Monitoring of European PRRSV strains using sequencing technologies

ESPHM-0203

Sandrine MOINE1, Anne QUILADA1, Stéphane DALY1, Nardy ROBBEN2, Alex RAEBER3

1Thermo Fisher Scientific, Lissieu, France
2Thermo Fisher Scientific, Bleiswijk, Netherlands
3Thermo Fisher Scientific, Schlieren-Zürich, Switzerland

INTRODUCTION

Porcine reproductive and respiratory syndrome (PRRS) is considered one of the most economically important infectious diseases of swine. PRRS is caused by a RNA virus with a high mutation rate.

Thermo Fisher Scientific has improved sequencing workflows over the years, resulting in a larger percentage of field samples which can be sequenced (either whole genome sequencing or targeted). The quality of the sample impacts the options for sequencing. With the optimized workflows, even samples with different viral load can be sequenced. Sequencing positive samples give additional information about the origin of the sample and if it could be related to used vaccines or new field infections. Having this information helps the veterinarians and farm manager to evaluate the PRRS management and biosecurity in farms.

MATERIALS AND METHODS

Thermo Fisher Scientific established different partnerships to collect more than 100 PRRSV positive samples in more than 10 different countries (Figure 1).

Sequencing strategy applied depends on PRRSV viral load and quality of the sampling process: sample collection, storage, shipment (Figure 2). For 82 samples containing a high/medium PRRS viral load with a high quality sampling, RNA-Seq or Long Range protocols on PGM instrument were applied in order to obtain whole PRRS genome sequences. For 20 samples containing a weak viral load or with a poor quality, capillary electrophoresis protocol on Genetic Analyzer was performed in order to obtain a specific target sequence of PRRS genome (ORF7 sequence).

RESULTS

Figure 4: Sequenced samples

Figure 5: Phylogenetic trees of sequenced samples

CONCLUSIONS

Compared to a Real Time PCR assays that enables the pathogen presence/absence, sequencing approaches offer the possibility to identify new PRRSV strains.

The monitoring of circulating European PRRSV strains using sequencing technologies enables to sequence RNA, directly isolated from various field samples.

Thermo Fisher Scientific offers a range of adapted workflows from the sampling, extraction methods to the sequencing solutions.

ACKNOWLEDGEMENTS

- Sarah McGuigan, Virology and Animal Health Agency (APHA), UK
- Katarzyna Podgorska, Swine Diseases Department, National Veterinary Research Institute (NVRI), Poland
- Tomasz Sladkiewicz, Warsaw University of Life Sciences, Faculty of Veterinary Medicine, Poland
- Ivan Topali, National Veterinary Institute (NVI), Slovenia
- Beatrice Bonini, Istituto Zooprofylattico Sperimentale (IZS), Italy
- Jordi Serra Martinez, BIOPHAR Laboratories, S.L, Spain
- Enric Mateu, CRESA, Spain
- Adolf Dienstl, Agentur für Gesundheit und Ernährungssicherheit GmbH (AGES), Austria

TRADEMARKS/LICENSING

- Applied Biosystems™ MagMAX™ Pathogen RNA/DNA Kit™
- Applied Biosystems™ LSI VeloMAX™ PRRSV ELUNA-kit™
- Applied Biosystems™ QuantStudio™ 5
- Thermo Scientific™ KingFisher™ pit
- Ion Torrent™
- Ion PGM™ next generation sequencers™

©2017 Thermo Fisher Scientific Inc. All rights reserved. All trademarks are the property of Thermo Fisher Scientific and its subsidiaries.

* For veterinary use only. Regulatory requirements may vary by country; products may not be available in your geographic area.
** For research use only. Not for use in diagnostic procedures.