



University of Southern Denmark

## Identification of Common Bacterial Antigenic Markers From Bovine Digital Dermatitis Lesions Using Meta-Transcriptomics in Combination With High-Density Peptide-Microarrays

Nielsen, Martin W.; Marcatili, Paoli; Sicheritz-Ponten, Thomas; Jensen, Tim K.; Schafer-Nielsen, Claus; Boye, Mette; Nielsen, Morten; Klitgaard, Kirstine

*Publication date:*  
2017

### *Citation for published version (APA):*

Nielsen, M. W., Marcatili, P., Sicheritz-Ponten, T., Jensen, T. K., Schafer-Nielsen, C., Boye, M., Nielsen, M., & Klitgaard, K. (2017). *Identification of Common Bacterial Antigenic Markers From Bovine Digital Dermatitis Lesions Using Meta-Transcriptomics in Combination With High-Density Peptide-Microarrays*. Abstract from 2nd International Symposium on Alternatives to Antibiotics, Challenges and Solutions in Animal Production, Paris, France.

### **Terms of use**

This work is brought to you by the University of Southern Denmark through the SDU Research Portal. Unless otherwise specified it has been shared according to the terms for self-archiving. If no other license is stated, these terms apply:

- You may download this work for personal use only.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying this open access version

If you believe that this document breaches copyright please contact us providing details and we will investigate your claim. Please direct all enquiries to [puresupport@bib.sdu.dk](mailto:puresupport@bib.sdu.dk)

## IDENTIFICATION OF COMMON BACTERIAL ANTIGENIC MARKERS FROM BOVINE DIGITAL DERMATITIS LESIONS USING META-TRANSCRIPTOMICS IN COMBINATION WITH HIGH-DENSITY PEPTIDE-MICROARRAYS

MW Nielsen<sup>1\*</sup>, P Marcatili<sup>2\*</sup>, T Sicheritz-Pontén<sup>2</sup>, TK Jensen<sup>1</sup>, C Schafer-Nielsen<sup>3</sup>, M Boye<sup>4</sup>, M Nielsen<sup>2,5</sup> & K Klitgaard<sup>1</sup>

<sup>1</sup>National Veterinary Institute, Technical University of Denmark, Bülowsvej 27, 1870 Frederiksberg C, Denmark, <sup>2</sup>Center for Biological Sequence analysis, Technical University of Denmark, Kemitorvet, 2800 Kgs. Lyngby, Denmark, <sup>3</sup>Schafer-N ApS, Lersø Parkallé 42, 2100 Copenhagen; <sup>4</sup>Molecular Diagnostic and Clinical Research Unit, Hospital of Southern Jutland, 6400 Sønderborg, Denmark; <sup>5</sup>Instituto de Investigaciones Biotecnológicas, Universidad Nacional de San Martín, Buenos Aires, Argentina.

\*These authors contributed equally to this work

[kksc@vet.dtu.dk](mailto:kksc@vet.dtu.dk), [mawen@vet.dtu.dk](mailto:mawen@vet.dtu.dk)

Bovine digital dermatitis (DD) is the most important infectious cause of lameness in dairy cattle, and a major contributing factor to welfare problems and economic losses in the dairy cattle industry worldwide. DD is a disease that involves chronic dermal inflammatory processes and destruction of collagenous and connective tissues. Multiple *Treponema* species, many of which are not-yet-cultivable, are strongly implicated in disease progression. Despite the economic and welfare importance of this disease, no effective vaccine is available; and there is presently very little knowledge concerning efficacious immunoprophylactic antigens against DD. It is highly likely that DD-associated treponemes possess considerable antigenic variation, as cows exhibit a variable humoral response against different isolates of *Treponema*. Hence, combinations of antigens from multiple *Treponema* species should be used for the development of disease prevention measures. As treponemes from DD lesions are extremely difficult to culture, identification of these antigens is challenging. To circumvent this problem, we studied the *in situ* gene expression patterns of the microbiome in DD-affected skin lesions and the host antibody response directed at the site of infection. By metatranscriptomics we measured the *in situ* genome-wide transcriptome of the bacterial population in DD-affected skin lesions from 21 dairy cows. From the transcriptome data, we identified a panel of *Treponema* genes that were highly expressed in multiple animals, and we monitored the host immune response to these target genes using high-density peptide microarrays. By this approach, we identified a small group of antigenic proteins, which were expressed in the majority of the samples, and demonstrated antigenicity when screened against sera from infected animal. Future studies will show if these proteins represent candidates for the development of novel biomarkers or vaccines.

**Desired presentation type:** poster presentation

**Applicable conference topic:** Vaccines that could reduce the use of medically important antibiotics.

