Distinction between infections with European and American/vaccine type PRRS virus after vaccination with a modified-live PRRS virus vaccine

In July 1996 a modified live Porcine reproductive and respiratory syndrome (PRRS) vaccine, based on an American (US) strain of the PRRS virus (PRRSV), was licensed in Denmark. The vaccine was licensed for use in 3-18 week old pigs, exclusively. Starting during the middle of October 1996, several herds who had recently begun vaccination, experienced acute PRRS-like symptoms including an increasing number of abortions and stillborn piglets and an increasing mortality in the nursing period. During the period from October 1996 until May 1997, the PRRS virus (PRRSV), identified as the vaccine/US type of PRRSV, was isolated from fetuses, dead piglets, pleural fluids and/or lung tissues from 114 of such herds. These findings indicated the spread of the vaccine virus to non-vaccinated sows followed by transplacental infection of fetuses. Also, a number of not previously PRRSV infected and non-vaccinated herds in Denmark have become infected with the vaccine-like PRRSV. Possible routes of transmission are the introduction of vaccinated pigs to the herd, use of semen from artificial insemination (AI) centres or airborne transmission. The situation of PRRS in Denmark is now complicated by the fact that both the European (EU) type and the US type of PRRSV are circulating among their herds. It is not clinically possible to differentiate between the two different types of infections. At the Danish Veterinary Institute for Virus Research (DVIVR), diagnostic tools have been developed to distinguish between the two types of infections, and both virological and serological methods are now available for distinction. The diagnostic tests used at DVIVR to diagnose PRRS and to differentiate between EU and US strains of PRRSV infections are described below. The distinction between infection with the two types of PRRSV was made on a serological basis. The immunoperoxidase monolayer assay (IPMA), carried out using a Danish strain (IPMA/DK) and the vaccine strain (IPMA/vac) in parallel, allows the distinction of infections with EU and US strains of PRRSV. In herds infected with the EU type, the titer in individual samples is higher in the IPMA/DK compared to the titer in the IPMA/vac, while in herds infected with the vaccine/US type, the titers are highest in the IPMA/vac. Furthermore, a double blocking ELISA has been developed, which enables large scale screening for and simultaneous distinction between antibodies against EU and US strains of PRRSV. This test is performed using a Danish PRRSV isolate and the vaccine strain in parallel. The results of the ELISA tests are given as negative or positive for each sample. For positive samples a ratio is calculated (ratio = ODp blocking ELISA-DK / ODp blocking ELISA-Vac), which enables us to serologically distinguish between EU and US strains of PRRSV infections. In herds infected with the Danish strain of PRRSV, most animals have a ratio below 1, while in herds infected with the vaccine/US strain most animals have a ratio above 2. The distinction between infections with the two types of PRRSV was made by virus isolation. As the porcine pulmonary alveolar macrophages (PPAM) are found to be the most sensitive system for isolation of PRRSV field strains, while the vaccine strain, when taken directly from the bottle, grows in the MARC 145 cell line and not in the PPAM, both cell types have routinely been used in parallel at our institute since the introduction of the PRRS vaccine in Denmark. However, from our experience, the vaccine virus becomes able to replicate in PPAM during in vivo passages. For typing of the PRRSV isolates as EU or US/vaccine isolates, three monoclonal antibodies (mAb) are used in an IPMA: SDOW 17 reacting with most EU and US isolates including the vaccine strain, VO 17 reacting with some US isolates including the vaccine strain but not with EU PRRSV isolates, and WBE 4 reacting with most EU isolates, but not with US isolates. The detection and typing of PRRSV was made by RT-PCR. An RT-PCR test which sensitively detects and types PRRSV from relevant biological material and provides a maximal amount of sequence information by amplification of whole viral open reading frames, has been developed at our institute. To provide maximal sequence information, complete viral open reading frames (ORFs 5 and 7) are targeted for amplification. Typing of viruses is accomplished by any one of three strategies: (a) DNA sequencing, (b) type-specific PCR primers, (c) size determination of ORF7 amplicons. All three typing strategies show complete concordance with the currently used method of typing with monoclonal antibodies when used on a panel of PRRSV field isolates covering the period 1992-1997. The ORF7-based test had particularly desirable characteristics, namely highly sensitive detection of PRRSV without apparent type bias, typing of the detected virus, discrimination between pure and mixed virus populations, and semi-quantitative assessment of type-ratios in mixed populations, all in a single PCR reaction. The blocking ELISA is routinely used at our institute for PRRSV antibody screening, making it possible to distinguish between the EU and US type PRRSV in infected herds. IPMA is mostly used for serologic herd profiles to determine the spread of PRRSV within herds, based on the level of the IPMA titers. However, the IPMA can also be used to differentiate between the two different PRRSV type of infections. For detection and typing of PRRSV, we routinely use virus isolation and mAb typing. For selected cases RT-PCR followed by DNA sequencing are performed to confirm mAb typing or get more detailed information.
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SJR 1.266 SNIP 1.139
Web of Science (2017): Impact factor 2.903
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.44 SNIP 1.303
Web of Science (2016): Impact factor 2.798
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.66 SJR 1.537 SNIP 1.153
Web of Science (2015): Impact factor 2.928
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.46 SJR 1.453 SNIP 1.423
Web of Science (2014): Impact factor 2.815
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3.13 SJR 1.681 SNIP 1.701
Web of Science (2013): Impact factor 3.383
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.97 SJR 1.461 SNIP 1.45
Web of Science (2012): Impact factor 3.426
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.85 SJR 1.712 SNIP 1.655
Web of Science (2011): Impact factor 4.06
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.531 SNIP 1.606
Web of Science (2010): Impact factor 3.765
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.489 SNIP 1.689
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.578 SNIP 2.002
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Scopus rating (2007): SJR 1.749 SNIP 2.189
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Scopus rating (2006): SJR 1.353 SNIP 1.936
Scopus rating (2005): SJR 0.885 SNIP 1.567
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.79 SNIP 1.3
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.727 SNIP 1.068
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