VETERINARY TODAY

Popular Article
ISSN: 2583-8288

Classical swine fever virus (CSFV) infection in pigs

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Abstract: Classical swine fever (syn. Hog cholera) is a notifiable disease caused by *Pestivirus* family *Flaviviridae*, CSFV. It is deemed a notifiable illness (each suspicious case must be looked upon, and when it is verified, the epidemic must be made aware) by the World Organisation of Animal Health (WOAH), is most likely the commercially significant viral infectious disease of farmed pigs. This disease is highly contagious and result in high morbidity and mortality as well as the rigorous trade and product limitations placed on pig and pork-derived goods, huge losses have occurred.The symptoms of the illness include a fever, lethargy, weakness, conjunctivitis, appetite loss, constipation, and diarrhoea. The article was prepared on the infection of CSFV in pigs, taking into consideration the severity of the illness and the financial losses it causes.

Introduction

CSF/Hog cholera is highly contagious disease which can easily widespread among swine population. The disease is having a noteworthy socioeconomic influence on the pig sector globally, including India (Nandi *et al.*,2011). Conjunctivitis, loss of hunger, dullness, weakness, fever, constipation and diarrhoea are some of the symptoms of the illness (Singh *et al.*,2017). The RNA virus known as the "classical swine fever virus" (CSFV) belongs to family *Flaviviridae* and genus *Pestivirus* (Patil *et al.*, 2019). CSFV is enveloped virus having a nucleocapsid that is icosahedral in shape and has a diameter of 40 to 60 nm. The enveloped virion incorporates glycosylated membrane proteins and this glycoprotein occur as a homodimer that is disulfide-bonded within the viral particle. The genetic material of virus is non-segmented, single chained RNA, having around 12,300 nucleotide sequences (Paton *et al.*, 2000).

Epidemiology

CSF is distributed worldwide and is considered as endemic in most of the parts of world including Europe, Africa and Central Asia (Arzt *et al.*,2010). First outbreak of the disease occurred in Ohio state of USA in the year 1833 but was considered bacterial (hog cholera bacillus) till CSFV discovery by Schweinitz and Dorset in 1903. In 1990's many number of CSF outbreaks were reported in different countries such as Italy (1995, 1996, 1997), Netherlands (1997), Belgium (1990, 1993, 1994) and Germany (1993-2000). Although it has been eliminated from Australia, Canada, the US, and nearly all of the other countries in Europe, outbreaks in domestic and wild pigs still happen in many areas on an irregular basis. Epidemiology and control of CSF is largely dependent on structure and density of pig population. Probability of spread of disease after outbreak is higher in locations with a higher density of pigs than places with a lower density. Pigs are the primary source of CSFV infection, either through raw pork products or infected live animals (through viral excretion via saliva, faeces, and urine). Moreover, the virus is also reported from semen causing natural breeding and artificial insemination as a additional sources of infection.

The disease has been described from several regions of India, although regular cases are documented from the north-eastern region, since vast amount of swines are raised by economically underprivileged segment of society (Paton *et al.*, 2000). The first case of the illness was discovered in Maharashtra in 1962, and it eventually spread to other states after first emerging in Uttar Pradesh (Shivraj *et al.*, 2015). Thes disease has been reported in many states of India such as Punjab (Patil *et al.*,2019), Kerala, Manipur, Tamil Nadu, Mizoram (Sapre *et*

al.,1962), Arunachal Pradesh, Karnataka, West Bengal, and Nagaland (Sandvik *et al.*, 1997),reports of the disease have been made.The phylogenetic analysis of specimens from epidemics that occurred between 2006 and 2008 found that the virus of Indian origin was divided into two subgroups, 1.1 and 2.2(Paton *et al.*,2000). Later studies carried out in 2014 revealed that the genotype 2.1 is circulating nort-eastern parts of India (Sapre *et al.*, 1962). But only one whole genome analysis of samples from Karnataka state has been reported in 2019 so far by NIVEDI-165CSV, and it identified subtype 1.1(Bhaskar *et al.*,2015). Wild pigs have also been shown to carry the CSFV, however there are very few data on its frequency and epidemiology in this community.

Pathogenesis

Traditional swine fever can be categorised into three different types: acute, which can be fatal or temporary, chronic, and persistent form. Infection during pregnancy is necessary for the persistent form of classical swine fever (Moennig *et al.*,2003). When a pig with an infection is unable to mount a sufficient immunological response it eventually leads to chronic cases, in which animal shows non-specific clinical signs and die after few months.

After infection virus replicates primarily in the tonsils and afterwards proceeds towards surrounding lymph nodes through lymphatic vessels. Main enmarks of the viruses is the immune system involving monocytes present in the peripheral blood and lymphocytes and granulocytes in the later stages of disease. In early stages of infection when animal is asymptomatic, high concentration of interferons (INF-α) are present and a progressive lymphopenia is discovered which ended up to extremerepression of immune system (Tarradas *et al.*,2014). Once incubation period is completed fever develops in animal and pathogen can be located in peripheral blood. Severe thrombocytopenia develops which may be due to abnormal expenditure of thrombocytes in peripheral blood and progressive degeneration of megakaryocytes is observed.

