Bacterial community analysis for investigating bacterial transfer from tonsils to the pig carcass

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Tonsils in the oral cavity are an important source of contamination during pig slaughter, but have not received as much attention as faecal contamination. In the present study, ten pigs were sampled from tonsils, faeces and three different areas on each carcass. The samples were analysed by both culturing of Escherichia coli and Yersinia enterocolitica and by 16S rRNA gene sequencing to characterize the bacterial communities. Comparing culture data from deep tonsil tissue and tonsil surface showed similar numbers of E. coli but significantly higher numbers of Y. enterocolitica in the deep tissue samples. Microbiota analysis showed similar bacterial communities in the two sample types at phylum level, while comparison at genus level showed significant differences between the relative abundance of several genera in the two sample types. The finding of a significantly higher relative abundance of Yersinia in tonsil tissue compared to tonsil surface supported the culture analysis. The microbiota analysis also investigated characteristics of the bacterial community that could discriminate bacterial transfer from tonsils and faeces to the carcass during slaughter. The microbiota analyses demonstrated that Fusobacteria and Proteobacteria are the most abundant phyla in tonsils, while Firmicutes showed the highest relative abundance in faeces. The dominating phylum on carcasses was Proteobacteria. Besides Proteobacteria, the swabbing area on the forepart of the carcass, showed a higher relative abundance of Firmicutes and Fusobacteria compared to swabbing areas on the rear part and mid-section of the carcass. Principal coordinate analysis showed clear clustering of samples based on sample source (tonsils, faeces and carcass). Carcass swab samples from the forepart tended to cluster closer to the tonsil samples compared to carcass swab samples from the rear part and mid-section.

Identification of the genera Fusobacterium, Moraxella, Actinobacillus and non-E. coli genera of the family Enterobacteriaceae in carcass swabs could indicate tonsil contamination, while faecal contamination would more likely include higher prevalence of bacteria belonging to the class of Clostridia. The present study supports that it is possible to identify bacterial groups that are indicative for either tonsil or faecal carcass contamination. The level and composition of Enterobacteriaceae on the carcasses did, however, indicate that other sources of meat contamination than tonsils and faeces may be important, such as the process environment.

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