



BACTERIAL DISEASES

BBD-035

ENTEROCOCCUS HIRAE- COMMENSAL OR PATHOGEN?

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Enterococcus (E.) hirae has been described as a potentially emerging cause of neonatal porcine diarrhoea (NPD). The bacterium is however also found in the intestinal flora of healthy piglets. The aim of this study was to investigate if strains associated with NPD are genetically different from strains found in healthy piglets.

E. hirae isolates associated with NPD were obtained from frozen intestinal samples from 18 piglets from six herds. All 18 animals displayed intestinal colonization with *E. hirae* on histopathology. *E. hirae* isolates from healthy animals were obtained from rectal samples from 35 healthy piglets from six different herds with no history of NPD. All animals were <1 week old. Swabs were cultured for enterococci on Slanetz/Bartley-agar. Up to ten pink colonies from each sample were analysed by MALDI-TOF for species identification. *E. hirae* isolates were subtyped by *cpn60* gene sequencing. Whole genome sequencing (WGS) was performed using Oxford Nanopore's MinION on six isolates from diarrhoeic and healthy piglets, respectively.

E. hirae could be cultured from all 18 diarrhoeic piglets and from 18 out of the 35 healthy piglets. A total of 160 isolates were recovered from the diarrhoeic piglets and 35 from the healthy. *Cpn60*-sequences were determined for 158 isolates from diarrhoeic piglets and 23 isolates from healthy piglets (12 isolates remain to be sequenced). Alignment of the ~500 bp sequences (CLC main workbench 7.9.1) revealed that the *cpn60*-sequence in 157 out of the 158 isolates from diarrhoeic animals were identical and differed from the isolates from healthy animals. Bioinformatics analyses of WGS data are on-going.

Preliminary data support a genetic difference between *E. hirae* associated with NPD and strains found in healthy animals. Comparative genomics of WGS data is however needed to confirm this and to characterise genetic features that are specific for *E. hirae* associated with NPD.