcine reproductive and respiratory syndrome virus spread among swine farms. Transbound Emerg Dis. 2019;66:810–820. https://doi.org/10.1111/tbed.13085
11. Wang X, Marthaler D, Rovira A, Rossow S, Murtaugh MP. Emergence of porcine reproductive and respiratory syndrome virus in Asia: current status and molecular epidemiology. Front Vet Sci. 2021;8:672731. https://doi.org/10.3389/fvets.2021.672731
12. Statistics Korea. Korean Statistical Information Service (KOSIS): Livestock Statistics Survey. Available from: https://kosis.kr/. Accessed 2025.
13. Lee MA, Jayaramaiah U, You SH, Shin EG, Song SM, Ju L, et al. Molecular characterization of porcine reproductive and respiratory syndrome virus in Korea from 2018 to 2022. Pathogens. 2023;12:757. https://doi.org/10.3390/pathogens12060757
14. Kim SC, Kang SC, Kim HJ, Park J, Kim HR, Park CK, et al. Nationwide emergence and spread of highly virulent PRRSV-2 mutants in Korea. Porcine Health Manag. 2025;11:58. https://doi.org/10.1186/s40813-025-00470-5
15. Yim-Im W, Anderson TK, Paploski IAD, VanderWaal K, Gauger P, Krueger K, et al. Refining PRRSV-2 genetic classification based on global ORF5 sequences and investigation of their geographic distributions and temporal changes. Microbiol Spectr. 2023;11:e0291623. https://doi.org/10.1128/spectrum.02916-23
16. Zhou L, Yang Y, Xia Q, Guan Z, Zhang J, Li B, et al. Genetic characterization of porcine reproductive and respiratory syndrome virus from Eastern China during 2017–2022. Front Microbiol. 2022;13:971817. https://doi.org/10.3389/fmicb.2022.971817
17. Li C, Fan A, Liu Z, Wang G, Zhou L, Zhang H, et al. Prevalence, time of infection, and diversity of porcine reproductive and respiratory syndrome virus in China. Viruses. 2024;16:774. https://doi.org/10.3390/v16050774

18. Zhang J, Wei X, Sun L, Yang C, Wang S, Wang W, et al. Epidemiological analysis based on ORF5 of porcine reproductive and respiratory syndrome virus in China in 2019-2024. Front Microbiol. 2026;17:1794268. https://doi.org/10.3389/fmicb.2026.1794268
19. Chandra S, Cezar G, Rupasinghe K, Magalhães E, Silva GS, Almeida M, et al. Harnessing sequencing data for porcine reproductive and respiratory syndrome virus (PRRSV): tracking genetic evolution dynamics and emerging sequences in US swine industry. Front Vet Sci. 2025;12:1571020. https://doi.org/10.3389/fvets.2025.1571020
20. Thakur KK, Sanchez J, Hurnik D, Poljak Z, Opps S, Revie CW. Development of a network based model to simulate the between-farm transmission of porcine reproductive and respiratory syndrome virus. Vet Microbiol. 2015;180:212–222. https://doi.org/10.1016/j.vetmic.2015.09.010
21. Stadejek T, Stankevicius A, Murtaugh MP, Oleksiewicz MB. Molecular evolution of PRRSV in Europe: current state of play. Vet Microbiol. 2013;165:21–8. https://doi.org/10.1016/j.vetmic.2013.02.029
22. Opriessnig T, Halbur PG. Concurrent infections are important for expression of porcine circovirus associated disease. Virus Res. 2012;164:20–32. https://doi.org/10.1016/j.virusres.2011.09.014
23. Karuppannan AK, Opriessnig T. Porcine circovirus type 2 (PCV2) vaccines in the context of current molecular epidemiology. Viruses. 2017;9:99. https://doi.org/10.3390/v9050099
24. Murtaugh MP, Genzow M. Immunological solutions for treatment and prevention of porcine reproductive and respiratory syndrome (PRRS). Vaccine. 2011;29:8192–204. https://doi.org/10.1016/j.vaccine.2011.09.013
25. Rossow KD. Porcine reproductive and respiratory syndrome. Vet Pathol. 1998;35:1–20.
26. Lunney JK, Fang Y, Ladinig A, Chen N, Li Y, Rowland B, et al. Porcine reproductive and respiratory syndrome virus (PRRSV): pathogenesis and interaction with the immune system. Annu Rev Anim Biosci. 2016;4:129–154. https://doi.org/10.1146/annurev-animal-022114-111025

27. Hermann JR, Hoff SJ, Muñoz-Zanzi C, Yoon KJ, Roof MB, Burkhardt AC, et al. Effect of temperature and relative humidity on the stability of infectious porcine reproductive and respiratory syndrome virus in aerosols. Vet Res. 2007;38(1):81–93. https://doi.org/10.1051/vetres:2006044

28. Linhares DCL, Torremorell M, Joo HS, Morrison RB. Infectivity of PRRS virus in pig manure at different temperatures. Vet Microbiol. 2012;160(1–2):23–28. https://doi.org/10.1016/j.vetmic.2012.05.009

29.

