THE SCIENCE WORLD
A Monthly e Magazine
ISSN:2583-2212
Oct, 2023; 3(10), 2504-2507

Popular Article

Porcine Circovirus (PCV) in pigs

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https://doi.org/10.5281/zenodo.8417984

Abstract

In India, pig farming is one of the most viable and lucrative animal industries, and the pork sector plays a significant role in ensuring food security. Pig diseases are frequently complicated and can result in multifactorial situations, particularly when they are respiratory illnesses brought on by the porcine circovirus. Porcine circovirus (PCV) infection in pigs develop wide variety of diseases. This is responsible for significant economic loss to the swine industry. The virus is categorised under the family *Circoviridae* of the genera *Circovirus*.The virus can cause substantial mortality which may reach up-to 50%. Keeping in view the severity of the disease and the economic losses caused by it, the article was written on the infection of Porcine Circovirus in swine population.

Introduction

A wide variety of disorders in pigs are brought on by PCV, which also has a significant economic impact. It covers a number of illnesses that affect pigs between the ages of 3 and 26 weeks, including Proliferative and Necrotizing Pneumonia (PNP), Porcine Respiratory Disease Complex (PRDC) and Porcine Dermatitis and Nephropathy Syndrome (PDNS), and (Oliver *et al.*, 2016). Symptoms of this illness include diarrhoea, slowed growth, spontaneous abortion, breathing problems and edoema of the appendages (Segales *et al.*, 2012).

Structure

The respiratory virus which is a DNA virus included in genus *Circovirus* of *Circoviridae* family. With a diameter of 17–22 nm and the ability to replicate on its own, PCV is a tiny animal virus (Tischer *et al*., 1982). They are single chained circular DNA pathogen with symmetry of an octahedron and capable of performing autonomous replication in cells of mammals (Mankertz *et al.*, 1997). Replication of virus takes place in the nucleus of cycling cells and produce large intracellular inclusion bodies. The DNA of virus is encapsulated in single viral capsid protein which has 60 subunits (Mankertz *et al.*, 1997). Three different strains of the virus have been recognised, designated as porcine circovirus class1 (PCV1), 2 (PCV2), and 3 (PCV3). Later in 2020 Zhang and his co-workers discovered new strain of PCV named PCV type 4. The genotypes of PCV2—PCV2a, PCV2b, PCV2c, PCV2d, and PCV2e—have been further discoveredon the basis of phylogenetic study of the cap gene and the entire genome.

Epidemiology

PCV is considered ubiquitous, highly prevalent in worldwide pig population. Porcine circovirus, now named as PCV1 was initially extracted as a source of contamination from the kidney cell line of porcine origin (PK-15) (Tischer *et al.,* 1974). The serological prevalence of PCV1 was reported in domestic pigs of North America and Europe but the virus did not show any correlation with other swine diseases. In the year 2016, PCV3 virus was identified in the sows of USA showing PDNS like physical symptoms or inflammation in multiple organs and the heart. Since that time, reports of the virus from numerous nations have been ongoing such as Brazil, China, Denmark, Japan, Italy, Russia, Spain, South Korea, Sweden and Thailand, indicating worldwide distribution of the disease (Hayashi *et al.,* 2018).

In 2006, India reported the first instance of PCV2 systemic disease (PCV2-SD) in pigs exhibiting Post-Weaning Multisystemic Wasting Syndrome (PMWS) symptoms. Diverse genotypes, such as PCV2a-2D, PCV2b-1C, and PCV2d, were discovered in the country through heterogenetic analysis of the PCV2genome. Recombination was also confirmed (Rajkhowa *et al.,* 2021). In 2015, Bhattacharjee *et al*. revealed the whole genomic sequence of the Indian porcine circovirus types 2a and 2b (north eastern states). Prior to this, the only virus known to cause common illnesses in pigs was PCV type 2, however later on, pigs were also found to have contaminationof 3rd strain of PCV (PCV3) (Phan *et al.,* 2016). In North eastern part of India, the positivity rate for mean PCV2 antibody was reported as 31.27% from 2011 to 2017, however in 2019, samples taken from all states of northern India, such asAssam, Manipur, Mizoram, Meghalaya, Nagaland, Tripura, and Sikkim, showed a positive rate of 49.35% (Barman *et al.,* 2018). Seropositivity of 6.28% was observed by Deka and co-workers in the pigs of north eastern states which were not vaccinated, however in Punjab, 34.07% seroprevalence was discovered (Deka *et al.,* 2021). Additionally, it has been discovered that the PCV2 is linked to 88.46% neonatal mortality and 20.00% stillbirth in a private pig farm in Tamil Nadu, India's Poosaripalayam village (Kumar *et al.,* 2014).

