Infectious African Swine Fever Virus in Spray-Dried Porcine Plasma Used as Feed Ingredient, South Korea, 2026

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We detected African swine fever virus DNA in feed and spray-dried porcine plasma (SDPP) used as a feed ingredient in South Korea. Pigs inoculated with SDPP developed fatal infection. An isolate phylogenetically clustered with South Korea strains. Our findings highlight the need for strengthened risk management of animal-derived feed ingredients like SDPP.

African swine fever (ASF), caused by ASF virus (ASFV), is a highly contagious and fatal hemorrhagic disease of domestic pigs and wild boars across Eurasia (*1*). In Africa, soft ticks (*Ornithodoros* spp.) act as biological vectors, whereas wild suids serve as asymptomatic reservoirs (*2*). In Eurasia, ASFV is primarily maintained and spread by wild boars, although transmission also occurs through contaminated pork products and swill feeding (*3*,*4*). Because of its environmental stability, ASFV remains infectious in meat and blood for weeks to months (*5*). Since its introduction from Africa into the country of Georgia in 2007 (*6*), ASFV has spread throughout Eastern Europe and Russia and subsequently into Asia (*4*,*6*). ASFV outbreaks were reported in China in 2018 and Mongolia in early 2019; rapid spread across Asia followed (*4*,*6*).

In South Korea, after the first outbreak in Paju in 2019 (*6*), ASFV had been detected in 79 domestic pig farms by March 2026, affecting ≈345,000 pigs (*7*). Before 2026, ASF outbreaks on domestic pig farms in South Korea occurred sporadically, and only a small number of outbreaks were reported each year. However, an unprecedented number of outbreaks occurred during January–March 2026, affecting 24 domestic pig farms. Epidemiologic investigations linked some affected farms to ASFV DNA–positive feed, whereas other farms had potential risk factors such as wild boar exposure and illegal livestock products (*8*). The investigations detected ASFV DNA in commercial compound feed (CF) and in spray-dried porcine plasma (SDPP), which is produced from slaughterhouse blood and used as a feed ingredient because of its high nutritional value and beneficial effects on growth (*9*). The ASFV DNA–positive CF was produced by a feed manufacturer using SDPP from the same batch as the ASFV DNA–positive SDPP. We experimentally administered ASFV DNA–positive SDPP and CF samples to pigs to determine if the compounds could cause disease and genetically characterized the virus to identify its origin.

The Study

We tested SDPP (n = 72) and CF (n = 219) samples collected from ASF outbreak pig farms in South Korea for ASFV at the Animal and Plant Quarantine Agency (Gimcheon, South Korea). In brief, we suspended 5 g of each sample in phosphate-buffered saline (PBS) for DNA extraction and real-time PCR. On February 19, 2026, we detected ASFV DNA in 2 SDPP samples (cycle threshold [Ct] values 28.48 and 31.18). On February 24, 2026, we also detected ASFV DNA in 2 commercial CFs produced using SDPP and stored at a pig farm (Ct values 35.97 and 37.71) (Appendix Table 1, https://wwwnc.cdc.gov/EID/article/32/12/26-1380-App1.pdf). However, virus isolation using primary porcine alveolar macrophages, as previously described (*10*), was unsuccessful.

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For the experiment, we used 9 healthy 4-week-old Landrace pigs from a commercial pig farm; blood samples from all pigs tested as previously described (*10*) were negative for ASFV and other swine pathogens. We housed the pigs in separate isolators within the Animal Biosafety Level 3 facility of the Animal and Plant Quarantine Agency under approved institutional protocols. We randomly assigned pigs to 3 experimental groups (n = 3 per group): an SDPP inoculation group, a CF-fed group, and a negative control group (Appendix Table 2). We prepared a 50% wt/vol ASFV-positive SDPP suspension in sterile PBS and filtered through a 0.45-μm syringe filter to remove bacterial contaminants. We then inoculated each pig in the SDPP group intramuscularly with 1 mL of the SDPP suspension. We provided pigs in the CF-fed group with 200 g of the 2 ASFV-positive CFs 1 time/day for 30 days. We monitored clinical signs and body temperature and performed necropsies on pigs that died. We tested viral shedding by real-time PCR using swab samples and viremia using blood samples, as previously described (*10*).