Figure Legends

Figure 1.

Annual and overall PRRSV detection and genotype distribution in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

(A) Annual and overall porcine reproductive and respiratory syndrome virus (PRRSV) positivity rates (%) during the study period. Values above the bars indicate positivity rates and the number of positive samples.

(B) Annual and overall distribution of PRRSV genotypes among PRRSV-positive samples. Stacked bars represent the proportions of PRRSV-1, PRRSV-2, and co-detection.

Figure 2.

PRRSV–PCV2 co-detection patterns in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

(A) Annual and overall proportions of PRRSV-positive samples concurrently positive for PCV2. Values above the bars indicate co-detection rates and sample counts.

(B) PRRSV positivity according to PCV2 detection. Bars represent annual and overall PRRSV positivity rates in PCV2-positive and PCV2-negative samples. Statistical significance was assessed using chi-square tests.

Figure 3.

Seasonal patterns of PRRSV detection in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

(A) Monthly PRRSV positivity rate trends by year. Lines represent monthly positivity rates for 2022, 2023, 2024, and the overall positivity rate for 2022–2024.

(B) Seasonal comparison of PRRSV positivity rates. Bars indicate positivity rates by season for each year (2022, 2023, and 2024) and the overall positivity rate for 2022–2024. Statistical significance was assessed using chi-square tests.

Figure 4.

Regional distribution of PRRSV positivity in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

2022–2024(Average) and annual PRRSV positivity rates by province. Horizontal bars represent positivity rates for each province. Values indicate positivity rates and the number of positive samples/total samples. Provinces with fewer than 10 samples were excluded from visualization.

Figure 5.

Multivariate logistic regression analysis of factors associated with PRRSV positivity in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

Forest plot showing odds ratios (ORs) and 95% confidence intervals (CIs) for variables associated with PRRSV positivity. The dashed vertical line indicates the null value (OR = 1.0). Reference categories were 2022 for year, summer for season, and PCV2-negative samples.

Figure 5.

Multivariate logistic regression analysis of factors associated with PRRSV positivity in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

Forest plot showing odds ratios (ORs) and 95% confidence intervals (CIs) for variables associated with PRRSV positivity. The dashed vertical line indicates the null value (OR = 1.0). Reference categories were 2022 for year, summer for season, and PCV2-negative samples.

Supplementary Figure S1.

Provincial distribution of the swine population in the Republic of Korea, 2022–2024.

(A) Geographic distribution of the average swine population by province in the Republic of Korea. Provinces were grouped according to the average number of pigs raised during 2022–2024.

(B) Average swine populations in the major swine-producing provinces during the same period. Bars represent the mean number of pigs, expressed in millions of heads. Data were obtained from the Korean Statistical Information Service (KOSIS) Livestock Statistics Survey, and quarterly provincial swine population data were averaged across 2022–2024.

Tables

Table 1.

Characteristics of lung samples collected from pigs with respiratory disease in the Republic of Korea, 2022–2024.

Variable	Category	n (%)
Year	2022	776 (31.3)
	2023	870 (35.1)
	2024	830 (33.5)
Season	Spring	614 (24.8)
	Summer	479 (19.3)
	Autumn	713 (28.8)
	Winter	670 (27.1)
Province	Chungnam	460 (18.6)
	Gyeonggi	489 (19.7)
	Jeonbuk	456 (18.4)
	Gyeongbuk	558 (22.5)
	Gyeongnam	94 (3.8)
	Jeonnam	119 (4.8)
	Gangwon	38 (1.5)
	Chungbuk	259 (10.5)

Values are presented as number of samples (n) and percentages. PCV2, porcine circovirus type 2; PRRSV, porcine reproductive and respiratory syndrome virus.

478

Table 2.

PRRSV positivity rates according to epidemiological variables in lung samples from pigs with respiratory symptoms from 2022 to 2024.

