VVD-PP-54

TITLE

PRRSV1 INFECTION IMPACT IN THE INTESTINAL MICROBIOME COMPOSITION: A COMPARATIVE STUDY WITH STRAINS OF DIFFERENT VIRULENCE

HECTOR ARGUELLO[1], Irene Magdalena Rodríguez-Gómez[2], Jose María Sánchez-Carvajal[3], Francisco José Pallares[4,5], Fiona Crispie[6], Raúl Cabrera[6], Enric Mateu[7], Gerard Martín-Valls[8], Librado Carrasco[3], Jaime Gómez-Laguna[9]

[1] Grupo genómica y mejora animal. Departamento de Genética. Universidad de Córdoba.
[2] Department of Anatomy and Comparative Pathology, Faculty of Veterinary Medicine, University of Cordoba, Cordoba, Spain.
[3] Department of Anatomy and Comparative Pathology, Faculty of Veterinary Medicine, University of Cordoba, Spain
[4] Dpto. Anatomía y Anatomía Patológica Comparadas. Facultad de Veterinaria. Universidad de Murcia. Spain
[5] Instituto Murciano de Investigación Bisoanitaria IMIB). Murcia.
[6] Teagasc
[7] Centre de Recerca en Sanitat Animal, Universitat Autónoma de Barcelona
[8] Departament de Sanitat i Anatomia animals, Universitat Autònoma de Barcelona (UAB), 08193, Barcelona
[9] Department of Anatomy and Comparative Pathology, Faculty of Veterinary Medicine, University of Cordoba, Cordoba, Spain

CONTENT

Background and Objectives
Porcine reproductive and respiratory syndrome virus (PRRSV) infection is characterised by respiratory lesions, viral replication in alveolar macrophages and lymphoid organs and a strong early local inflammatory response together with a loss of the global condition of the animal. Infection outcome depends on PRRSV strain virulence and clearly impacts the respiratory tract microbiome directly. Here we aim at deciphering the indirect impact of an experimental infection with highly pathogenic PRRSV strain (Lena) and a low pathogenic strain (3249) in the intestinal microbiota through the first 13 days post-infection.
Material & Methods
Seventy four-week old piglets were distributed in three different groups: (i) control, (ii) 3249 strain (low virulent) and (iii) Lena strain (high virulent). Animals were euthanised at 1, 3, 6, 8 and 13 days post-infection (dpi) to analyse lung lesions and blood and faeces samples were collected and routinely processed to determine viraemia (RT-qPCR) and analyse the microbiome by 16S rRNA amplicon sequencing (MiSeq) (Illumina Inc., Cambridge, UK).
Results
Study results showed that PRRS infection ($p=0.02$) and strain virulence ($p=0.05$) alter the diversity of the faecal gut microbiota, with clear changes in microbiome richness and evenness from 6 dpi onwards. Similarly, the infection altered the ordination of the microbiome composition, although no apparent differences were observed between strains. These global microbiome changes were reproduced at taxonomic level. Significant differences in operational taxonomic units (OTUs) belonging to genera Ruminococcus, Prevotella or Oscillibacter were observed between infected and non-infected pigs. There were also differences in abundance of OTUs such as Fusobacterium, Cloabacillus or Anaerovibrio between Lena- and 3249- infected groups.
Discusssion & Conclusion
Our results reflect the indirect impact of PRRSV infection and strain virulence in faecal microbiome composition. Further analysis are addressed to correlate early inflammatory response to microbial changes in the gut.