Diagnosis

Quick and authentic diagnostic measures are of need of hour for the control of disease and its further spread. Initial diagnosis of disease can be done on the basis of clinical signs, serological tests, virus isolation and PCR test but most of the CSF outbreaks are tentatively diagnosed on clinical symptoms. For direct diagnosis, virus isolation through porcine cell culture is still regarded as standard protocol but virus sometimes does not show specific CPE and infection observed through staining cells. RT qPCR technology has been developed for detection of CSFV and can distinguish between distinct virus types (Paton *et al.*,2000; Hoffmann *et al.*,2005). Since the 5'-UTR region of all pestiviruses is highly conserved, it is routinely targeted for CSFV detection. The test based on Nested PCR has high sensitivity and specificity compared to viral isolation which is recognized as gold standard test. In order to conduct comparative sequence analyses and investigate the genetic relationships between various CSFV isolates, the 5'UTR, E2, and NS5b genes were additionally amplified using RT-PCR (Paton *et al.*,2019). The prevalence of CSFV across India has been determined using ELISA based of antibody and antigen present in serum samples collected from different parts (Nandi *et al.*,2011). Recently, field based diagnostic test such as loop-mediated isothermal amplification (LAMP) assays (Zhang *et al.*,2010), is developed and can be employed for the detection of CSFV virus.

References

1. Arzt, J., White, W. R., Thomsen, B. V., & Brown, C. C. (2010). Agricultural diseases on the move early in the third millennium. Veterinary Pathology, 47(1), 15-27.
2. Bhaskar, N., Ravishankar, C., Rajasekhar, R., Sumod, K., Sumithra, T. G., John, K., ... &Aishwarya, J. (2015) Molecular typing and phylogenetic analysis of classical swine fever virus isolates from Kerala, India. Virus Disease, 26, 260-266.

3. Hoffmann, B., Beer, M., Schelp, C., Schirrmeier, H., &Depner, K. (2005) Validation of a real-time RTPCR assay for sensitive and specific detection of classical swine fever. Journal of Virological Methods, 130(1-2), 36-44.
4. Moennig, V., Floegel-Niesmann, G., &Greiser-Wilke, I. (2003) Clinical signs and epidemiology of classical swine fever: a review of new knowledge. The Veterinary Journal, 165(1), 11-20.
5. Nandi, S., Muthuchelvan, D., Ahuja, A., Bisht, S., Chander, V., Pandey, A. B., & Singh, R. K. (2011) Prevalence of Classical Swine Fever Virus in India: A 6-Year Study (2004– 2010). Transboundary and Emerging Diseases, 58(5), 461-463.
6. Patil, S. S., Suresh, K. P., Amachawadi, R. G., Meekins, D. A., Richt, J. A., Mondal, M., Hiremath, J., Hemadri, D., Rahman, H. & Roy, P. (2019) Genome sequence of classical swine fever virus NIVEDI-165, subtype 1.1, a field virus strain isolated from the Southern part of India. Microbiology Resource Announcements, 8(21), e00295-19.
7. Paton, D. J., McGoldrick, A., Greiser-Wilke, I., Parchariyanon, S., Song, J. Y., Liou, P. P., Stadejek, T., Lowings, J.P., Björklund, H. &Belak, S. (2000) Genetic typing of classical swine fever virus. Veterinary Microbiology, 73(2-3), 137-157.
8. Sandvik, T., Paton, D. J., &Lowings, P. J. (1997) Detection and identification of ruminant and porcine pestiviruses by nested amplification of 5′ untranslated cDNA regions. Journal of Virological Methods, 64(1), 43-56.
9. Sapre, S. N., Moghe, R. G., Bhagwat, S. V., Choudhary, D. G., &Purohit, B. L. (1962) A note on observations and investigation into an outbreak of swine fever in Bombay. Indian Veterinary Journal, 39, 527-534.
10. Shivaraj, D. B., Patil, S. S., Rathnamma, D., Hemadri, D., Isloor, S., Geetha, S., Manjunathareddy, G.B., Gajendragad, M.R. & Rahman, H. (2015) Genetic clustering of recent classical swine fever virus isolates from Karnataka, India revealed the emergence of subtype 2.2 replacing subtype 1.1. Virus Disease, 26, 170-179.
11. Singh, V. K., Rajak, K. K., Kumar, R., Raut, S. D., Saxena, A., Muthuchelvan, D., Singh, R.K. & Pandey, A. B. (2017) Changing pattern of classical swine fever virus genogroup from classical 1.1 to emerging 2.2 in India. Virus Disease, 28, 174-181.
12. Tarradas, J., de la Torre, M. E., Rosell, R., Perez, L. J., Pujols, J., Muñoz, M., Muñoz, I., Muñoz, S., Abad, X., Domingo, M. & Ganges, L. (2014) The impact of CSFV on the immune response to control infection. Virus Research, 185, 82-91.
13. Zhang, C., Wang, C., Chen, X., Yang, C., Li, K., Wang, J., Dai, J., Hu, Z., Zhou, X., Chen, L. & Zhang, C. Y. (2010) Expression profile of microRNAs in serum: a fingerprint for esophageal squamous cell carcinoma. Clinical Chemistry, 56(12), 1871-1879.