Variable	Category	Positive / Total	Positivity (%)	p-value
Year	2022	463/776	59.7	0.0004
	2023	520/870	59.8	
	2024	563/830	67.8	
Season	Autumn	485/713	68.0	<0.001
	Spring	326/614	53.1	
	Summer	269/479	56.2	
	Winter	466/670	69.6	
Province	Chungnam	339/460	73.7	<0.001
	Gyeonggi	310/489	63.4	
	Jeonbuk	289/456	63.4	
	Gyeongbuk	341/558	61.1	
	Gyeongnam	57/94	60.6	
	Jeonnam	72/119	60.5	
	Gangwon	18/38	47.4	
	Chungbuk	119/259	45.9	
PCV2 status	Negative	899/1536	58.5	<0.001
	Positive	647/940	68.8	

Positivity rates are presented as percentages. Statistical significance was assessed using chi-square tests. PRRSV, porcine reproductive and respiratory syndrome virus; PCV2, porcine circovirus type 2.

479

480

481

Table 3.

Annual detection rates of PRRSV and PCV2 in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

Year	Sample No.	PRRSVpositive / total	PRRSV positivity (%)	PCV2 positive / total	PCV2 positivity (%)
2022	776	463/776	59.7	220/776	28.4
2023	870	520/870	59.8	316/870	36.3
2024	830	563/830	67.8	404/830	48.7
Total	2476	1,546/2,476	62.4	940/2,476	38

Values are presented as number of positive samples and positivity rates. PRRSV, porcine reproductive and respiratory syndrome virus; PCV2, porcine circovirus type 2.

482

483

484

485

Table 4.

Multivariate logistic regression analysis of factors associated with PRRSV positivity in lung samples from pigs with respiratory symptoms from 2022 to 2024.

Variable	Category	OR (95% CI)	*p*-value
Year	2023 vs 2022	0.97 (0.79–1.18)	0.740
	2024 vs 2022	1.33 (1.08–1.64)	0.008
Season	Spring vs Summer	0.89 (0.69–1.13)	0.324
	Autumn vs Summer	1.61 (1.26–2.05)	<0.001
	Winter vs Summer	1.78 (1.39–2.28)	<0.001
PCV2 detection	Positive vs Negative	1.45 (1.21–1.73)	<0.001

Odds ratios (ORs) and 95% confidence intervals (CIs) are presented. Reference categories were defined as 2022 for year, summer for season, and PCV2-negative samples.

PRRSV, porcine reproductive and respiratory syndrome virus; PCV2, porcine circovirus type 2.

