

SHORT REPORT

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Characterization of a PCV2d-2 isolate by experimental infection of pigs

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Abstract

Porcine circovirus type 2 (PCV2), a highly prevalent, economically important swine pathogen is classified into different genotypes (PCV2a-f) based on phylogenetic analysis. Since the introduction of extensive vaccination programs, at least two major shifts have been observed in the prevalence of PCV2 genotypes. The first genotype shift from 2a towards 2b occurred around 2003, while in recent years, we are witnessing the second change in genotype prevalence from the predominant 2b towards 2d. In this study, a PCV2d-2 isolate was characterized as a potential challenge virus for the evaluation of PCV2 vaccine efficacy. Ten-week-old pigs carrying low to moderate levels of maternally derived antibodies to PCV2 were infected with the isolate by the nasal route. Over the next 4 weeks post-infection, the pigs were monitored for the presence of viremia, fecal virus excretion, and humoral immune responses. At the end of the post-infection observation period, samples were taken from the mediastinal and mesenteric lymph nodes of the animals and tested for viral load. The gradual depletion of maternally derived antibodies in the sera of piglets was demonstrated by ELISA and virus neutralization tests. Following experimental infection by PCV2d-2, specific IgM antibodies were first detected at 14 days post challenge (dpch), while IgG class antibodies were first detected at 21 dpch. Both viremia and virus shedding could be detected at 7 dpch, in 36 and 50% of the pigs, respectively. The proportion of shedders reached 100% by 14 dpch and remained at this level, while viremia was demonstrated in 86, 100, and 100% of the pigs at 14, 21, and 28 dpch, respectively. Both the mediastinal and mesenteric lymph nodes contained high levels of virus (7.6 and 8.5 log₁₀ copies/mg tissue, respectively).

Keywords: PCV2d-2, Viremia, Excretion, Virus neutralization

Main text

Porcine circovirus type 2 (PCV2) was first described in 1998 [1], and since then, it has become one of the most important pig pathogens, contributing to considerable economic losses by a syndrome called porcine circovirus disease (PCVD). The virus has demonstrated the highest evolution rate among similar DNA viruses, resulting in genetic shifts even over the rather short period of time since its recognition [2]. Today six genotypes of PCV2 are known, PCV2a-f [3]. PCV2d is the most widespread genotype [4], which is further subdivided into PCV2d-1 and 2 [5]. Pathogenicity of PCV2 is complex, and presumably involves the infection of pig fetuses, especially their thymus, where the virus establishes a latent infection. Changes of this fetal viral pool due to environmental

factors such as stress, vaccination and last but not least, the genetics of the host, will determine the outcome of the infection [6].

In the field, PCVD is controlled by vaccination and intensifying the biosecurity measures on pig farms, and by the development of high hygiene systems of environmental control based on the recommendations of Madec et al. [7]. Current vaccines, comprising PCV2a strains or their proteins, have proven effective for protecting against clinical disease in pigs when challenged with PCV2a, PCV2b, or PCV2d, especially in controlled conditions [2]. Evaluating vaccines presumes access to appropriate challenge strain(s). Therefore, the aim of this study was to characterize a PCV2d-2 isolate, by using parameters such as viremia, virus shedding, and viral load in lymph nodes. Also, different assays to monitor humoral immune responses after challenge were assessed.

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