Pathogenesis

In the world's pig population, PCV is extremely common. A retrospective serological study indicates that PCV2 infection in pigs' dates back more than 50 years and phylogenetic studies indicate that virus is circulating in pigs since 100 years (Rose *et al.,* 2012). PCV has a high level of environmental resistance and persistent shedding in respiratory and oral secretions. It's difficult to achieve absolute inactivation of the virus and extended exposure time is required for disinfection (Rose *et al.,* 2012). This virus can spread through faeces, urine, direct contact, through colostrum, through seminal fluid and through placental contact (Gillespie *et al.,* 2009). Pathogenesis of the PCV depends on the type of virus strain infecting the pig. Out of three strains of PCV type 1 is considered non-infectious causing no disease in swine while type 2 and 3 are considered highly pathogenic (Mettenleiter & Sobrino, 2008). PCV2 causes PMWS (post weaning multisystemic syndrome) which results into lymphocyte depletion and enlargement of lymph nodes. Impairment of immune system is the main characteristic of PCV2 directly infecting macrophages and endothelial cells leading to acquired immunodeficiency in infected pigs. Endothelial cell infection causes vascular thrombi, perivascular and intramural edoema, fibrinoid necrosis, the activation of the phenotypic, and endothelial cell degeneration.Infected animals' thymus, bone marrow, and thymic lymphocyte macrophages exhibit PCV2 positivity. Pigs infected with PCV3 show characteristic lesions of PDNS such as destructive inflammation of

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Published: 7.10.2023

blood vessels, bronchointerstitial pneumonia, glomerulonephritis and granulomatous lymphadenitis.

Diagnosis

Diagnosis of PCV infection in pigs involves 3 main criteria i.e. accordant clinical symptoms, distinctmicroscopic lesions and presence of virus specific antigens or DNA in the lesions (Rosell *et al.,* 2000). The disease is difficult to diagnose since PCV2 is linked to so many disorders and because an infected animal may not exhibit any clinical symptoms. A conclusive detection of the disease related to PCV infection were made on the basis of the identification of pathogenic antigen and/or genomic content connected to injuriesin sick animals. When determining whether a virus is present in the pig population, histopathological studies are extremely helpful (Sharma *et al.,* 2010). Localized death of the living cells in growing organs, such as kidneys, liver, heart, brain, spleens, lymph nodes, as well as organs of respiratory system and hepatic system, accounted for the majority of the histological changes observed in aborted foetuses. The enzyme-linked immune sorbent assay (ELISA), which detects serum antigen and antibody, have been quite helpful in determining the seroprevalence of the virus in the nation (Rajkhowa *et al.,* 2021; Deka *et al.,* 2021). In the country's north-eastern region, the PCV2 was amplified with the help of PCR targeting ORF2 gene to identify the disease (Mukherjee *et al.,* 2018). A variety of real-time PCR assays such as Taq-man-based and SYBR Green-based have been described globally for the identificationof PCV2 (Ouyang *et al.,* 2019). Recently, isothermal assays such as Loop-mediated isothermal amplification (LAMP), and Recombinase polymerase amplification (RPA) and indirect enzyme-linked immunosorbent assays (ELISAs) are a few of the diagnostic tests that have been developed to detect PCV3 infection in pigs (Chen *et al.,* 2018).

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Published: **7.10.2023**

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