486

487

Figures

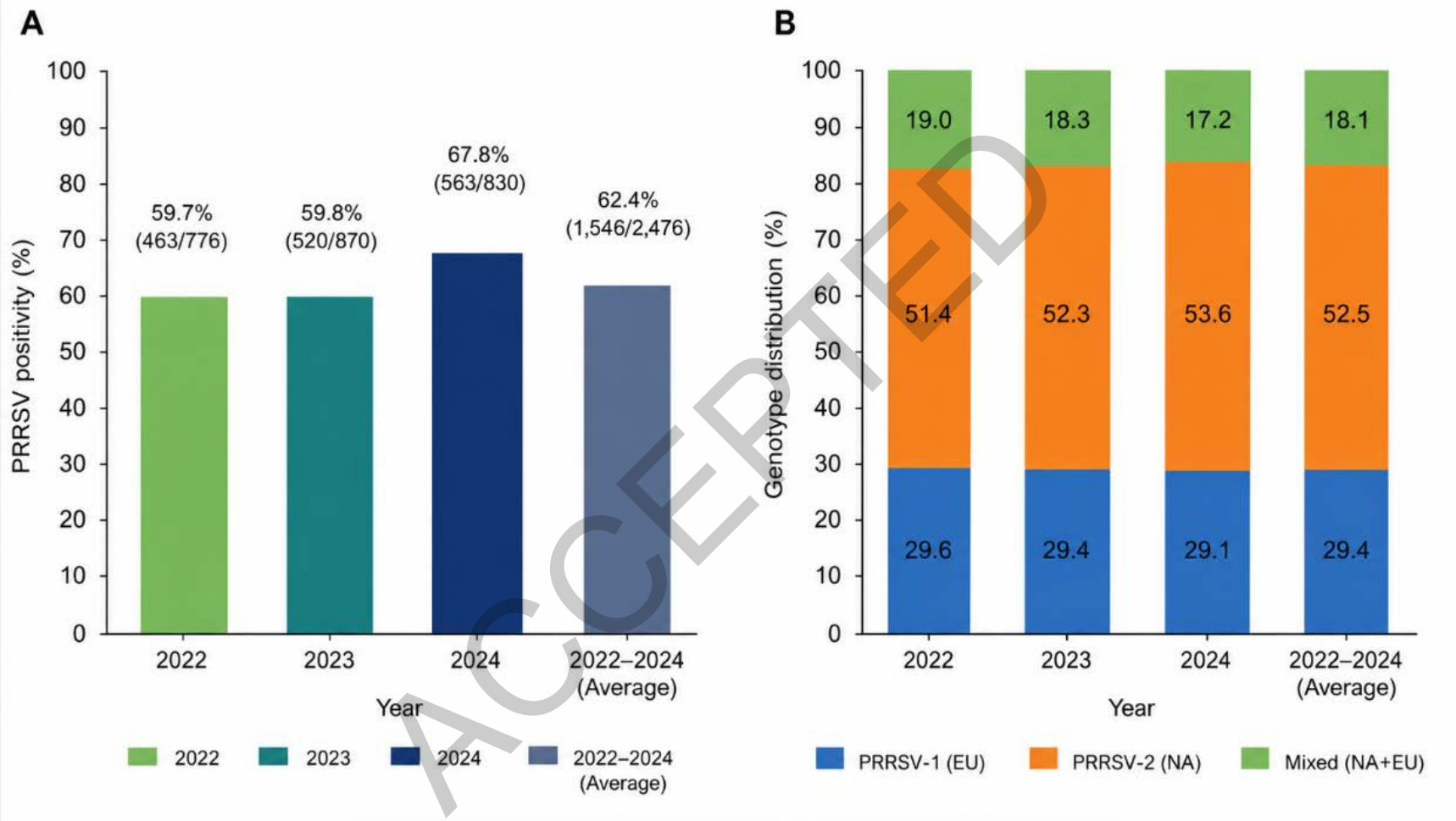


Figure 1. Annual and overall PRRSV detection and genotype distribution in lung samples from pigs with respiratory symptoms in the Republic of Korea between 2022 and 2024.

(A) Annual and overall PRRSV positivity rates (%) during the study period. Values above bars indicate positivity rates and the number of positive samples.

(B) Annual and overall distribution of PRRSV genotypes among PRRSV-positive samples. Stacked bars represent the proportions of PRRSV-1, PRRSV-2, and co-detection.