Two SDPP-inoculated pigs developed acute pyrexia (body temperature >40.5°C) at 5 days postchallenge (dpc) and a third pig at 6 dpc. Rectal temperatures peaking at 41.2°C shortly before death (Figure 1, panel A). Pyrexia was accompanied by rapidly progressive clinical signs, including severe lethargy, anorexia, huddling, and depression (Figure 1, panel B). All SDPP-inoculated pigs died; mean time to death (±SD) was 8.0 ±0.8 dpc (Figure 1, panel C). In the SDPP-inoculated group, we detected viremia in whole blood and viral shedding via the oral and rectal routes from 4 dpc onward; blood samples showed

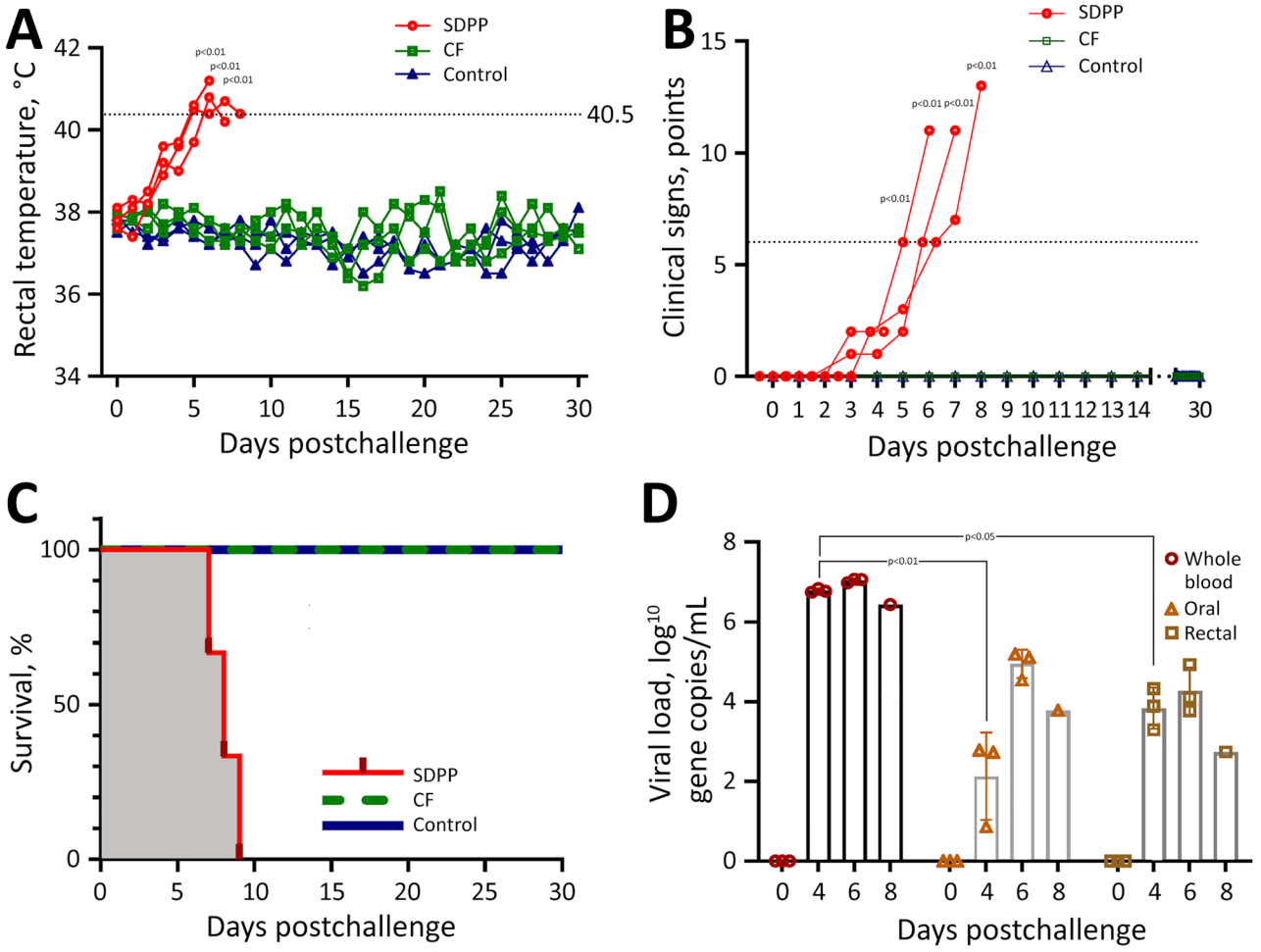


Figure 1. Clinical characterization of pigs experimentally infected in investigation of African swine fever virus in SDPP used as feed ingredient, South Korea, 2026. Nine pigs were divided into 3 groups of 3; 1 group was experimentally inoculated with African swine fever virus DNA–positive SDPP and 1 group was fed commercial CF collected in 2026; the third group was the control. A–C) Rectal temperatures (A), clinical sign scores (B), and survival (C) for all 3 groups. Gray shading in panel C indicates survival for SDPP animals, all of which died. D) Viremia in whole blood samples and virus shedding in oral and rectal samples among the SDPP group; all 3 animals in this group died. Error bars indicate SD. CF, compound feed; SDPP, spray-dried porcine plasma.

