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**Thermo Fisher Scientific Research Monitors Genetic Diversity of European PRRSV**  
*Diagnostic research presented at International Pig Veterinary Society Congress*

**DUBLIN, Ireland** — June 7, 2016 — The porcine reproductive and respiratory syndrome (PRRS) virus mutates rapidly, especially European strains, creating a challenge for diagnostic laboratories to monitor the disease. Today, Thermo Fisher Scientific presented research at the Pig Veterinary Society (IPVS) Congress showing the genetic diversity of the PRRS virus and how the company is monitoring and evolving its diagnostic tools to ensure highly accurate results.

PRRS is caused by a single stranded RNA enveloped virus with a high mutation rate which leads to greater heterogeneity of the nucleotide sequence between the individual strains.

“The high genetic virus diversity we see with PRRS increases the risk of reduced sensitivity for a real-time PCR diagnostic tool,” said Nardy Robben, product manager at Thermo Fisher Scientific and research presenter at the IPVS Congress in Dublin. “To monitor and understand the virus diversity and to test our diagnostic tools’ capabilities, we regularly monitor circulating PRRS strains in Europe by both target sequencing and whole genome sequencing.”

**Study Monitors PRRSV Strains, Diagnostic Design**

Thermo Fisher analyzed more than 120 PRRSV positive samples collected by collaborating laboratories and research institutes in Spain, Italy, United Kingdom, Belgium, the Netherlands, Czech Republic, Poland, Slovenia and Russia. Samples with a high PRRS viral load were sequenced using RNA-Seq workflow on Ion Torrent PGM instrument to obtain whole genome sequences. For samples with low PRRS viral load, target sequencing was performed using capillary electrophoresis.

The results showed that the main subtypes of the PRRS Type 1 (European strain) were present in the collected samples. Target (ORF7) sequencing, the method traditionally used, was very useful to highlight important variability on this viral gene region. Whole genome sequencing, using the RNA-Seq workflow on Ion Torrent, recognized that many gene regions outside of ORF 7 also displayed high variability.

To detect new strains, primers are designed using bioinformatics analysis software, followed by internal validation of the resulting diagnostic PCR test to show that Thermo Fisher has designed a primer to match the new PRRS sequences, while not interfering with the detection of the old PRRS sequences.

“Monitoring the circulating strains is necessary to identify new variants,” said Nardy Robben. “Employing new sequencing technologies allows us to keep our knowledge of the virus up to date which is essential to deliver accurate diagnostic tools to our customers.”

For more information about PRRS virus and our diagnostic tools, please visit [www.thermofisher.com/animalhealth](http://www.thermofisher.com/animalhealth).

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