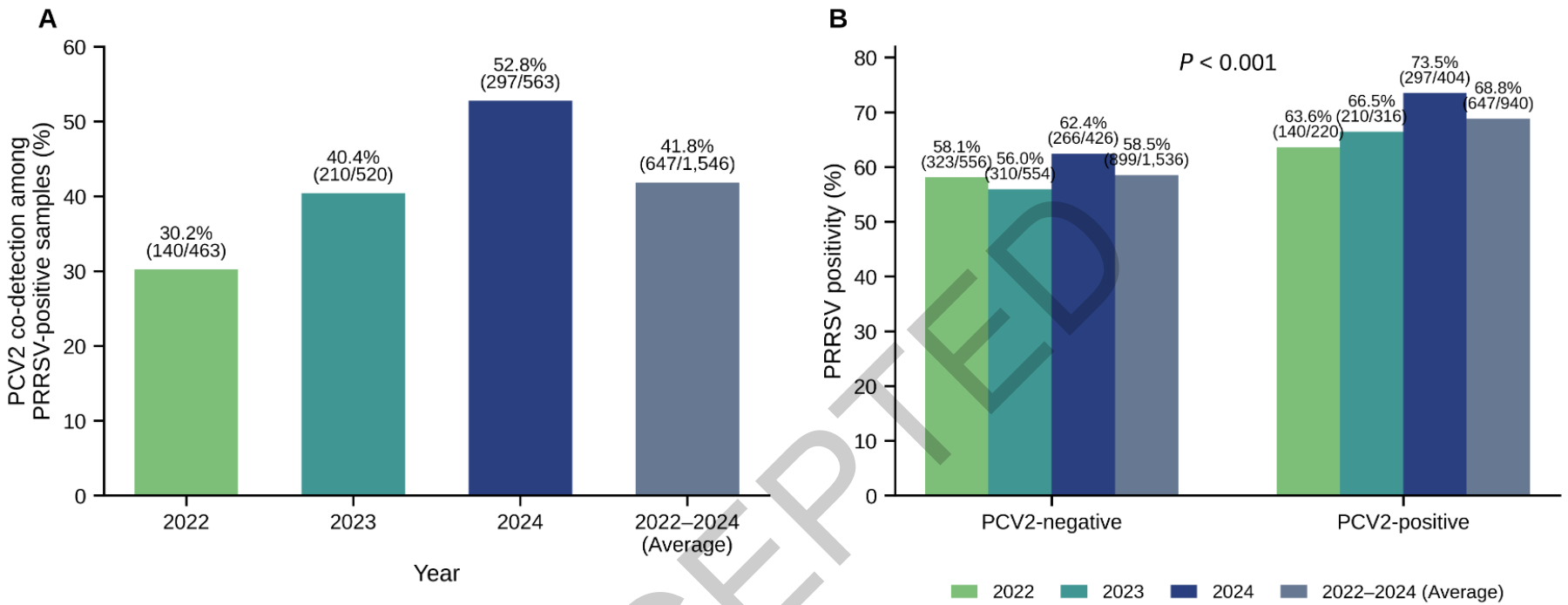


Figure 2. PRRSV–PCV2 co-detection patterns in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

(A) Annual and overall proportions of PRRSV-positive samples concurrently positive for PCV2. Values above bars indicate co-detection rates and sample counts.

(B) PRRSV positivity according to PCV2 detection. Bars represent annual and overall PRRSV positivity rates in PCV2-positive and PCV2-negative samples. Statistical significance was assessed using chi-square tests.

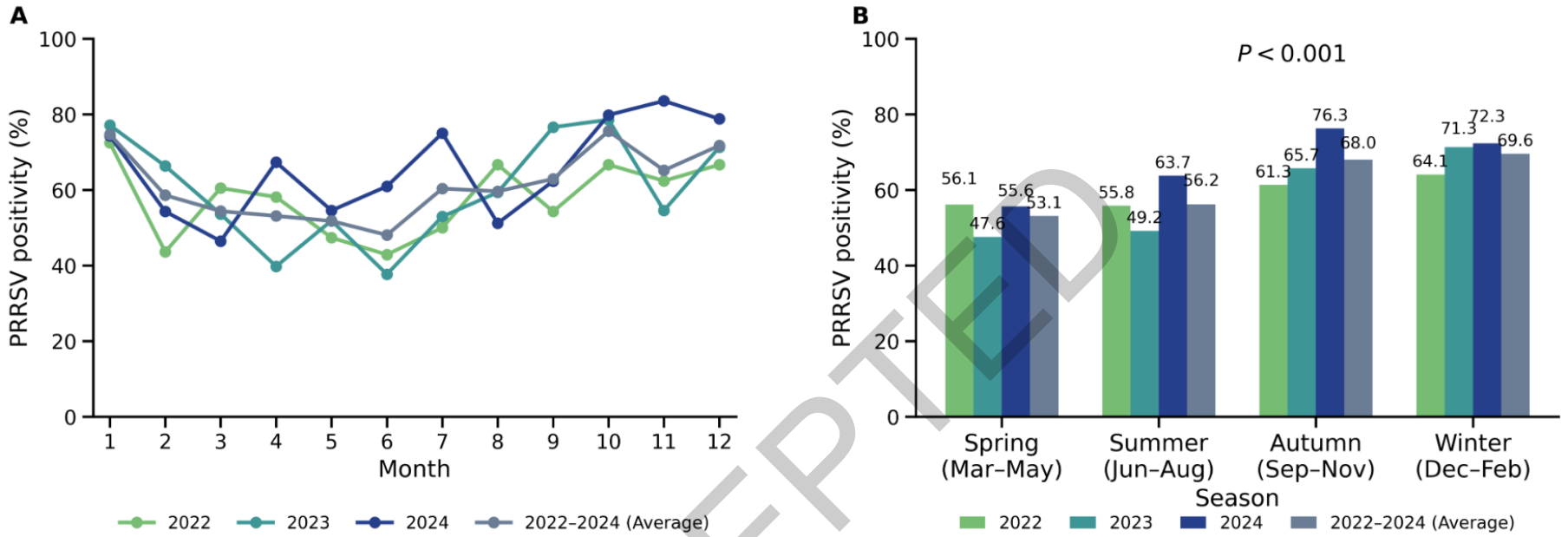


Figure 3. Seasonal patterns of PRRSV detection in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024. (A) Monthly PRRSV positivity trends by year. Lines represent monthly positivity rates for 2022, 2023, 2024, and the overall positivity rate for 2022–2024. (B) Seasonal comparison of PRRSV positivity rates. Bars indicate positivity rates by season for each year (2022, 2023, and 2024) and the overall positivity rate for 2022–2024. Statistical significance was assessed using chi-square tests.

