Abstract

The high organic content of abattoir-associated process water provides an alternative for low-cost and non-invasive sample collection. This study investigated the association of microbial diversity from an abattoir processing environment with that of chicken meat. Water samples from scalders, defeathering, evisceration, carcass-washer, chillers, and post-chill carcass rinsate were collected from a large-scale abattoir in Australia. DNA was extracted using the Wizard® Genomic DNA Purification Kit, and the 16S rRNA v3-v4 gene region was sequenced using Illumina MiSeq. The results revealed that the Firmicutes decreased from scalding to evisceration (72.55%) and increased with chilling (23.47%), with the Proteobacteria and Bacteroidota changing inversely. A diverse bacterial community with 24 phyla and 392 genera was recovered from the post-chill chicken, with *Anoxybacillus* (71.84%), *Megamonas* (4.18%), *Gallibacterium* (2.14%), Unclassified Lachnospiraceae (1.87%), and *Lactobacillus* (1.80%) being the abundant genera. The alpha diversity increased from scalding to chilling, while the beta diversity revealed a significant separation of clusters at different processing points (p = 0.01). The alpha- and beta-diversity revealed significant contamination during the defeathering, with a redistribution of the bacteria during the chilling. This study concluded that the genetic diversity during the defeathering is strongly associated with the extent of the post-chill contamination, and may be used to indicate the microbial quality of the chicken meat.