Transcriptional profiling at different sites in lungs of pigs during acute bacterial respiratory infection - DTU Orbit (27/03/2019)

Transcriptional profiling at different sites in lungs of pigs during acute bacterial respiratory infection
The local transcriptional response was studied in different locations of lungs from pigs experimentally infected with the respiratory pathogen Actinobacillus pleuropneumoniae serotype 5B, using porcine cDNA microarrays. This infection gives rise to well-demarcated infection loci in the lung, characterized by necrotic and haemorrhagic lesions. Lung tissue was sampled from necrotic areas, from visually unaffected areas and from areas bordering on necrotic areas. Expression pattern of these areas from infected pigs was compared to healthy lung tissue from un-infected pigs. Transcription of selected genes important in the innate defence response were further analysed by quantitative realtime reverse-transcriptase PCR. A clear correlation was observed between the number of differentially expressed genes as well as the magnitude of their induction and the sampling location in the infected lung, with the highest number of differentially expressed genes, and the most highly induced genes found in necrotic areas. Interestingly, a group of differently regulated genes was represented in all three areas, comprising genes encoding cytokines, acute phase proteins, and factors related to regulation of apoptosis and the complement system. Interferon-g was downregulated in both necrotic and bordering areas. Evidence of neutrophil recruitment was seen by the up-regulation of chemotactic factors for neutrophils. In conclusion, we found subsets of genes expressed at different levels in the three selected areas of the infected lung as compared to the control group. Thus it is demonstrated that an infection with clearly defined infected loci leads to a rapid disseminated intra-organ response in neighbouring seemingly unaffected tissue areas of the infected organ. Within the lung, we found a clear division of induced genes as, in unaffected areas a large part of differently expressed genes were involved in systemic reactions to infections, while differently expressed genes in necrotic areas were mainly concerned with homeostasis regulation.

General information
State: Published
Organisations: Innate Immunology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Aarhus University
Contributors: Mortensen, S., Skovgaard, K., Hedegaard, J., Bendixen, C., Heegaard, P. M. H.
Pages: 41-53
Publication date: 2011
Peer-reviewed: Yes

Publication information
Journal: Innate Immunity
Volume: 17
Issue number: 1
ISSN (Print): 1753-4259
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.34 SJR 1.031 SNIP 0.686
Web of Science (2017): Impact factor 2.312
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.7 SJR 1.169 SNIP 0.816
Web of Science (2016): Impact factor 2.342
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.55 SJR 1.264 SNIP 0.836
Web of Science (2015): Impact factor 2.83
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.65 SJR 1.275 SNIP 0.965
Web of Science (2014): Impact factor 3.271
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.47 SJR 1.146 SNIP 0.825
Web of Science (2013): Impact factor 2.459
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1