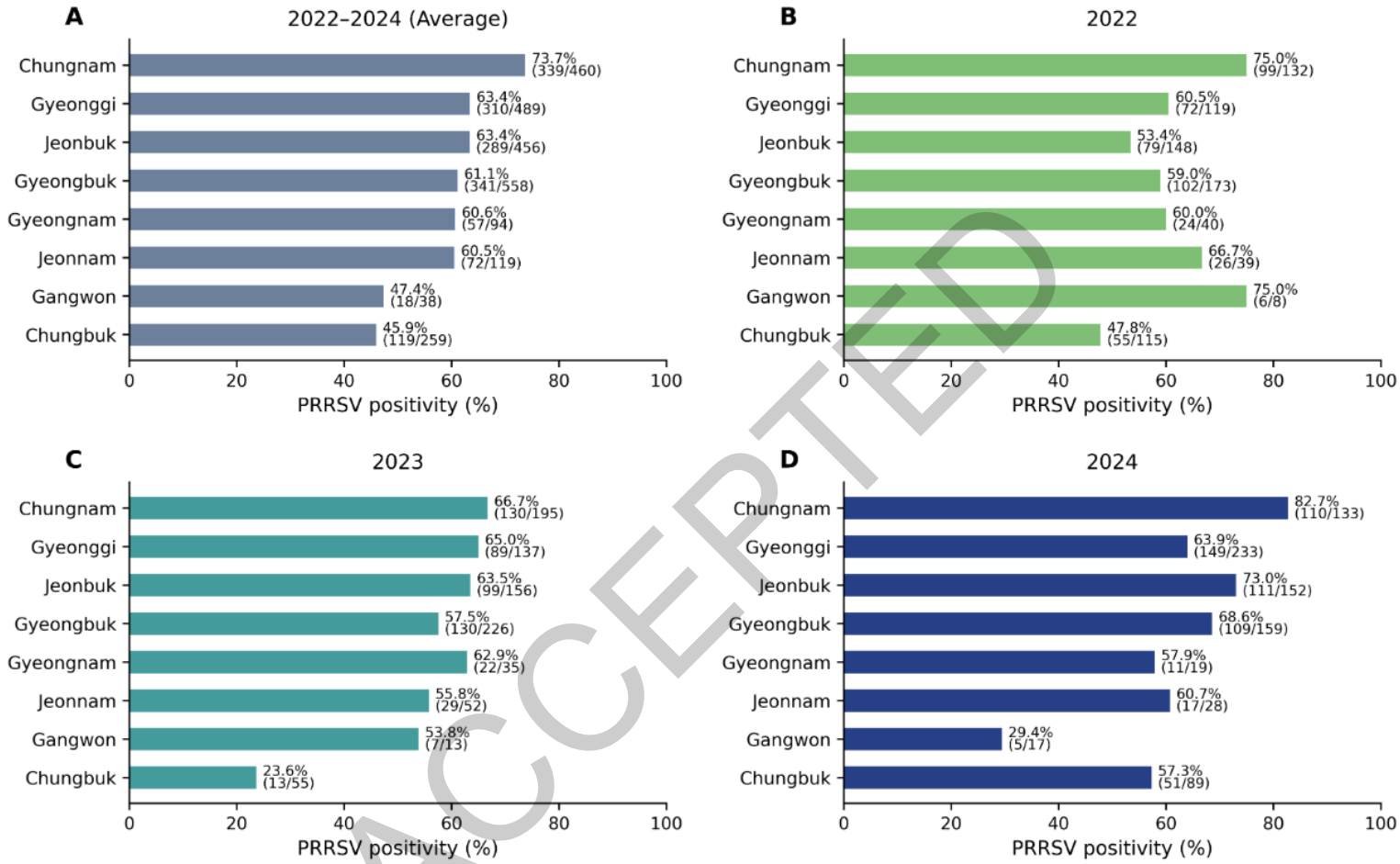


Figure 4. Regional distribution of PRRSV positivity in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

2022–2024(Average) and annual PRRSV positivity rates by province. Horizontal bars represent positivity rates for each province. Values indicate positivity rates and the number of positive samples/total samples. Provinces with fewer than 10 samples were excluded from visualization.

