





## SARS-associated Coronavirus transmitted from human to pig

Weijun Chen, Minghua Yan, Ling Yang, Boliang Ding, Bo He, Yingzhen Wang, Xiuli Liu, Chenhui Liu, Hui Zhu, Bo You, Shengyong Huang, Jiangguo Zhang, Feng Mu, Zhao Xiang, Xiaoli Feng, Jie Wen, Jianqiu Fang, Jun Yu, Huanming Yang, and Jian Wang (For institutional affiliations see paper)

Key Points:

- Detection antibodies and RNA of SARS-CoV was attempted in blood and feces from pigs, cattle, dogs, cats, chickens, ducks, with positive RNA and antibody detection in 1 and 2 pigs, respectively.
- SARS-CoV was isolated from the one pig and sequenced.

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Sever acute respiratory syndrome (SARS) was first identified in the Chinese province of Guangdong in November 2002. A novel coronavirus, SARS-CoV was the causative agent. Several possible origins of the coronavirus were suggested such as Himalayan palm civets and racoon dogs. The virus infects other wild and domesticated animals, such as *Mustela furo*, *felis domesticus*, and *Nyctereutes procyonoides*, but infection of domesticated pigs has not been previously reported.

The study surveyed 6 major domestic animal species (e.g. pigs, cattle, dogs, cats, chickens, ducks) that are in close contact with humans and that could be infected by SARS-CoV if transmission were possible. The survey was conducted in a suburban area and its extended farming villages where the SARS outbreak occurred in late spring of 2003. Animal samples of blood and fecal swab specimens were collected and transported on ice to a laboratory within 24 hours. For the initial viral screen, immunological assays to identify antibodies and reverse transcription-polymerase chain reaction (RT-PCR) to detect viral genome were used.

Of 242 animals surveyed, 2 pigs were identified as antibody-positive. Of the 93 blood specimens and 15 fecal swabs tested with PCR, 1 of the previously cited 2 pigs tested positive. Viral isolates from its blood and fecal samples were obtained and designated TJB and TJF, respectively. Follow up studies were performed for 4 weeks until its blood tested PCR negative. Serum samples from the swineherd on the farm and a few persons who may have had contact with the swine herd were also obtained. All serum samples tested negative.

The TJF isolate was completely sequenced (GenBank accession no. AY654624) and compared its sequence to that of an early viral isolate, BJ01. With that, the authors suggested a human origin for the TJF strain. First it is only distantly related to SZ16, which was isolated from Himalayan palm civets of Southern China. Second, a sequence signature, GD01, which is found only in an early isolate but is absent from all the SARS-CoV isolates so far, is also absent in the TJF sequence. This sequence signature has been found in all coronavirus isolates of animal origin except from the pig identified in this study. Therefore, authors suggest that direct viral transmission of SARS-CoV from a human host to the pig bearing TJF is the most likely cause of infection. Additionally, a phylogenetic tree based on S-gene sequences shows that TJF is more closely related to human SARS-CoV isolates than to animal coronaviruses.

The authors raised the hypothesis that direct source of SARS-CoV transmission to the identified infected pigs was most likely virus contaminated animal feed because the farm where the infected pig was identified is rather remote, more than 1 KM away from the nearest village. The only person routinely in close contact with the animals is the swineherd owner, whose serum samples were negative for SARS-CoV on all tests. Swineherds in rural areas often obtain leftovers from restaurants in the cities to feed pigs without being cooked. Even if no direct evidence for human-to-swine SARS-CoV transmission exists, a strong warning should be issued to prevent such a practice, or regulatory procedures should be instituted to block this route of disease propagation.

Whether or not other domesticated (such as dogs and cats) and wild animals that are common in and around human settlements can easily contract and pass on SARS-CoV remains to be seen in future studies. Intensive surveillance and investigations on animals, especially during and after an outbreak of SARS, will lead to a better understanding and ability to control this disease's natural animal reservoirs and to prevent interspecies transmission events.

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