Spillover of Canine Parvovirus Type 2 to Pigs, South Dakota, USA, 2020

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Canine parvovirus type 2 (CPV-2) is a variant of the species *Carnivore protoparvovirus 1*, which can cause severe disease in carnivores of many species (1–3). Besides CPV-2, which causes enteritis in dogs of all ages and myocarditis in puppies, the virus species includes feline panleukopenia virus, which causes severe enteritis and leukopenia in cats of all ages (4). In 1978, CPV-2 emerged and caused a worldwide pandemic of enteritis and myocarditis among canids. In 2020, the virus was identified in pigs in South Dakota, USA, by PCR, sequencing, in situ hybridization, and serology. Genetic analysis suggests spillover from wildlife.

In October 2020, a dead pig was submitted to South Dakota State University (Brookings, SD, USA) for diagnostic testing. Histopathologic examination revealed mild to moderate enteritis, hepatitis, and visceral edema. Hemolytic *Escherichia coli* was isolated. No significant lung lesions were noted. Approximately 8 months later, we performed viral metagenomic sequencing on archived lung tissue for an unrelated research project and unexpectedly identified CPV-2. Using a 5′-nuclease PCR (Integrated DNA Technologies, https://www.idtdna.com), we confirmed that the sample was CPV-2 positive; cycle threshold (Ct) was 24.4. Sanger sequencing of overlapping amplicons confirmed the CPV-2 genome sequence determined by metagenomic sequencing. We submitted the strain SDS21601 sequence to GenBank (accession no. MZ666397).

We used a 5′-nuclease PCR to test 90 archived porcine lung samples submitted for respiratory disease diagnostic testing for CPV-2. Of the 90 samples, 9 (10%) were positive for CPV-2, including those with strain SDS21601, and Ct values were 22.4–36.3. The samples were collected September–November 2020 from swine farms within 150 miles of Brookings. We sequenced the genome from a second strongly positive sample (Ct 22.4) and submitted strain SDS21608 to GenBank (accession no. MZ666398). An amplicon from 4 of the remaining 7 samples positive by PCR was generated by PCR and confirmed as CPV-2 by Sanger sequencing. The 3 samples that failed to yield a CPV-2–specific amplicon had Ct values >32. Sequence comparison showed 99.9% nt identity between SDS21601 and SDS21608. blastp (https://blast.ncbi.nlm.nih.gov) analysis of SDS21601 virus capsid protein (VP) 2 found 100% identity to CPV-2 from a coyote sampled in Montana in 2012. Analysis of the VP2 amino acid sequences identified an F212I mutation previously identified only from US wildlife, mainly coyotes.

We performed in situ hybridization on archived formalin-fixed paraffin-embedded tissues from SDS21608 by using a commercially available CPV-2 probe. CPV-2 nucleic acids were hybridized sporadically as intracytoplasmic punctate signals in few monocyte–macrophage lineage cells in the medullary and subcapsular sinuses of a bronchial lymph node (Figure). However, the primary anatomic site of CPV-2 infection and replication was not determined. In other examined tissues, we observed neither typical...
of different species (7). Glycine 300 and tyrosine 305, observed in the VP2 of both swine CPV-2 strains (SDS21601 and SDS21608), are diagnostic of CPV-2 isolates from canids (7). The F212I mutation present in both swine CPV-2 strains, which was previously found only in wildlife, suggests a sylvatic origin. Of the species in which F212I has been identified, only coyotes are common in the agricultural areas of the upper US Midwest and are peridomestic. We hypothesize that the source of swine CPV-2 infection is CPV-2–positive coyote feces.

Our results demonstrate spillover of CPV-2 to swine. CPV-2 has been associated with severe enteritis in insectivorous Taiwanese pangolin (Manis pentadactyla pentadactyla), further demonstrating the propensity of CPV-2 to overcome host barriers (8). The ability of CPV-2 to cause disease in swine remains unknown; further surveillance is warranted because this spillover may threaten the health of swine herds.

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Dr. Temeeyasen is a research associate at the Animal Disease Research and Diagnostic Laboratory, South Dakota State University, in Brookings. His primary research interest is pathogenic porcine and bovine viruses.

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### Table

Antibody titers for CPV-2 and PPV-1 in serum collected from multiparous sows at origin farm of CPV-2 strain SDS21601 ≥8 months after collection of CPV-2–positive lungs, South Dakota, USA, 2020.

| Sow no. | CPV-2 titer | PPV-1 titer |
|---------|-------------|-------------|
| 3818    | 20          | 16          |
| 8985    | 10          | 256         |
| 3407    | 20          | 1024        |
| 4344    | 0           | 256         |
| 4345    | 10          | 512         |
| 3406    | 0           | 2048        |
| 3410    | 0           | 4096        |
| 37681   | 10          | 4096        |
| 38679   | 20          | 4096        |
| 39692   | 0           | 1024        |
| 4347    | 20          | 64          |
| 37683   | 20          | 2048        |
| 37673   | 40          | 2048        |
| 8980    | 0           | 256         |
| 445     | 10          | 512         |
| 8952    | 10          | 512         |
| 8953    | 0           | 2048        |
| 8981    | 20          | 1024        |
| 3817    | 20          | 0           |
| 10040   | 0           | 128         |

* Determined by hemagglutination inhibition. CPV-2, canine parovirus type 2; PPV-1, porcine parovirus type 1.
Antenatal Seroprevalence of Zika and Chikungunya Viruses, Kingston Metropolitan Area, Jamaica, 2017–2019

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To determine the extent of exposure to Zika virus (ZIKV) and chikungunya virus (CHIKV) in Jamaica, we collected serum from 584 pregnant women during 2017–2019. We found that 15.6% had antibodies against ZIKV and 83.6% against CHIKV. These results indicate potential recirculation of ZIKV but not CHIKV in the near future.

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1Preliminary results from this study were presented at the 2nd International Conference on Zika Virus and Aedes Related Infections; June 14–17, 2018; Tallinn, Estonia.

2Members of the ZIKAction Consortium are listed at the end of this article.

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