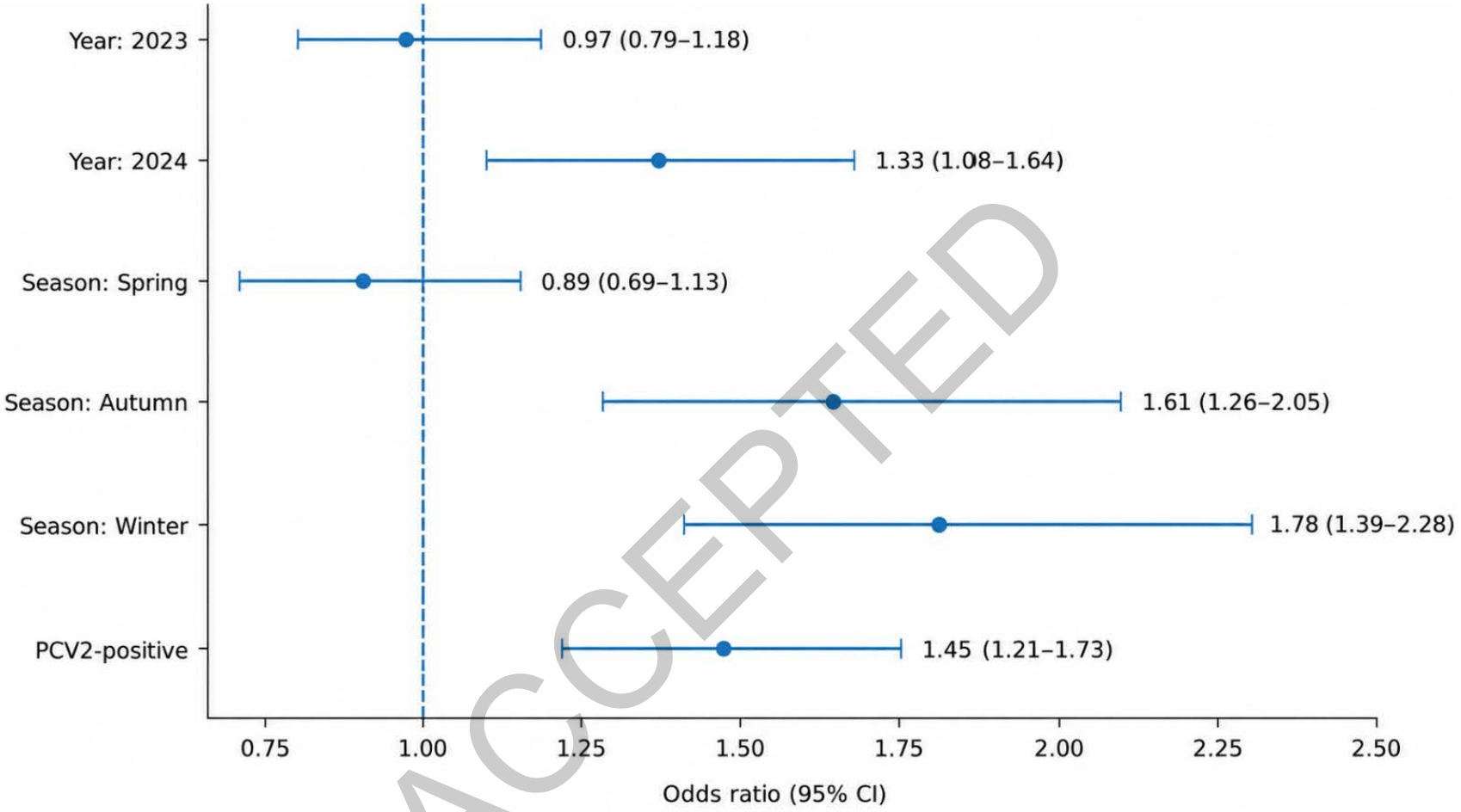
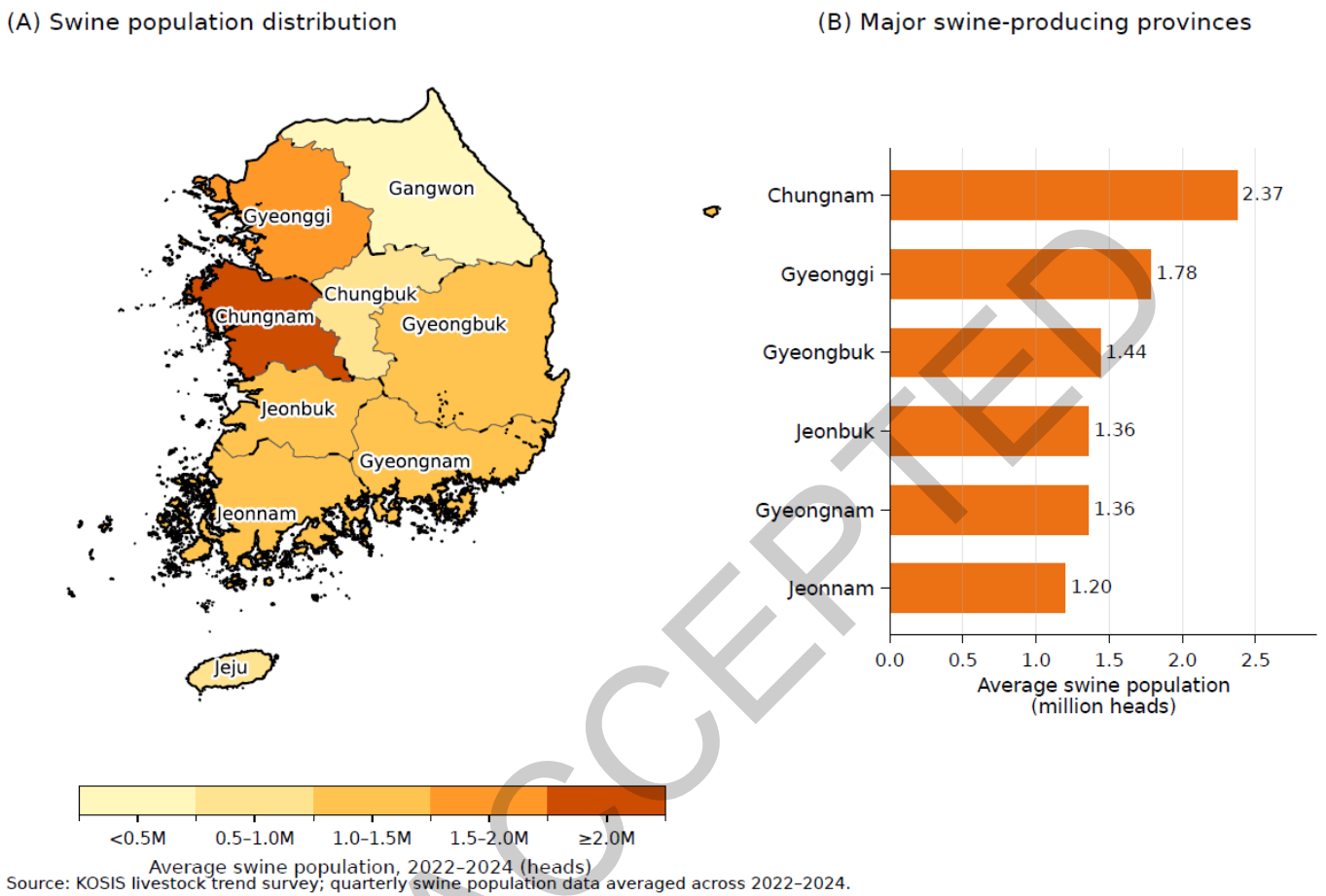


Figure 5. Multivariate logistic regression analysis of factors associated with PRRSV positivity in lung samples from pigs with respiratory symptoms in the Republic of Korea from 2022 to 2024.

Forest plot showing odds ratios (ORs) and 95% confidence intervals (CIs) for variables associated with PRRSV positivity. The dashed vertical line indicates the null value (OR = 1.0). Reference categories were 2022 for year, summer for season, and PCV2-negative samples.



Source: KOSIS livestock trend survey; quarterly swine population data averaged across 2022–2024.

Supplementary Figure S1. Provincial distribution of the swine population in the Republic of Korea, 2022–2024.

(A) Geographic distribution of the average swine population by province in the Republic of Korea. Provinces were grouped according to the average number of pigs raised during 2022–2024.

(B) Average swine populations in the major swine-producing provinces during the same period. Bars represent the mean number of pigs, expressed in millions of heads. Data were obtained from the Korean Statistical Information Service (KOSIS) Livestock Statistics Survey, and quarterly provincial swine population data were averaged across 2022–2024.