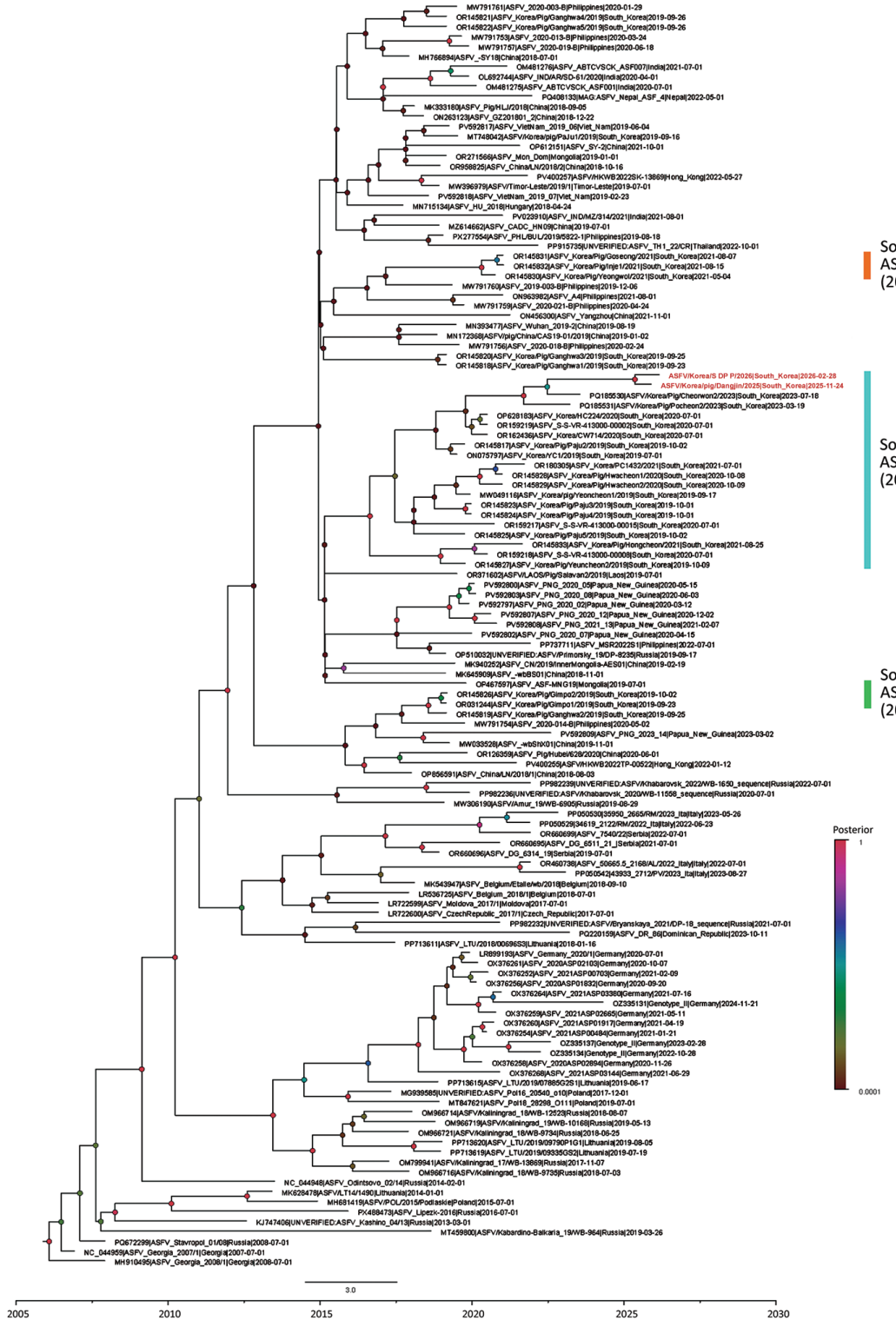


Figure 2. Time-scaled maximum clade credibility tree of the ASFV isolated from pigs inoculated with spray-dried porcine plasma in investigation of African swine fever virus in spray-dried porcine plasma used as feed ingredient, South Korea, 2026. Red indicates the ASFV isolate recovered from the inoculated pig and the reference virus from the Dangjin outbreak farm. The size and color of each node (circle) indicate the posterior probability supporting the corresponding monophyletic group. South Korea ASFV isolates were classified into 3 groups according to a previous study (*9*). GenBank accession numbers are shown. Scale bar indicates nucleotide substitutions per site. ASF, African swine fever; ASFV, ASF virus.

higher viral loads than oral and rectal swab samples (Figure 1, panel D). However, pigs in the CF-fed and control groups remained clinically stable and uninfected throughout the experimental period.

In all 3 pigs that died in the SDPP-inoculated group, necropsy revealed severe multiorgan lesions characterized by extensive congestion and systemic hemorrhage. Major pathologic findings included splenomegaly with severe hemorrhagic infarction and enlarged and hemorrhagic mandibular, gastrohepatic, and renal lymph nodes with evident erythema (Appendix Figure 1). We further detected ASFV DNA in examined postmortem tissues; all tissues with gross lesions tested positive (Appendix Figure 2).

We characterized ASFV DNA detected in SDPP and CF by Sanger sequencing of the *B646L* (*p72*), *E183L* (*p54*), and *EP402R* (*CD2v*) genes; the central variable region of the *B602L* gene; and the *I73R/I329L* intergenic region (IGR). The ASFV genomes were assigned to p72 genotype II and carried the IGR-I variant (Appendix Figures 3, 4). We isolated viable virus from spleen homogenates of SDPP-inoculated pigs (Appendix Figure 5). We determined the whole-genome sequence of the isolate, ASFV/Korea/SDPP/2026 (GenBank accession no. PZ617907), by using next-generation sequencing, as previously described (*11*). The genome shared 99.98% nucleotide identity with ASFV/Korea/pig/Dangjin/2025 (GenBank accession no. PZ617906), a strain detected during an ASF outbreak on a pig farm. The isolate further harbored characteristic insertion/deletion polymorphisms, including a 706-bp deletion across *MGF 110–7L* and *285L* within the left variable region and a 9-bp insertion in the *MGF 110–10L* to *110–14L* region. Of note, whereas most previously characterized South Korea ASFV isolates belonged to IGR type II, both the Dangjin and SDPP isolates belonged to IGR type I.

After excluding G/C homopolymer regions and inverted terminal repeats, we constructed a time-scaled phylogenetic tree using BEAST version 1.10.4 (*12*), as described in our previous study (*11*). The Dangjin and SDPP isolates clustered with South Korea ASFV isolates previously detected on affected pig farms and in wild boar (Figure 2). Those findings suggest the emergence of an IGR type I variant during domestic ASFV circulation in South Korea, rather than a recent independent introduction.

Conclusions

Infected wild boars, contaminated vehicles, illegal pork products, and the movement of pigs and farm workers are major risk factors for ASFV introduction and spread (*13*). In this study, however, we identified infectious ASFV in a feed ingredient, suggesting a potential risk for ASFV transmission. The interval between feed manufacturing and farm outbreaks ranged from 56 to 116 days (*8*). Given that infectious ASFV can persist for >100 days at 4°C, ASFV in the SDPP and CF could have remained infectious during the outbreak period (*14*). The absence of infection in CF-fed pigs might reflect reduced viral infectivity during farm storage, although infectious virus was isolated after SDPP inoculation. Oral infection also requires a higher viral dose than does direct inoculation (*15*). Given the small number of pigs tested (n = 3), the possibility of infection through CF consumption cannot be excluded.

Considering the epidemiologic context in South Korea, contaminated SDPP represents a potential risk factor that could contribute to feedborne ASFV dissemination associated with some of the 2026 outbreaks in South Korea, although further investigation is warranted. Our findings support strengthened surveillance of porcine blood products and feed to reduce the risk for feedborne ASFV transmission.

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Dr. Hong is a veterinary researcher at the Animal and Plant Quarantine Agency, South Korea. His research focuses on animal viral diseases and their molecular epidemiology via genomic analyses and the characterization of viral pathogenicity.

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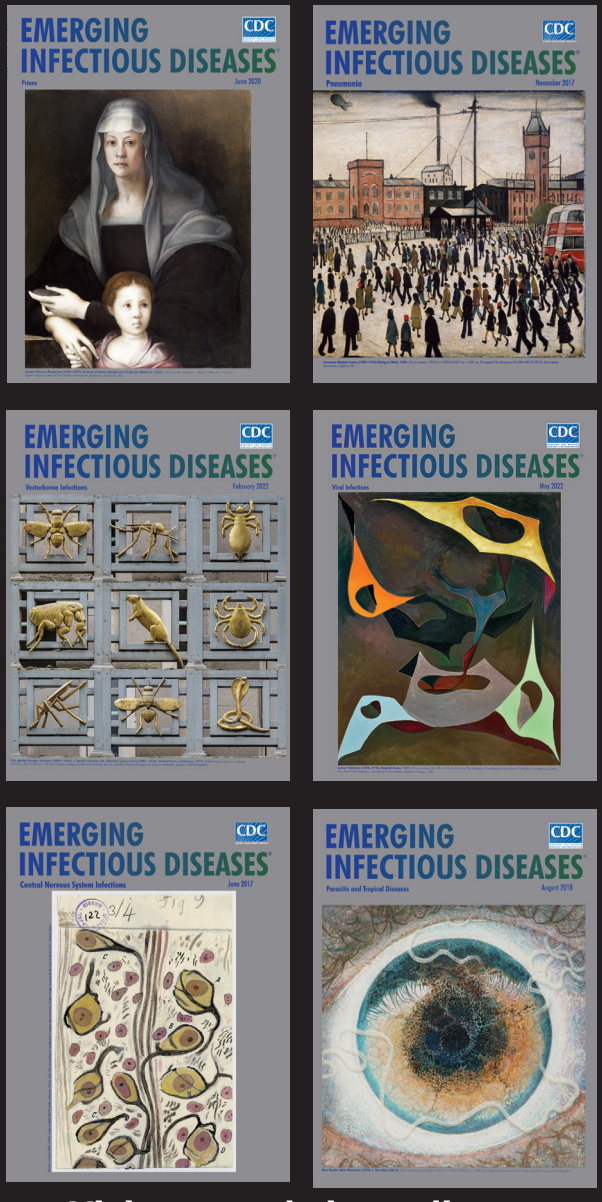
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